GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 16:24:39 ; Search time 7268 Seconds
(without alignments)
11340.441 Million cell updates/sec

Title: US-10-063-583-73
Perfect score: 1701
Sequence: 1 gagactgcagagggagataa.....aaattaaagtttctgacttt 1701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1700	99.9	1701	6	AX092342	AX092342 Sequence
2	1700	99.9	1701	6	AX376200	AX376200 Sequence
3	1700	99.9	1701	6	AX697354	AX697354 Sequence
4	1700	99.9	1701	9	AY358689	AY358689 Homo sapi
5	1698.4	99.8	1743	6	CQ728278	CQ728278 Sequence
6	1696.8	99.8	1757	9	AB025904	AB025904 Homo sapi
7	1680.2	98.8	1771	6	CQ782700	CQ782700 Sequence
8	1680.2	98.8	1771	6	BD127270	BD127270 Primer fo
9	1680.2	98.8	1771	9	AK074765	AK074765 Homo sapi
10	1668.4	98.1	1767	9	BC034412	BC034412 Homo sapi
11	1496	87.9	1657	6	AX574386	AX574386 Sequence
12	1486.6	87.4	1673	6	AX593027	AX593027 Sequence
13	1201.4	70.6	1537	6	BD205641	BD205641 97 human
14	842.6	49.5	188217	9	AL451074	AL451074 Human DNA
15	842.6	49.5	203959	2	AC064827	AC064827 Homo sapi
16	795.6	46.8	1624	6	AX700281	AX700281 Sequence
17	795.6	46.8	1624	10	AB005450	AB005450 Mus muscu
18	795.6	46.8	1654	10	BC046995	BC046995 Mus muscu
19	679.8	40.0	865	6	CQ780142	CQ780142 Sequence
20	679.8	40.0	865	6	CQ781541	CQ781541 Sequence
21	679.8	40.0	865	6	BD124851	BD124851 Primer fo
22	679.8	40.0	865	6	BD126250	BD126250 Primer fo
23	522.2	30.7	552	6	AR426563	AR426563 Sequence
24	522.2	30.7	552	6	AX987257	AX987257 Sequence
25	522.2	30.7	552	6	BD122116	BD122116 EST and e
26	482.4	28.4	132823	9	AL138795	AL138795 Human DNA
c 27	482.4	28.4	159707	2	AL365403	AL365403 Homo sapi
28	362.8	21.3	1227	9	BC012108	BC012108 Homo sapi
29	267.8	15.7	458	6	CQ458664	CQ458664 Sequence
c 30	240	14.1	241	11	G25174	G25174 human STS E
c 31	240	14.1	241	11	G41862	G41862 SHGC-32182
32	222.2	13.1	297	6	AR251789	AR251789 Sequence
33	213.6	12.6	1104	6	AR014371	AR014371 Sequence
34	213.6	12.6	1104	6	AR156362	AR156362 Sequence
35	213.6	12.6	1104	6	I32995	I32995 Sequence 1
36	213.6	12.6	1104	6	AX057576	AX057576 Sequence
37	213.6	12.6	2134	6	AR014373	AR014373 Sequence
38	213.6	12.6	2669	9	AF051882	AF051882 Homo sapi
39	213.6	12.6	2771	6	BD176858	BD176858 A method
40	213.6	12.6	2771	9	AF037335	AF037335 Homo sapi
41	213.6	12.6	2775	6	CQ776642	CQ776642 Sequence
42	213.6	12.6	2803	9	BC023981	BC023981 Homo sapi
43	213.6	12.6	3171	6	CQ414663	CQ414663 Sequence
44	211.6	12.4	1032	9	BT006656	BT006656 Homo sapi
45	211.6	12.4	1032	12	BT008173	BT008173 Synthetic
46	211.6	12.4	1718	9	BC000278	BC000278 Homo sapi
47	211.6	12.4	2743	9	BC011691	BC011691 Homo sapi
48	211	12.4	2679	6	AR025464	AR025464 Sequence
49	211	12.4	2679	6	AR060379	AR060379 Sequence
50	211	12.4	2679	6	AR117873	AR117873 Sequence
51	211	12.4	2679	6	I85575	I85575 Sequence 1
52	211	12.4	2679	6	AR287595	AR287595 Sequence
53	211	12.4	2679	6	AX114022	AX114022 Sequence
54	211	12.4	2679	6	AX719098	AX719098 Sequence
55	206	12.1	822	6	AR014379	AR014379 Sequence
56	206	12.1	986	6	AR014372	AR014372 Sequence
57	206	12.1	986	6	AR014381	AR014381 Sequence
58	206	12.1	986	6	I32996	I32996 Sequence 3
59	206	12.1	986	6	I33002	I33002 Sequence 12
60	205.2	12.1	813	6	AR014378	AR014378 Sequence
61	205.2	12.1	813	6	I33000	I33000 Sequence 9
62	203	11.9	1190	6	AR060382	AR060382 Sequence
63	203	11.9	1190	6	AR117876	AR117876 Sequence
64	203	11.9	1190	6	AR287598	AR287598 Sequence
65	203	11.9	1190	6	AX114025	AX114025 Sequence
66	203	11.9	1190	6	AX719101	AX719101 Sequence
67	200.8	11.8	3629	10	BC033432	BC033432 Mus muscu
68	200.8	11.8	3674	10	BC035941	BC035941 Mus muscu
69	200.6	11.8	2776	6	CQ725112	CQ725112 Sequence
70	192.8	11.3	3642	10	BC031385	BC031385 Mus muscu
71	188.6	11.1	1830	5	CR761051	CR761051 Xenopus t
72	178.4	10.5	1068	4	AF263367	AF263367 Oryctolag
73	146	8.6	2556	6	AX834407	AX834407 Sequence
74	146	8.6	2556	9	AK096845	AK096845 Homo sapi
c 75	146	8.6	249205	10	AC092855	AC092855 Mus muscu
c 76	134.2	7.9	87233	2	AC141102	AC141102 Rattus no
77	123.6	7.3	5403	5	GGU38349	U38349 Gallus gall
78	122	7.2	1755	5	BC072918	BC072918 Xenopus l
79	119	7.0	1289	6	CQ726696	CQ726696 Sequence
80	118.4	7.0	1399	6	AR095263	AR095263 Sequence
81	118.4	7.0	1519	9	HAJ10588	AJ010588 Homo sapi
82	118.4	7.0	1522	6	AR074439	AR074439 Sequence
83	118.4	7.0	1522	6	AR081119	AR081119 Sequence
84	118.4	7.0	1522	6	AR085316	AR085316 Sequence
85	118.4	7.0	1522	6	AR088064	AR088064 Sequence
86	118.4	7.0	1522	6	AR104223	AR104223 Sequence
87	118.4	7.0	1522	6	AR143487	AR143487 Sequence
88	118.4	7.0	1522	6	AR171392	AR171392 Sequence
89	118.4	7.0	1522	6	AR171563	AR171563 Sequence
90	118.4	7.0	1522	6	BD243152	BD243152 MN gene a
91	118.4	7.0	1552	6	CQ834035	CQ834035 Sequence
92	118.4	7.0	1552	6	AX330007	AX330007 Sequence

93	118.4	7.0	1552	6	AX332607	AX332607 Sequence
94	118.4	7.0	1552	6	AX333244	AX333244 Sequence
95	118.4	7.0	1552	6	AX336174	AX336174 Sequence
96	118.4	7.0	1552	9	HSMATUMN	X66839 H.sapiens M
97	118.4	7.0	1639	9	BC014950	BC014950 Homo sapi
98	117.2	6.9	4338	6	AR069915	AR069915 Sequence
99	117.2	6.9	4338	6	BD145125	BD145125 Novel rec
100	117.2	6.9	4338	6	I23305	I23305 Sequence 1
101	117.2	6.9	4707	9	HUMPTPRG	L09247 Human recep
102	112	6.6	2581	10	AY177706	AY177706 Rattus no
103	112	6.6	3721	10	AY177705	AY177705 Rattus no
104	112	6.6	4391	10	AY177704	AY177704 Rattus no
105	112	6.6	4478	10	AY177703	AY177703 Rattus no
106	111.8	6.6	1965	10	MMU245857	AJ245857 Mus muscu
107	107.4	6.3	4620	10	MUSPTPRG	L09562 Mouse recep
108	106.6	6.3	960	10	S57181	S57181 Ptprg=recep
109	102.2	6.0	1976	5	AB055617	AB055617 Tribolodo
110	94.6	5.6	1351	4	AB080972	AB080972 Canis fam
111	94.4	5.5	1319	6	CQ720132	CQ720132 Sequence
112	91.2	5.4	1316	9	HUMCA6	M57892 Human carbo
113	88.2	5.2	5617	10	BC079595	BC079595 Mus muscu
114	85	5.0	828	6	AX817267	AX817267 Sequence
115	84	4.9	769	10	AF291660	AF291660 Mus muscu
116	84	4.9	1568	10	AY075021	AY075021 Mus muscu
117	83	4.9	4330	5	BC057412	BC057412 Danio rer
118	82.4	4.8	145	6	AX920647	AX920647 Sequence
119	82.4	4.8	145	6	BD056180	BD056180 Sequence
120	82.4	4.8	1931	10	BC038270	BC038270 Mus muscu
121	82.2	4.8	1789	5	BC059693	BC059693 Danio rer
122	82.2	4.8	1833	5	BC049309	BC049309 Danio rer
123	82	4.8	2665	5	BC067635	BC067635 Danio rer
124	81.8	4.8	833	6	AX817269	AX817269 Sequence
125	81.8	4.8	1023	6	AX458348	AX458348 Sequence
126	81.8	4.8	1237	9	BC052602	BC052602 Homo sapi
127	81.8	4.8	3564	6	AX833515	AX833515 Sequence
128	81.8	4.8	3564	9	AK095314	AK095314 Homo sapi
129	81.6	4.8	1344	4	BTCARANVI	X96503 B.taurus mR
130	80.2	4.7	688	6	BD276051	BD276051 48 Human
131	79.8	4.7	881	4	RABCAI	M10412 Rabbit eryt
132	78.6	4.6	87233	2	AC141102	AC141102 Rattus no
133	78.4	4.6	2486	5	AB117757	AB117757 Oncorhync
134	77.8	4.6	1560	5	BC078387	BC078387 Danio rer
135	76.4	4.5	1964	5	AY322477	AY322477 Oreochrom
c 136	76	4.5	2594	3	AK113979	AK113979 Ciona int
137	74.8	4.4	1107	5	AY514870	AY514870 Oncorhync
c 138	73.8	4.3	408	6	AX198178	AX198178 Sequence
139	73.8	4.3	1671	10	AB086322	AB086322 Mus muscu
140	73.6	4.3	1542	10	BC011129	BC011129 Mus muscu
c 141	73.2	4.3	521	6	AX197674	AX197674 Sequence
142	73	4.3	1240	10	BC030174	BC030174 Mus muscu
143	73	4.3	1548	5	BC065611	BC065611 Danio rer
144	72.2	4.2	331	6	CQ667014	CQ667014 Sequence
145	72	4.2	1067	6	AX305956	AX305956 Sequence
146	72	4.2	1067	10	MUSCAIIIA	M27796 Mouse carbo
147	71.8	4.2	1040	3	AF140537	AF140537 Anthopleu
148	71.4	4.2	1574	5	DRU55177	U55177 Danio rerio
149	71.2	4.2	927	4	RABCAHIV	L48928 Oryctolagus
150	71.2	4.2	1066	4	OCU58871	U58871 Oryctolagus
c 151	70	4.1	418	6	AX197911	AX197911 Sequence
152	70	4.1	1853	10	BC034413	BC034413 Mus muscu
c 153	69.2	4.1	184611	2	CR391977	CR391977 Danio rer
154	69.2	4.1	215604	2	CR376804	CR376804 Danio rer
155	69.2	4.1	231864	2	AC097246	AC097246 Rattus no
156	69	4.1	1052	10	AF231123	AF231123 Mus muscu
157	69	4.1	1082	10	BC064050	BC064050 Mus muscu
158	69	4.1	1231	4	MDO417908	AJ417908 Monodelph
159	68.6	4.0	786	5	AY125007	AY125007 Lepisoste
160	68.6	4.0	1792	10	BC081872	BC081872 Rattus no
161	68.4	4.0	1201	10	AF192978	AF192978 Mus muscu
162	68.4	4.0	1232	3	RPA439711	AJ439711 Riftia pa
163	68.2	4.0	6801	6	AX683146	AX683146 Sequence
164	68.2	4.0	6801	10	RNU04998	U04998 Rattus norv
165	68.2	4.0	7851	10	RNU09357	U09357 Rattus norv
166	67.6	4.0	1248	6	AX552095	AX552095 Sequence
c 167	66.6	3.9	304	6	AX208508	AX208508 Sequence
168	66.4	3.9	1570	9	AY075019	AY075019 Homo sapi
169	66.4	3.9	1580	9	BC033865	BC033865 Homo sapi
170	66.4	3.9	1717	9	AY075020	AY075020 Homo sapi
171	66.2	3.9	1437	5	AY641852	AY641852 Gekko jap
172	66.2	3.9	1440	4	SHPCAI	L42178 Ovis aries
173	65.2	3.8	1053	6	AX827359	AX827359 Sequence
174	65.2	3.8	1053	10	AF037072	AF037072 Rattus no
175	65.2	3.8	1164	9	AB021660	AB021660 Homo sapi
176	65.2	3.8	2285	9	BC028142	BC028142 Homo sapi
c 177	64.4	3.8	297	6	AX208752	AX208752 Sequence
178	64	3.8	1083	9	HUMCARBANH	L19297 Human nucle
179	63.8	3.8	911	6	AX350366	AX350366 Sequence
180	63.8	3.8	1650	5	BC078205	BC078205 Danio rer
181	63.6	3.7	802	10	AB030830	AB030830 Rattus no
182	63.6	3.7	1502	10	AB030829	AB030829 Rattus no
183	63.6	3.7	1737	10	BC061980	BC061980 Rattus no
184	63.4	3.7	1201	6	AX402001	AX402001 Sequence
185	63.4	3.7	1201	6	AX827773	AX827773 Sequence
186	63.4	3.7	1201	10	RNU12268	U12268 Rattus norv
187	63.4	3.7	3784	10	MMU428208	AJ428208 Mus muscu
188	63.4	3.7	6887	6	CQ777575	CQ777575 Sequence
189	63.4	3.7	6887	10	MMU133130	AJ133130 Mus muscu
c 190	62.8	3.7	157590	9	AC087525	AC087525 Homo sapi
191	62.8	3.7	171456	9	AC023591	AC023591 Homo sapi
192	62.2	3.7	434	6	AX197552	AX197552 Sequence
193	62	3.6	146575	2	AC135571	AC135571 Rattus no
c 194	62	3.6	174426	10	AC142504	AC142504 Mus muscu
c 195	62	3.6	180602	10	AC134429	AC134429 Mus muscu
196	62	3.6	215985	2	AC137029	AC137029 Rattus no
197	62	3.6	240453	2	AC103204	AC103204 Rattus no
198	61.8	3.6	2880	5	BC077855	BC077855 Xenopus l
c 199	61.2	3.6	157159	2	AC026279	AC026279 Homo sapi
200	60.2	3.5	1226	10	MMCARBAN	X51971 Mouse mRNA
201	59.8	3.5	1116	5	BX931094	BX931094 Gallus ga
202	59.8	3.5	1513	5	CR406508	CR406508 Gallus ga
203	59.6	3.5	1412	10	AF079835	AF079835 Mus muscu
204	59.6	3.5	1475	10	AF079834	AF079834 Mus muscu
205	59	3.5	60	6	CQ539505	CQ539505 Sequence
206	58.8	3.5	305	6	AX208168	AX208168 Sequence
c 207	58.8	3.5	417	6	AX070048	AX070048 Sequence
208	58.8	3.5	988	6	AX402000	AX402000 Sequence
209	58.8	3.5	988	10	RATCAIII	M22413 Rat carboni
210	58.8	3.5	3369	6	CQ721425	CQ721425 Sequence
211	58.6	3.4	1741	5	BX934845	BX934845 Gallus ga
212	58.6	3.4	185079	2	AC135702	AC135702 Rattus no
213	58.6	3.4	249871	2	AC118150	AC118150 Rattus no
214	58.4	3.4	810	9	CHPCAIPRO	L11621 Pan troglod
215	58.4	3.4	914	9	HSCAIR	X05014 Human cDNA
216	58.4	3.4	1307	9	BC027890	BC027890 Homo sapi
217	58.4	3.4	2785	6	AX926618	AX926618 Sequence
218	58.4	3.4	2785	6	AX926667	AX926667 Sequence
219	58.4	3.4	2785	9	HUMCAIX	M33987 Human carbo
220	58.4	3.4	2785	11	G28544	G28544 human STS S
221	58	3.4	261397	2	AC127658	AC127658 Rattus no
c 222	57.4	3.4	267093	2	AC109408	AC109408 Rattus no
223	57.2	3.4	248378	2	AC128989	AC128989 Rattus no
224	57.2	3.4	259933	2	AC106643	AC106643 Rattus no
225	57	3.4	1740	5	AB117756	AB117756 Oncorhync
226	56.8	3.3	810	9	GORCAIPRO	L11622 Gorilla gor
227	56.8	3.3	1202	6	CQ718744	CQ718744 Sequence
228	56.2	3.3	783	5	AY307082	AY307082 Oncorhync
229	56	3.3	783	6	CQ732664	CQ732664 Sequence
230	56	3.3	1266	6	AR448501	AR448501 Sequence
231	56	3.3	1266	6	AX473375	AX473375 Sequence
232	56	3.3	1734	9	BC004897	BC004897 Homo sapi
233	56	3.3	1748	9	AK096880	AK096880 Homo sapi
234	56	3.3	2286	6	AX399834	AX399834 Sequence
c 235	55.6	3.3	227423	2	AC111960	AC111960 Rattus no
236	55.6	3.3	242290	2	AC106076	AC106076 Rattus no
c 237	55.2	3.2	98062	2	RN516O10	AL603719 Rattus no
238	55.2	3.2	211901	10	AL772310	AL772310 Mouse DNA

	239	55	3.2	7218	6	I66494 I66494 Sequence 14
	240	55	3.2	178653	10	AC121820 AC121820 Mus muscu
	241	54.8	3.2	953	10	BC039657 BC039657 Mus muscu
	242	54.8	3.2	1195	10	BC011223 BC011223 Mus muscu
	243	54.8	3.2	1372	10	BC055437 BC055437 Mus muscu
	244	54.8	3.2	1380	10	BC049973 BC049973 Mus muscu
c	245	54.8	3.2	240200	2	AC122075 AC122075 Rattus no
c	246	54.6	3.2	224	3	SRU45263 U45263 Strongyloid
	247	54.6	3.2	1834	5	BC042287 BC042287 Xenopus l
c	248	54.4	3.2	231412	2	AC129647 AC129647 Rattus no
c	249	54.4	3.2	240766	2	AC114048 AC114048 Rattus no
	250	54.2	3.2	1179	10	AB079601 AB079601 Mus muscu
	251	54.2	3.2	1390	10	BC019393 BC019393 Mus muscu
	252	54.2	3.2	1456	10	AY075026 AY075026 Mus muscu
	253	54.2	3.2	158952	5	BX005434 BX005434 Zebrafish
	254	54	3.2	97387	9	AC105939 AC105939 Homo sapi
	255	54	3.2	165849	9	AC104849 AC104849 Homo sapi
c	256	54	3.2	173361	2	CR377220 CR377220 Danio rer
	257	53.8	3.2	1125	9	MACCAANI L25082 Macaca neme
	258	53.8	3.2	1481	4	AY240020 AY240020 Bos tauru
	259	53.8	3.2	6924	6	I35776 I35776 Sequence 2
c	260	53.8	3.2	33163	2	AC151617 AC151617 Emiliania
c	261	53.8	3.2	188342	2	AC117698 AC117698 Mus muscu
c	262	53.8	3.2	206930	10	AC113533 AC113533 Mus muscu
	263	53.6	3.2	321	6	BD177377 BD177377 Carbonate
	264	53.6	3.2	200774	10	AC116324 AC116324 Mus muscu
c	265	53.6	3.2	207505	2	AC091306 AC091306 Mus muscu
	266	53.6	3.2	245447	2	AC098666 AC098666 Rattus no
	267	53.6	3.2	265361	2	AC125800 AC125800 Rattus no
	268	53.4	3.1	592	6	CQ724691 CQ724691 Sequence
	269	53.4	3.1	719	6	CQ723965 CQ723965 Sequence
	270	53.4	3.1	719	6	CQ726074 CQ726074 Sequence
c	271	53.4	3.1	158398	10	AL929020 AL929020 Mouse DNA
c	272	53.4	3.1	188400	2	AC119102 AC119102 Rattus no
c	273	53.4	3.1	188754	10	AC091260 AC091260 Mus muscu
	274	53.4	3.1	232166	2	AC123218 AC123218 Rattus no
c	275	53.4	3.1	246516	2	AC120725 AC120725 Rattus no
	276	53.4	3.1	273544	2	AC099419 AC099419 Rattus no
	277	53.2	3.1	440	9	HSPTPRG07 U46095 Human recep
	278	53.2	3.1	1224	10	MUSCAIA M32452 Mouse carbo
	279	53.2	3.1	2207	5	AF093622 AF093622 Platichth
c	280	53	3.1	181059	2	AC119628 AC119628 Rattus no
c	281	53	3.1	259289	2	AC096268 AC096268 Rattus no
c	282	52.8	3.1	106625	2	AC147421 AC147421 Didelphis
c	283	52.8	3.1	110000	2	AC151904_2 Continuation (3 of
	284	52.8	3.1	151891	10	AL732585 AL732585 Mouse DNA
	285	52.8	3.1	167522	2	AC124476 AC124476 Mus muscu
c	286	52.8	3.1	191975	10	AC147045 AC147045 Mus muscu
c	287	52.8	3.1	192351	10	AC132355 AC132355 Mus muscu
	288	52.8	3.1	196580	10	AC125191 AC125191 Mus muscu
c	289	52.8	3.1	200997	10	AC123842 AC123842 Mus muscu
c	290	52.8	3.1	207340	10	AC139885 AC139885 Mus muscu
	291	52.6	3.1	612	10	AF050105 AF050105 Mus muscu
c	292	52.6	3.1	164296	10	AC117783 AC117783 Mus muscu
c	293	52.6	3.1	174259	2	AC119836 AC119836 Mus muscu
c	294	52.6	3.1	184466	2	AC105681 AC105681 Rattus no
	295	52.6	3.1	204343	2	AC102169 AC102169 Mus muscu
c	296	52.6	3.1	210851	10	AC117686 AC117686 Mus muscu
c	297	52.6	3.1	212115	2	AC116701 AC116701 Mus muscu
c	298	52.6	3.1	216860	2	AC134702 AC134702 Rattus no
c	299	52.6	3.1	217464	2	AC139061 AC139061 Mus muscu
	300	52.6	3.1	224973	2	AC118082 AC118082 Rattus no
	301	52.6	3.1	246577	2	AC136124 AC136124 Rattus no
	302	52.6	3.1	258988	2	AC103322 AC103322 Rattus no
	303	52.4	3.1	1934	5	CR352666 CR352666 Gallus ga
c	304	52.4	3.1	90365	2	AC139132 AC139132 Mus muscu
c	305	52.4	3.1	237498	2	AC108595 AC108595 Rattus no
	306	52.2	3.1	65	6	CQ556585 CQ556585 Sequence
	307	52.2	3.1	3350	9	HSU88967 U88967 Human tyros
	308	52.2	3.1	6807	6	CQ725791 CQ725791 Sequence
	309	52.2	3.1	7941	6	CQ776705 CQ776705 Sequence
	310	52.2	3.1	7941	6	AR231695 AR231695 Sequence
	311	52.2	3.1	7941	6	AX334330 AX334330 Sequence
	312	52.2	3.1	7941	9	HUMPTPRZ M93426 Human prote
	313	52.2	3.1	7941	11	G20044 G20044 sWSS1987 Er
	314	52.2	3.1	186022	10	AC102517 AC102517 Mus muscu
c	315	52.2	3.1	192273	9	AC091754 AC091754 Papio anu
c	316	52.2	3.1	201891	2	AC103601 AC103601 Mus muscu
	317	52.2	3.1	233707	2	AC106337 AC106337 Rattus no
c	318	52	3.1	113964	9	AL589872 AL589872 Human DNA
c	319	52	3.1	157088	10	AL662855 AL662855 Mouse DNA
c	320	52	3.1	158829	2	AC130068 AC130068 Rattus no
	321	52	3.1	167869	10	AC126437 AC126437 Mus muscu
c	322	52	3.1	171474	2	AC135752 AC135752 Rattus no
c	323	52	3.1	177207	2	AC119946 AC119946 Mus muscu
c	324	52	3.1	177581	10	AC110380 AC110380 Mus musc
	325	52	3.1	179430	2	AC131826 AC131826 Rattus no
	326	52	3.1	185059	2	AC102292 AC102292 Mus muscu
	327	52	3.1	198835	2	CR388001 CR388001 Danio rer
c	328	52	3.1	228840	2	AC097835 AC097835 Rattus no
c	329	52	3.1	242816	2	AC107474 AC107474 Rattus no
c	330	52	3.1	247625	2	AC127105 AC127105 Rattus no
	331	52	3.1	253877	2	AC106328 AC106328 Rattus no
c	332	52	3.1	321384	2	AC097810 AC097810 Rattus no
c	333	51.8	3.0	398	6	AX071058 AX071058 Sequence
	334	51.8	3.0	941	9	HUMCARP L04656 Homo sapien
	335	51.8	3.0	1620	9	AY075022 AY075022 Homo sapi
	336	51.8	3.0	2148	9	BC069744 BC069744 Homo sapi
	337	51.8	3.0	2183	9	BC069794 BC069794 Homo sapi
	338	51.8	3.0	2191	9	AK090655 AK090655 Homo sapi
	339	51.8	3.0	3271	9	BC082971 BC082971 Homo sapi
c	340	51.8	3.0	119922	9	AC099804 AC099804 Homo sapi
c	341	51.8	3.0	157795	10	AC123047 AC123047 Mus muscu
	342	51.8	3.0	166457	2	AC131895 AC131895 Didelphis
c	343	51.8	3.0	184139	9	AC022966 AC022966 Homo sapi
c	344	51.8	3.0	214571	10	AC134535 AC134535 Mus muscu
c	345	51.8	3.0	231926	10	AL662779 AL662779 Mouse DNA
c	346	51.6	3.0	174669	10	AC127698 AC127698 Mus muscu
c	347	51.6	3.0	175495	2	AC023938 AC023938 Mus muscu
c	348	51.6	3.0	178870	2	AC021555 AC021555 Homo sapi
c	349	51.6	3.0	186585	2	CR450689 CR450689 Danio rer
	350	51.6	3.0	198578	10	AC134571 AC134571 Mus muscu
	351	51.6	3.0	200102	5	AC145955 AC145955 Gallus ga
c	352	51.6	3.0	200704	2	AC120892 AC120892 Rattus no
c	353	51.6	3.0	207779	2	AC134631 AC134631 Rattus no
c	354	51.6	3.0	213715	2	AC118879 AC118879 Rattus no
	355	51.6	3.0	224628	10	AL513351 AL513351 Mouse DNA
c	356	51.6	3.0	239781	2	AC106535 AC106535 Rattus no
	357	51.6	3.0	244946	2	AC110706 AC110706 Rattus no
c	358	51.6	3.0	246767	2	AC097955 AC097955 Rattus no
	359	51.6	3.0	248366	2	AC096062 AC096062 Rattus no
c	360	51.6	3.0	267392	2	AC099071 AC099071 Rattus no
c	361	51.6	3.0	279907	2	AC115053 AC115053 Mus muscu
	362	51.6	3.0	293507	2	AC097292 AC097292 Rattus no
	363	51.4	3.0	408	6	AX884433 AX884433 Sequence
	364	51.4	3.0	408	6	BD024043 BD024043 Sequence
	365	51.4	3.0	1902	5	CR760774 CR760774 Xenopus t
c	366	51.4	3.0	166703	2	BX927394 BX927394 Danio rer
c	367	51.4	3.0	197630	9	AC011676 AC011676 Homo sapi
c	368	51.4	3.0	202214	2	AC135818 AC135818 Rattus no
c	369	51.4	3.0	203230	10	AL589670 AL589670 Mouse DNA
	370	51.4	3.0	225746	2	AC127882 AC127882 Rattus no
c	371	51.4	3.0	229883	2	AC116276 AC116276 Rattus no
	372	51.4	3.0	238007	10	AC097745 AC097745 Rattus no
	373	51.2	3.0	353	8	AF409184 AF409184 Pseudotsu
	374	51.2	3.0	570	6	CQ718748 CQ718748 Sequence
	375	51.2	3.0	591	5	AF309796 AF309796 Clupea pa
c	376	51.2	3.0	2851	10	BC012406 BC012406 Mus muscu
c	377	51.2	3.0	4653	10	AY591642 AY591642 Mus muscu
	378	51.2	3.0	143813	10	AC126247 AC126247 Mus muscu
c	379	51.2	3.0	148125	2	AC079873 AC079873 Mus muscu
	380	51.2	3.0	150308	10	AC098294 AC098294 Rattus no
	381	51.2	3.0	161205	2	AC132108 AC132108 Mus muscu
c	382	51.2	3.0	176563	10	AC101142 AC101142 Mus muscu
	383	51.2	3.0	192133	2	AC104555 AC104555 Mus muscu
c	384	51.2	3.0	199101	10	MMAE000665 AE000665 Mus muscu

	385	51.2	3.0	203073	10	AC122322 AC122322 Mus muscu
c	386	51.2	3.0	215067	2	AC114214 AC114214 Rattus no
	387	51.2	3.0	218800	2	AC094410 AC094410 Rattus no
c	388	51.2	3.0	225433	2	AC106484 AC106484 Rattus no
c	389	51.2	3.0	237199	10	AC094830 AC094830 Rattus no
	390	51.2	3.0	243191	2	AC098147 AC098147 Rattus no
	391	51.2	3.0	253462	2	AC096477 AC096477 Rattus no
c	392	51.2	3.0	290569	2	AC105809 AC105809 Rattus no
c	393	51.2	3.0	318959	2	AY657023 AY657023 Mus muscu
c	394	51	3.0	110000	2	AC115674_1 Continuation (2 of
	395	51	3.0	182736	2	AC139133 AC139133 Mus muscu
c	396	51	3.0	219763	10	AC093175 AC093175 Mus muscu
	397	51	3.0	237376	2	AC124949 AC124949 Rattus no
	398	51	3.0	309506	10	AY363102S1 AY363102 Mus muscu
c	399	51	3.0	321034	2	AC118305 AC118305 Rattus no
	400	50.8	3.0	939	9	CR541766 CR541766 Homo sapi
	401	50.8	3.0	1010	9	BC074768 BC074768 Homo sapi
	402	50.8	3.0	1035	9	BC069649 BC069649 Homo sapi
	403	50.8	3.0	1104	6	AX511612 AX511612 Sequence
	404	50.8	3.0	1105	6	AX329659 AX329659 Sequence
	405	50.8	3.0	1105	6	AX333747 AX333747 Sequence
	406	50.8	3.0	1105	9	HUMCAIVA M83670 Human carbo
	407	50.8	3.0	1106	6	CQ725314 CQ725314 Sequence
	408	50.8	3.0	1170	9	BC057792 BC057792 Homo sapi
	409	50.8	3.0	1199	5	GCAIIR X12639 Chicken mRN
	410	50.8	3.0	1797	5	BC054242 BC054242 Xenopus l
c	411	50.8	3.0	81390	10	AC109603 AC109603 Mus muscu
c	412	50.8	3.0	106098	10	CR392009 CR392009 Mouse DNA
	413	50.8	3.0	112560	9	HSJ513G18 AL109760 Human DNA
	414	50.8	3.0	128949	10	AC100738 AC100738 Mus muscu
c	415	50.8	3.0	136490	8	CNS08CCE AL929350 Oryza sat
	416	50.8	3.0	151878	8	CNS08CD0 AL954632 Oryza sat
	417	50.8	3.0	220428	2	AC122586 AC122586 Rattus no
c	418	50.8	3.0	227769	2	AC112437 AC112437 Rattus no
	419	50.8	3.0	236698	2	AC132037 AC132037 Rattus no
	420	50.8	3.0	238046	2	AC095003 AC095003 Rattus no
	421	50.8	3.0	244814	2	AC098223 AC098223 Rattus no
	422	50.8	3.0	245863	2	AC118761 AC118761 Rattus no
	423	50.8	3.0	246100	2	AC095492 AC095492 Rattus no
c	424	50.8	3.0	246716	2	AC096699 AC096699 Rattus no
	425	50.8	3.0	254175	2	AC096015 AC096015 Rattus no
c	426	50.8	3.0	271586	2	AC126739 AC126739 Rattus no
c	427	50.8	3.0	286106	2	AC105829 AC105829 Rattus no
	428	50.8	3.0	328736	2	AC107298 AC107298 Homo sapi
	429	50.6	3.0	683	6	AX525925 AX525925 Sequence
	430	50.6	3.0	1331	4	OACALP Y07785 Ovis aries
c	431	50.6	3.0	4309	10	MMPAXP2 AF098640 Mus muscu
	432	50.6	3.0	144310	10	AL929277 AL929277 Mouse DNA
	433	50.6	3.0	181262	2	AC129783 AC129783 Rattus no
c	434	50.6	3.0	186761	2	AC131795 AC131795 Mus muscu
	435	50.6	3.0	196484	2	AC129435 AC129435 Rattus no
c	436	50.6	3.0	198388	10	AC100506 AC100506 Mus muscu
	437	50.6	3.0	211960	10	AC128737 AC128737 Mus muscu
c	438	50.6	3.0	212046	10	BX005167 BX005167 Mouse DNA
	439	50.6	3.0	230343	2	AC098073 AC098073 Rattus no
	440	50.6	3.0	256608	10	AL589699 AL589699 Mouse DNA
c	441	50.6	3.0	327654	2	AC020816 AC020816 Mus muscu
c	442	50.4	3.0	142	10	MMDNDS13 X55231 M.musculus
	443	50.4	3.0	261	6	BD177372 BD177372 Carbonate
	444	50.4	3.0	41308	9	AC004196 AC004196 Homo sapi
c	445	50.4	3.0	85801	9	AL805909 AL805909 Human DNA
c	446	50.4	3.0	109514	9	AL162254 AL162254 Human DNA
	447	50.4	3.0	113907	10	AL646002 AL646002 Mouse DNA
	448	50.4	3.0	128790	2	AC146561 AC146561 Medicago
c	449	50.4	3.0	144224	2	AC105948 AC105948 Mus muscu
c	450	50.4	3.0	145153	9	AL590031 AL590031 Human DNA
	451	50.4	3.0	167439	2	AC104672 AC104672 Rattus no
	452	50.4	3.0	183639	10	AC127329 AC127329 Mus muscu
c	453	50.4	3.0	186555	9	AC006313 AC006313 Homo sapi
c	454	50.4	3.0	188125	10	AC122213 AC122213 Mus muscu
c	455	50.4	3.0	190277	2	AC079474 AC079474 Mus muscu
c	456	50.4	3.0	192154	10	BX293555 BX293555 Mouse DNA
c	457	50.4	3.0	197951	10	AC130723 AC130723 Mus muscu
c	458	50.4	3.0	198161	6	CQ861419 CQ861419 Sequence
c	459	50.4	3.0	198161	9	HS232K4 AL021938 Human DNA
	460	50.4	3.0	199101	10	MMAE000665 AE000665 Mus muscu
	461	50.4	3.0	219470	10	AC132458 AC132458 Mus muscu
c	462	50.4	3.0	223387	2	AC079470 AC079470 Mus muscu
	463	50.4	3.0	232538	10	AC111647 AC111647 Rattus no
	464	50.4	3.0	237829	2	AC120475 AC120475 Rattus no
	465	50.4	3.0	242820	2	AC093939 AC093939 Rattus no
	466	50.4	3.0	244224	2	AC125992 AC125992 Rattus no
c	467	50.4	3.0	244727	2	AC127633 AC127633 Rattus no
c	468	50.4	3.0	249899	2	AC132469 AC132469 Mus muscu
c	469	50.4	3.0	349980	6	AX344554 AX344554 Sequence
c	470	50.2	3.0	129970	10	BX005231 BX005231 Mouse DNA
	471	50.2	3.0	177116	10	AC117249 AC117249 Mus muscu
	472	50.2	3.0	182661	10	AC121602 AC121602 Mus muscu
	473	50.2	3.0	184636	10	AC140218 AC140218 Mus muscu
	474	50.2	3.0	192015	2	AC119223 AC119223 Mus muscu
c	475	50.2	3.0	192152	2	AC102581 AC102581 Mus muscu
c	476	50.2	3.0	197217	2	AC150748 AC150748 Mus muscu
c	477	50.2	3.0	198835	2	CR388001 CR388001 Danio rer
c	478	50.2	3.0	199065	10	AC116503 AC116503 Mus muscu
	479	50.2	3.0	235803	2	AC097591 AC097591 Rattus no
	480	50.2	3.0	240536	10	AC126046 AC126046 Mus muscu
	481	50.2	3.0	241679	2	AC020861 AC020861 Mus muscu
	482	50.2	3.0	246030	2	AC126591 AC126591 Rattus no
	483	50.2	3.0	250577	2	AC105702 AC105702 Rattus no
c	484	50.2	3.0	254454	2	AC121447 AC121447 Rattus no
c	485	50.2	3.0	263744	2	AF401201 AF401201 Mus muscu
c	486	50.2	3.0	270992	2	AC105620 AC105620 Rattus no
c	487	50.2	3.0	294494	2	AC098385 AC098385 Rattus no
	488	50	2.9	1959	10	BC010773 BC010773 Mus muscu
	489	50	2.9	2551	5	BC081201 BC081201 Xenopus l
c	490	50	2.9	104805	10	BX324122 BX324122 Mouse DNA
c	491	50	2.9	125020	9	AF429315 AF429315 Homo sapi
	492	50	2.9	143096	2	CR387991 CR387991 Danio rer
c	493	50	2.9	173051	2	AC101905 AC101905 Mus muscu
c	494	50	2.9	207360	2	BX324222 BX324222 Mus muscu
	495	50	2.9	213549	10	AL844489 AL844489 Mouse DNA
c	496	50	2.9	219463	10	AL807763 AL807763 Mouse DNA
	497	50	2.9	232419	10	AC091463 AC091463 Mus muscu
	498	50	2.9	251740	2	AC123460 AC123460 Rattus no
	499	50	2.9	252580	2	AC121227 AC121227 Rattus no
	500	50	2.9	254778	2	AC126532 AC126532 Rattus no
c	501	50	2.9	257645	2	AC103094 AC103094 Rattus no
	502	50	2.9	261224	10	AL645527 AL645527 Mouse DNA
c	503	50	2.9	271532	2	AC122958 AC122958 Rattus no
c	504	50	2.9	283066	2	AC126991 AC126991 Rattus no
	505	49.8	2.9	1890	5	BC041213 BC041213 Xenopus l
	506	49.8	2.9	5281	5	BC070850 BC070850 Xenopus l
	507	49.8	2.9	151503	10	AL732319 AL732319 Mouse DNA
c	508	49.8	2.9	175802	10	AL805929 AL805929 Mouse DNA
	509	49.8	2.9	187715	2	AC135305 AC135305 Rattus no
	510	49.8	2.9	194333	2	AC130536 AC130536 Mus muscu
	511	49.8	2.9	210427	10	AC124757 AC124757 Mus muscu
c	512	49.8	2.9	234998	2	AC108266 AC108266 Rattus no
	513	49.8	2.9	246203	2	AC111705 AC111705 Rattus no
	514	49.8	2.9	265423	2	AC128960 AC128960 Rattus no
	515	49.8	2.9	296111	2	AC120083 AC120083 Rattus no
c	516	49.6	2.9	23169	6	AX695410 AX695410 Sequence
c	517	49.6	2.9	86684	9	AC010605 AC010605 Homo sapi
c	518	49.6	2.9	128991	10	AC117775 AC117775 Mus muscu
c	519	49.6	2.9	136777	2	AC146986 AC146986 Strongylo
	520	49.6	2.9	154561	10	AL929071 AL929071 Mouse DNA
	521	49.6	2.9	166591	2	AC120180 AC120180 Mus muscu
c	522	49.6	2.9	187418	10	AL672278 AL672278 Mouse DNA
	523	49.6	2.9	192971	10	AC118012 AC118012 Mus muscu
	524	49.6	2.9	196365	2	AC110528 AC110528 Mus muscu
c	525	49.6	2.9	197992	2	AC020715 AC020715 Homo sapi
c	526	49.6	2.9	203000	10	AL596130 AL596130 Mouse DNA
c	527	49.6	2.9	209365	2	BX005177 BX005177 Mus muscu
c	528	49.6	2.9	214627	10	AC046160 AC046160 Mus muscu
c	529	49.6	2.9	221080	2	AC106160 AC106160 Rattus no
	530	49.6	2.9	225630	2	AC134035 AC134035 Rattus no

c 531	49.6	2.9	227340	2	AC095000	AC095000 Rattus no
c 532	49.6	2.9	234087	2	AC098149	AC098149 Rattus no
c 533	49.6	2.9	237179	2	AC128466	AC128466 Rattus no
c 534	49.6	2.9	237467	2	AC133689	AC133689 Rattus no
535	49.6	2.9	239049	2	AC111870	AC111870 Rattus no
536	49.6	2.9	240483	2	AC095955	AC095955 Rattus no
c 537	49.6	2.9	244224	2	AC125992	AC125992 Rattus no
538	49.6	2.9	244322	2	AC123135	AC123135 Rattus no
c 539	49.6	2.9	256086	2	AC097863	AC097863 Rattus no
540	49.6	2.9	260164	2	AC098181	AC098181 Rattus no
541	49.6	2.9	260331	2	AC135400	AC135400 Rattus no
c 542	49.6	2.9	267672	2	AC093934	AC093934 Rattus no
543	49.6	2.9	311774	2	AC118873	AC118873 Rattus no
544	49.6	2.9	347801	2	AC118786	AC118786 Rattus no
c 545	49.4	2.9	462	11	BV006616	BV006616 ORS 1264
546	49.4	2.9	1092	4	BTU58870	U58870 Bos taurus
547	49.4	2.9	57729	9	AL449284	AL449284 Human DNA
c 548	49.4	2.9	101511	2	AC109574	AC109574 Rattus no
549	49.4	2.9	104360	10	AC124038	AC124038 Mus Muscu
c 550	49.4	2.9	118473	10	AL671969	AL671969 Mouse DNA
c 551	49.4	2.9	134412	10	AC124037	AC124037 Mus Muscu
c 552	49.4	2.9	154195	2	AC142242	AC142242 Atelerix
553	49.4	2.9	172498	2	AC127998	AC127998 Rattus no
554	49.4	2.9	179980	2	AC121271	AC121271 Mus muscu
c 555	49.4	2.9	185437	2	AC135488	AC135488 Rattus no
556	49.4	2.9	189741	10	AC125053	AC125053 Mus muscu
c 557	49.4	2.9	191186	2	AC115077	AC115077 Mus muscu
c 558	49.4	2.9	192252	2	AC148944	AC148944 Gasterost
559	49.4	2.9	194060	10	AC125349	AC125349 Mus muscu
560	49.4	2.9	195805	10	AC102666	AC102666 Mus muscu
561	49.4	2.9	198761	10	AL607041	AL607041 Mouse DNA
c 562	49.4	2.9	199521	2	AC079371	AC079371 Mus muscu
563	49.4	2.9	210747	2	AC125880	AC125880 Rattus no
c 564	49.4	2.9	215137	10	AC128672	AC128672 Mus muscu
565	49.4	2.9	215759	2	AC128417	AC128417 Rattus no
566	49.4	2.9	223252	2	AC116686	AC116686 Mus muscu
567	49.4	2.9	223843	10	AC102595	AC102595 Mus muscu
c 568	49.4	2.9	224267	2	AC126623	AC126623 Rattus no
569	49.4	2.9	224522	2	AC106627	AC106627 Rattus no
c 570	49.4	2.9	230041	10	AC111047	AC111047 Mus muscu
571	49.4	2.9	230447	10	AL671866	AL671866 Mouse DNA
c 572	49.4	2.9	230994	2	AC130120	AC130120 Rattus no
573	49.4	2.9	237402	2	AC114709	AC114709 Rattus no
c 574	49.4	2.9	238797	2	AC110480	AC110480 Rattus no
c 575	49.4	2.9	239114	2	AC129936	AC129936 Mus muscu
c 576	49.4	2.9	239786	2	AC129377	AC129377 Rattus no
577	49.4	2.9	242080	2	AC124897	AC124897 Rattus no
578	49.4	2.9	242866	2	AC096889	AC096889 Rattus no
c 579	49.4	2.9	244034	2	AC122326	AC122326 Mus muscu
580	49.4	2.9	244707	2	AC098994	AC098994 Rattus no
581	49.4	2.9	246911	2	AC097084	AC097084 Rattus no
582	49.4	2.9	250548	2	AC128521	AC128521 Rattus no
c 583	49.4	2.9	266229	2	AC073676	AC073676 Mus muscu
c 584	49.4	2.9	281021	2	AC111415	AC111415 Rattus no
c 585	49.4	2.9	318435	2	AC118697	AC118697 Mus muscu
586	49.4	2.9	321034	2	AC118305	AC118305 Rattus no
587	49.4	2.9	336710	2	AC130999	AC130999 Rattus no
588	49.2	2.9	1256	8	AK070276	AK070276 Oryza sat
589	49.2	2.9	1486	5	GGCAIIR	X04810 Chicken mRN
590	49.2	2.9	54465	2	BX663500	BX663500 Mus muscu
591	49.2	2.9	160339	10	AC132600	AC132600 Mus muscu
c 592	49.2	2.9	168580	2	AC120415	AC120415 Mus muscu
593	49.2	2.9	179068	10	AL627125	AL627125 Mouse DNA
594	49.2	2.9	184420	2	AC118373	AC118373 Rattus no
595	49.2	2.9	191310	10	AC079365	AC079365 Mus muscu
c 596	49.2	2.9	226694	2	AC117060	AC117060 Rattus no
597	49.2	2.9	228976	2	AC099218	AC099218 Rattus no
c 598	49.2	2.9	251375	2	AC109422	AC109422 Rattus no
c 599	49.2	2.9	268202	2	AC115443	AC115443 Rattus no
c 600	49.2	2.9	271898	2	AC106311	AC106311 Rattus no
c 601	49.2	2.9	300830	2	AC096498	AC096498 Rattus no
c 602	49	2.9	851	11	BV062282	BV062282 S212P6041
603	49	2.9	1189	10	AY075025	AY075025 Rattus no
604	49	2.9	1250	5	BX929589	BX929589 Gallus ga
605	49	2.9	1277	5	CR352958	CR352958 Gallus ga
606	49	2.9	1439	6	CQ589506	CQ589506 Sequence
607	49	2.9	1457	3	AY058327	AY058327 Drosophil
608	49	2.9	5284	5	AB045238	AB045238 Xenopus l
609	49	2.9	7725	5	AB045237	AB045237 Xenopus l
610	49	2.9	8352	6	CQ589505	CQ589505 Sequence
c 611	49	2.9	13498	10	AB084948S1	AB084948 Mus muscu
612	49	2.9	17340	10	MMU57691	U57691 Mus musculu
c 613	49	2.9	53583	2	AC013160	AC013160 Drosophil
c 614	49	2.9	115003	2	AC109164	AC109164 Mus muscu
615	49	2.9	161682	3	AC092236	AC092236 Drosophil
616	49	2.9	161978	10	AL645965	AL645965 Mouse DNA
617	49	2.9	164914	9	AC027801	AC027801 Homo sapi
618	49	2.9	171598	3	AC092223	AC092223 Drosophil
c 619	49	2.9	176872	10	AL772313	AL772313 Mouse DNA
620	49	2.9	178673	10	BX539316	BX539316 Mouse DNA
c 621	49	2.9	179943	10	AC123822	AC123822 Mus muscu
c 622	49	2.9	183554	10	AC122230	AC122230 Mus muscu
623	49	2.9	184583	10	AL772347	AL772347 Mouse DNA
c 624	49	2.9	198907	2	AC139912	AC139912 Rattus no
625	49	2.9	204915	10	AC079134	AC079134 Mus muscu
c 626	49	2.9	215384	10	AC125221	AC125221 Mus muscu
c 627	49	2.9	219491	2	AC137244	AC137244 Rattus no
628	49	2.9	223541	10	AC125010	AC125010 Mus muscu
c 629	49	2.9	227835	10	AC141426	AC141426 Mus muscu
c 630	49	2.9	241630	2	AC131881	AC131881 Rattus no
c 631	49	2.9	245320	2	AC095444	AC095444 Rattus no
632	49	2.9	256632	10	AC139378	AC139378 Mus muscu
633	49	2.9	259237	2	AC108540	AC108540 Rattus no
c 634	49	2.9	285718	2	AC117571	AC117571 Mus muscu
635	49	2.9	303885	3	DROSADH01	AE003407 Drosophil
636	49	2.9	304771	3	AE003641	AE003641 Drosophil
c 637	49	2.9	322522	2	AC115351	AC115351 Rattus no
638	49	2.9	342544	2	AC120678	AC120678 Rattus no
639	48.8	2.9	428	6	AX069777	AX069777 Sequence
640	48.8	2.9	9359	10	BX323005	BX323005 Mouse DNA
c 641	48.8	2.9	10270	9	CR762477	CR762477 Human DNA
642	48.8	2.9	48500	10	AL772259	AL772259 Mouse DNA
c 643	48.8	2.9	90027	2	AC079522	AC079522 Mus muscu
644	48.8	2.9	99999	9	AP000510	AP000510 Homo sapi
c 645	48.8	2.9	106093	9	AC007561	AC007561 Homo sapi
c 646	48.8	2.9	117327	9	AL663093	AL663093 Human DNA
647	48.8	2.9	125020	9	AF429315	AF429315 Homo sapi
c 648	48.8	2.9	126222	2	AL844492	AL844492 Homo sapi
c 649	48.8	2.9	135396	9	BX927139	BX927139 Human DNA
650	48.8	2.9	135695	10	BX005114	BX005114 Mouse DNA
c 651	48.8	2.9	136906	2	RN86I20	AL603805 Rattus no
652	48.8	2.9	137628	10	AL672153	AL672153 Mouse DNA
653	48.8	2.9	138376	2	AC102877	AC102877 Mus muscu
c 654	48.8	2.9	141678	10	AC124688	AC124688 Mus muscu
655	48.8	2.9	144625	2	AC105735	AC105735 Rattus no
c 656	48.8	2.9	152269	2	AC121498	AC121498 Mus muscu
657	48.8	2.9	154195	2	AC142242	AC142242 Atelerix
c 658	48.8	2.9	161492	9	AC007780	AC007780 Homo sapi
c 659	48.8	2.9	167658	2	AC139358	AC139358 Mus muscu
660	48.8	2.9	174375	2	AC128360	AC128360 Rattus no
c 661	48.8	2.9	176278	10	AC126557	AC126557 Mus muscu
662	48.8	2.9	177066	9	AC091001	AC091001 Papio anu
663	48.8	2.9	179998	2	AC141350	AC141350 Rattus no
664	48.8	2.9	184006	2	AC121110	AC121110 Mus muscu
665	48.8	2.9	184151	2	AC116386	AC116386 Mus muscu
666	48.8	2.9	186734	10	BX005053	BX005053 Mouse DNA
c 667	48.8	2.9	187710	10	AC123807	AC123807 Mus muscu
c 668	48.8	2.9	188938	10	AC116875	AC116875 Mus muscu
c 669	48.8	2.9	191338	2	AC127650	AC127650 Rattus no
c 670	48.8	2.9	191692	2	AC023834	AC023834 Mus muscu
c 671	48.8	2.9	192013	10	AL845442	AL845442 Mouse DNA
672	48.8	2.9	192650	9	AB023048	AB023048 Homo sapi
c 673	48.8	2.9	198368	10	AC134903	AC134903 Mus muscu
c 674	48.8	2.9	199245	2	AC138622	AC138622 Mus muscu
675	48.8	2.9	202920	2	AC139392	AC139392 Rattus no
c 676	48.8	2.9	204298	9	AL662844	AL662844 Human DNA

c 677	48.8	2.9	205030	10	AL669911	AL669911 Mouse DNA
c 678	48.8	2.9	209156	2	AC114696	AC114696 Rattus no
c 679	48.8	2.9	214856	10	AC134434	AC134434 Mus muscu
680	48.8	2.9	214857	10	AC122899	AC122899 Mus muscu
681	48.8	2.9	217062	2	CR547130	CR547130 Mus muscu
c 682	48.8	2.9	224249	2	AC113691	AC113691 Rattus no
c 683	48.8	2.9	224617	10	AC099930	AC099930 Mus muscu
c 684	48.8	2.9	226724	10	AC125199	AC125199 Mus muscu
685	48.8	2.9	226957	2	AC140800	AC140800 Mus muscu
c 686	48.8	2.9	228623	10	AL772145	AL772145 Mouse DNA
687	48.8	2.9	228644	2	AC102879	AC102879 Mus muscu
c 688	48.8	2.9	228930	10	AC110919	AC110919 Mus muscu
c 689	48.8	2.9	235803	2	AC115551	AC115551 Rattus no
690	48.8	2.9	245633	2	AC112666	AC112666 Mus muscu
c 691	48.8	2.9	251266	2	AC096356	AC096356 Rattus no
692	48.8	2.9	251806	2	AC135284	AC135284 Rattus no
c 693	48.8	2.9	252108	10	AC138642	AC138642 Mus muscu
c 694	48.8	2.9	259213	2	AC096050	AC096050 Rattus no
695	48.8	2.9	265185	2	AC117637	AC117637 Mus muscu
c 696	48.8	2.9	282685	2	AC094597	AC094597 Rattus no
c 697	48.6	2.9	617	11	BV050912	BV050912 S208P6415
698	48.6	2.9	952	5	BX931926	BX931926 Gallus ga
699	48.6	2.9	48839	10	AL627227	AL627227 Mouse DNA
700	48.6	2.9	110000	2	AC098559_6	Continuation (7 of
c 701	48.6	2.9	136448	2	AC133662	AC133662 Rattus no
702	48.6	2.9	142344	2	AC128740	AC128740 Rattus no
c 703	48.6	2.9	146396	10	AL929449	AL929449 Mouse DNA
704	48.6	2.9	151804	2	AC008161	AC008161 Mus muscu
c 705	48.6	2.9	157224	2	AC105701	AC105701 Rattus no
c 706	48.6	2.9	158807	10	AC122017	AC122017 Mus muscu
c 707	48.6	2.9	159736	10	AC122292	AC122292 Mus muscu
c 708	48.6	2.9	161907	2	AC133897	AC133897 Mus muscu
709	48.6	2.9	173967	2	AC122093	AC122093 Rattus no
710	48.6	2.9	180922	10	AC124176	AC124176 Mus muscu
711	48.6	2.9	183376	2	AC129621	AC129621 Rattus no
712	48.6	2.9	190916	10	AC122470	AC122470 Mus muscu
713	48.6	2.9	193709	10	AC126685	AC126685 Mus muscu
c 714	48.6	2.9	197585	10	AC114552	AC114552 Mus muscu
715	48.6	2.9	198244	2	CR381546	CR381546 Danio rer
716	48.6	2.9	202391	10	AC110040	AC110040 Mus muscu
c 717	48.6	2.9	203388	2	AC132189	AC132189 Mus muscu
c 718	48.6	2.9	206189	10	AC133101	AC133101 Mus muscu
c 719	48.6	2.9	206806	10	AL772342	AL772342 Mouse DNA
c 720	48.6	2.9	207322	2	AC144632	AC144632 Mus muscu
c 721	48.6	2.9	208739	2	AC116104	AC116104 Mus muscu
722	48.6	2.9	210988	2	AC139449	AC139449 Rattus no
723	48.6	2.9	214489	10	AC145554	AC145554 Mus muscu
724	48.6	2.9	215217	2	AC127984	AC127984 Rattus no
725	48.6	2.9	217745	10	AC141647	AC141647 Mus muscu
726	48.6	2.9	219304	2	AC099700	AC099700 Mus muscu
c 727	48.6	2.9	223779	2	AC120443	AC120443 Rattus no
c 728	48.6	2.9	228741	10	AC134902	AC134902 Mus muscu
729	48.6	2.9	230313	10	AC132480	AC132480 Mus muscu
c 730	48.6	2.9	233326	10	AC111111	AC111111 Mus muscu
c 731	48.6	2.9	234508	2	AC113757	AC113757 Rattus no
c 732	48.6	2.9	238226	2	AC111396	AC111396 Rattus no
c 733	48.6	2.9	243412	2	AC127769	AC127769 Rattus no
734	48.6	2.9	245468	2	AC109534	AC109534 Rattus no
c 735	48.6	2.9	246823	2	AC079483	AC079483 Mus muscu
c 736	48.6	2.9	247394	10	AC139034	AC139034 Mus muscu
737	48.6	2.9	248906	2	AC111777	AC111777 Rattus no
c 738	48.6	2.9	252580	2	AC121227	AC121227 Rattus no
c 739	48.6	2.9	255258	2	AC097614	AC097614 Rattus no
740	48.6	2.9	336977	2	AC130770	AC130770 Rattus no
c 741	48.4	2.8	428	6	AX069777	AX069777 Sequence
742	48.4	2.8	1769	3	AY051620	AY051620 Drosophil
743	48.4	2.8	1983	10	MMCARP	X61397 Mouse mRNA
c 744	48.4	2.8	110000	2	AC024562_2	Continuation (3 of
c 745	48.4	2.8	113285	10	AL732606	AL732606 Mouse DNA
746	48.4	2.8	120808	10	AL662862	AL662862 Mouse DNA
747	48.4	2.8	138404	10	AC117187	AC117187 Mus muscu
748	48.4	2.8	144026	10	AC115304	AC115304 Mus muscu
749	48.4	2.8	145975	2	AC126238	AC126238 Felis cat
c 750	48.4	2.8	156869	2	AC136078	AC136078 Rattus no
c 751	48.4	2.8	157771	2	AC148432	AC148432 Sorex ara
c 752	48.4	2.8	160719	10	AC121267	AC121267 Mus muscu
c 753	48.4	2.8	161821	10	AL645968	AL645968 Mouse DNA
c 754	48.4	2.8	190699	2	AC128249	AC128249 Rattus no
755	48.4	2.8	192020	2	AC102311	AC102311 Mus muscu
c 756	48.4	2.8	196203	2	AC128953	AC128953 Rattus no
c 757	48.4	2.8	196662	2	AC129737	AC129737 Rattus no
c 758	48.4	2.8	199702	2	AC133988	AC133988 Rattus no
c 759	48.4	2.8	203022	2	AC127637	AC127637 Rattus no
c 760	48.4	2.8	205757	10	AL672186	AL672186 Mouse DNA
761	48.4	2.8	229303	2	AC115340	AC115340 Rattus no
762	48.4	2.8	235613	2	AC096257	AC096257 Rattus no
c 763	48.4	2.8	238387	2	AC103224	AC103224 Rattus no
c 764	48.4	2.8	239507	2	AC136588	AC136588 Rattus no
c 765	48.4	2.8	241199	2	AC095503	AC095503 Rattus no
766	48.4	2.8	241286	2	AC096065	AC096065 Rattus no
c 767	48.4	2.8	243818	2	AC134657	AC134657 Rattus no
c 768	48.4	2.8	243833	2	AC097386	AC097386 Rattus no
769	48.4	2.8	243870	2	AC094341	AC094341 Rattus no
c 770	48.4	2.8	246362	2	AC137868	AC137868 Mus muscu
771	48.4	2.8	251079	2	AC099134	AC099134 Rattus no
c 772	48.4	2.8	270268	2	AC130516	AC130516 Rattus no
773	48.4	2.8	271275	2	AC135198	AC135198 Rattus no
774	48.4	2.8	282387	2	AC103337	AC103337 Rattus no
c 775	48.4	2.8	339033	2	AC106969	AC106969 Rattus no
c 776	48.4	2.8	346644	2	AC098097	AC098097 Rattus no
c 777	48.2	2.8	313	11	BV007205	BV007205 LS308 Mea
778	48.2	2.8	27858	9	HSL118GB	Z68883 Human DNA s
779	48.2	2.8	98324	10	AL627408	AL627408 Mouse DNA
c 780	48.2	2.8	110000	2	AC099211_4	Continuation (5 of
781	48.2	2.8	136630	2	AC023572	AC023572 Homo sapi
c 782	48.2	2.8	138830	9	AP004281	AP004281 Homo sapi
783	48.2	2.8	143681	2	AC115934	AC115934 Mus muscu
c 784	48.2	2.8	147075	2	AC139166	AC139166 Rattus no
c 785	48.2	2.8	148818	2	AC098700	AC098700 Felis cat
c 786	48.2	2.8	149936	2	AC099320	AC099320 Felis cat
c 787	48.2	2.8	160180	10	AC129016	AC129016 Mus muscu
788	48.2	2.8	163230	2	AC122506	AC122506 Mus muscu
789	48.2	2.8	164617	2	AC102624	AC102624 Mus muscu
c 790	48.2	2.8	164733	2	AC117341	AC117341 Rattus no
791	48.2	2.8	165212	10	AL596125	AL596125 Mouse DNA
c 792	48.2	2.8	166926	10	AC134335	AC134335 Mus muscu
c 793	48.2	2.8	168912	2	AC116800	AC116800 Mus muscu
794	48.2	2.8	169661	10	AC132344	AC132344 Mus muscu
c 795	48.2	2.8	170737	10	AC129180	AC129180 Mus muscu
c 796	48.2	2.8	175222	2	AC132922	AC132922 Mus muscu
c 797	48.2	2.8	176830	2	BX901899	BX901899 Danio rer
798	48.2	2.8	176871	10	AC124687	AC124687 Mus muscu
799	48.2	2.8	178400	2	AC132941	AC132941 Mus muscu
c 800	48.2	2.8	182942	10	AC135110	AC135110 Mus muscu
801	48.2	2.8	184018	2	AC129540	AC129540 Mus muscu
802	48.2	2.8	187065	10	AC113014	AC113014 Mus muscu
803	48.2	2.8	187669	10	AL671874	AL671874 Mouse DNA
804	48.2	2.8	199674	10	AC125328	AC125328 Mus muscu
c 805	48.2	2.8	200627	2	AC101673	AC101673 Mus muscu
806	48.2	2.8	205230	2	AC126307	AC126307 Rattus no
c 807	48.2	2.8	205509	10	AL731853	AL731853 Mouse DNA
c 808	48.2	2.8	205958	2	AC117781	AC117781 Mus muscu
809	48.2	2.8	210594	2	AC117868	AC117868 Rattus no
810	48.2	2.8	211117	2	AC132627	AC132627 Rattus no
c 811	48.2	2.8	214461	10	AC113598	AC113598 Mus muscu
812	48.2	2.8	220221	2	AC141211	AC141211 Rattus no
813	48.2	2.8	221428	10	AC108782	AC108782 Mus muscu
c 814	48.2	2.8	221860	10	AC091473	AC091473 Mus muscu
815	48.2	2.8	223778	2	AC148811	AC148811 Canis fam
816	48.2	2.8	226939	2	AC113474	AC113474 Mus muscu
c 817	48.2	2.8	229482	2	AC074149	AC074149 Mus muscu
818	48.2	2.8	232193	2	AC130163	AC130163 Rattus no
c 819	48.2	2.8	232473	2	AC114212	AC114212 Rattus no
c 820	48.2	2.8	233034	2	AC116318	AC116318 Mus muscu
c 821	48.2	2.8	233369	2	AC099210	AC099210 Rattus no
822	48.2	2.8	233882	2	AC095414	AC095414 Rattus no

	823	48.2	2.8	234560	2	AC111539
	824	48.2	2.8	234840	2	AC133062
	825	48.2	2.8	236836	2	AC108530
	826	48.2	2.8	239009	2	AC113733
	827	48.2	2.8	240742	2	AC096830
c	828	48.2	2.8	241809	10	AC139848
	829	48.2	2.8	244220	10	AC122941
	830	48.2	2.8	249043	2	AC103197
	831	48.2	2.8	250391	2	AC096453
c	832	48.2	2.8	251932	2	AC137952
c	833	48.2	2.8	252660	2	AC138176
	834	48.2	2.8	278208	2	AC125728
	835	48.2	2.8	333664	2	AC128334
	836	48.2	2.8	338015	2	AC131401
	837	48	2.8	54068	10	AC095996
c	838	48	2.8	67702	9	AC104091
c	839	48	2.8	101509	2	AC027353
c	840	48	2.8	113006	9	AC006978
c	841	48	2.8	132932	10	AL928879
	842	48	2.8	151741	2	AC018609
c	843	48	2.8	154674	2	AC101753
	844	48	2.8	163284	10	AC131768
	845	48	2.8	165077	10	AC084382
	846	48	2.8	166819	2	AC129076
c	847	48	2.8	167448	10	AC133603
c	848	48	2.8	172110	10	AC122047
	849	48	2.8	174032	2	AC128150
c	850	48	2.8	174536	10	AC125079
	851	48	2.8	175022	2	AC134481
	852	48	2.8	175392	10	AL928635
	853	48	2.8	187191	9	AC007222
c	854	48	2.8	188390	10	AC140416
c	855	48	2.8	188782	10	AL713870
c	856	48	2.8	193458	10	AL645606
c	857	48	2.8	202768	10	AC122849
	858	48	2.8	202928	10	AC112147
c	859	48	2.8	208661	10	AC072048
	860	48	2.8	210648	10	AL772306
	861	48	2.8	212177	10	AC099468
	862	48	2.8	214604	10	AC104898
	863	48	2.8	218010	2	AC116052
c	864	48	2.8	220627	10	AC120843
	865	48	2.8	220893	2	AC106234
c	866	48	2.8	222451	10	AL845478
	867	48	2.8	227844	2	AC096134
c	868	48	2.8	236559	2	AC095895
c	869	48	2.8	236571	2	AC126595
	870	48	2.8	239344	2	AC133310
	871	48	2.8	246444	2	AC130772
	872	48	2.8	247282	2	AC126652
	873	48	2.8	250323	2	AC119713
c	874	48	2.8	251231	2	AC095505
	875	48	2.8	254269	2	AC112018
	876	48	2.8	256683	2	AC098307
c	877	48	2.8	257790	10	AC115767
c	878	48	2.8	262320	2	AC106419
	879	48	2.8	263388	2	AC094260
c	880	48	2.8	265001	2	AC121746
c	881	48	2.8	274343	2	AC115208
	882	48	2.8	281021	2	AC111415
c	883	47.8	2.8	507	4	AF252444
c	884	47.8	2.8	32626	9	AC002295
c	885	47.8	2.8	36091	2	AC012815
	886	47.8	2.8	37938	2	AC144846
	887	47.8	2.8	43342	2	AC144845
c	888	47.8	2.8	45802	9	AC027824
c	889	47.8	2.8	101093	2	AC136177
	890	47.8	2.8	110000	2	AC112373_03
c	891	47.8	2.8	110000	2	AC126804_0
c	892	47.8	2.8	135717	2	AC125921
	893	47.8	2.8	139995	10	AC131797
c	894	47.8	2.8	144055	10	AC120400
c	895	47.8	2.8	153481	2	AC092524

AC111539	Rattus no
AC133062	Rattus no
AC108530	Rattus no
AC113733	Rattus no
AC096830	Rattus no
AC139848	Mus muscu
AC122941	Mus muscu
AC103197	Rattus no
AC096453	Rattus no
AC137952	Mus muscu
AC138176	Mus muscu
AC125728	Rattus no
AC128334	Rattus no
AC131401	Rattus no
AC095996	Rattus no
AC104091	Homo sapi
AC027353	Homo sapi
AC006978	Homo sapi
AL928879	Mouse DNA
AC018609	Mus muscu
AC101753	Mus muscu
AC131768	Mus muscu
AC084382	Mus muscu
AC129076	Mus muscu
AC133603	Mus muscu
AC122047	Mus muscu
AC128150	Rattus no
AC125079	Mus muscu
AC134481	Rattus no
AL928635	Mouse DNA
AC007222	Homo sapi
AC140416	Mus muscu
AL713870	Mouse DNA
AL645606	Mouse DNA
AC122849	Mus muscu
AC112147	Mus muscu
AC072048	Mus muscu
AL772306	Mouse DNA
AC099468	Rattus no
AC104898	Mus muscu
AC116052	Mus muscu
AC120843	Mus muscu
AC106234	Rattus no
AL845478	Mouse DNA
AC096134	Rattus no
AC095895	Rattus no
AC126595	Rattus no
AC133310	Rattus no
AC130772	Rattus no
AC126652	Rattus no
AC119713	Rattus no
AC095505	Rattus no
AC112018	Rattus no
AC098307	Rattus no
AC115767	Mus muscu
AC106419	Rattus no
AC094260	Rattus no
AC121746	Rattus no
AC115208	Rattus no
AC111415	Rattus no
AF252444	Bos tauru
AC002295	Genomic s
AC012815	Drosophil
AC144846	Homo sapi
AC144845	Homo sapi
AC027824	Homo sapi
AC136177	Rattus no
Continuation (4 of	
AC126804	Mus muscu
AC125921	Rattus no
AC131797	Mus muscu
AC120400	Mus muscu
AC092524	Papio anu

c	896	47.8	2.8	154328	2	AC134145
c	897	47.8	2.8	154485	2	AC116894
c	898	47.8	2.8	162502	10	AC105062
c	899	47.8	2.8	164885	2	AC132365
c	900	47.8	2.8	167612	2	AC119140
c	901	47.8	2.8	169544	9	AC008573
c	902	47.8	2.8	172134	2	AC138589
c	903	47.8	2.8	172487	10	AL954375
	904	47.8	2.8	172949	10	AC122231
c	905	47.8	2.8	176416	10	AL805906
	906	47.8	2.8	179071	2	AC146665
	907	47.8	2.8	179334	2	AC131817
c	908	47.8	2.8	183863	2	AC110455
	909	47.8	2.8	185436	2	AC141216
c	910	47.8	2.8	185729	10	AC129602
	911	47.8	2.8	186115	10	AC117647
	912	47.8	2.8	188854	10	AL626770
	913	47.8	2.8	190760	10	AC122551
	914	47.8	2.8	196474	10	AC079957
c	915	47.8	2.8	200415	2	AC125886
c	916	47.8	2.8	201223	10	AL731735
c	917	47.8	2.8	203548	2	AC102094
	918	47.8	2.8	204605	2	AL160259
c	919	47.8	2.8	204684	10	AC127581
c	920	47.8	2.8	205029	10	AC140315
	921	47.8	2.8	209013	10	AL844846
	922	47.8	2.8	209936	10	AC111096
c	923	47.8	2.8	210923	2	AC111663
c	924	47.8	2.8	212789	10	AC124676
c	925	47.8	2.8	217080	10	AC110519
c	926	47.8	2.8	222565	2	CR318603
	927	47.8	2.8	224867	2	AC097751
c	928	47.8	2.8	227781	2	AC129745
	929	47.8	2.8	230706	2	AC134261
	930	47.8	2.8	235343	2	AC121745
c	931	47.8	2.8	236652	2	AC129111
	932	47.8	2.8	239807	2	AC096797
c	933	47.8	2.8	239880	2	AC095415
	934	47.8	2.8	240277	2	AC126559
c	935	47.8	2.8	249083	2	AC098753
	936	47.8	2.8	249995	2	AC121434
	937	47.8	2.8	252792	2	AC105667
c	938	47.8	2.8	254350	2	AC135408
	939	47.8	2.8	255469	2	AC112031
c	940	47.8	2.8	255682	2	AC122572
c	941	47.8	2.8	259702	2	AC119031
c	942	47.8	2.8	261979	10	AC118695
c	943	47.8	2.8	269739	10	AC139108
	944	47.8	2.8	287501	2	AC098561
c	945	47.8	2.8	295321	2	AC123894
	946	47.8	2.8	322522	2	AC115351
	947	47.6	2.8	1445	5	GDCARANH
	948	47.6	2.8	34046	2	AC141683
c	949	47.6	2.8	34914	2	AC102932
c	950	47.6	2.8	75849	2	AC101259
	951	47.6	2.8	81950	10	AL928665
	952	47.6	2.8	91526	9	AC114732
	953	47.6	2.8	110000	2	AC095769_0
	954	47.6	2.8	110000	2	AC098243_1
	955	47.6	2.8	122211	10	AL844555
c	956	47.6	2.8	135317	10	AC121998
c	957	47.6	2.8	145382	10	AL928925
	958	47.6	2.8	150491	2	AC116375
c	959	47.6	2.8	155843	2	AC104192
	960	47.6	2.8	159546	2	AC113419
c	961	47.6	2.8	161350	10	AC121983
c	962	47.6	2.8	164617	2	AC102624
c	963	47.6	2.8	167632	2	AC068604
	964	47.6	2.8	168570	2	AC119472
c	965	47.6	2.8	173136	10	AC103380
	966	47.6	2.8	178896	10	AC122504
c	967	47.6	2.8	180254	2	AC110187
	968	47.6	2.8	180916	10	AL844195

AC134145 Rattus no
AC116894 Mus muscu
AC105062 Mus muscu
AC132365 Mus muscu
AC119140 Rattus no
AC008573 Homo sapi
AC138589 Mus muscu
AL954375 Mouse DNA
AC122231 Mus muscu
AL805906 Mouse DNA
AC146665 Homo sapi
AC131817 Rattus no
AC110455 Rattus no
AC141216 Rattus no
AC129602 Mus muscu
AC117647 Mus muscu
AL626770 Mouse DNA
AC122551 Mus muscu
AC079957 Mus muscu
AC125886 Rattus no
AL731735 Mouse DNA
AC102094 Mus muscu
AL160259 Homo sapi
AC127581 Mus muscu
AC140315 Mus muscu
AL844846 Mouse DNA
AC111096 Mus muscu
AC111663 Rattus no
AC124676 Mus muscu
AC110519 Mus muscu
CR318603 Danio rer
AC097751 Rattus no
AC129745 Rattus no
AC134261 Rattus no
AC121745 Rattus no
AC129111 Rattus no
AC096797 Rattus no
AC095415 Rattus no
AC126559 Rattus no
AC098753 Rattus no
AC121434 Rattus no
AC105667 Rattus no
AC135408 Rattus no
AC112031 Rattus no
AC122572 Rattus no
AC119031 Rattus no
AC118695 Mus muscu
AC139108 Mus muscu
AC098561 Rattus no
AC123894 Rattus no
AC115351 Rattus no
Z14957 G.domesticu
AC141683 Apis mell
AC102932 Mus muscu
AC101259 Mus muscu
AL928665 Mouse DNA
AC114732 Homo sapi
AC095769 Rattus no
Continuation (2 of
AL844555 Mouse DNA
AC121998 Mus muscu
AL928925 Mouse DNA
AC116375 Mus muscu
AC104192 Mus muscu
AC113419 Homo sapi
AC121983 Mus muscu
AC102624 Mus muscu
AC068604 Mus muscu
AC119472 Rattus no
AC103380 Mus muscu
AC122504 Mus muscu
AC110187 Mus muscu
AL844195 Mouse DNA

c 969	47.6	2.8	183342	9	AL450345	AL450345 Human DNA
c 970	47.6	2.8	184201	10	BX088698	BX088698 Mouse DNA
c 971	47.6	2.8	188098	2	AC108396	AC108396 Mus muscu
c 972	47.6	2.8	195328	10	AC125153	AC125153 Mus muscu
c 973	47.6	2.8	200624	10	AL592065	AL592065 Mouse DNA
974	47.6	2.8	200955	10	AC131658	AC131658 Mus muscu
c 975	47.6	2.8	204919	2	AC151051	AC151051 Mus muscu
976	47.6	2.8	205318	10	AC122894	AC122894 Mus muscu
977	47.6	2.8	210516	2	AC079870	AC079870 Mus muscu
c 978	47.6	2.8	215042	2	AC136823	AC136823 Rattus no
979	47.6	2.8	215180	2	AC113180	AC113180 Mus muscu
c 980	47.6	2.8	215800	2	AC137947	AC137947 Mus muscu
c 981	47.6	2.8	216315	10	AL928963	AL928963 Mouse DNA
c 982	47.6	2.8	217584	2	AC113299	AC113299 Mus muscu
c 983	47.6	2.8	219409	2	AC134858	AC134858 Mus muscu
c 984	47.6	2.8	221911	2	AC114095	AC114095 Rattus no
985	47.6	2.8	224562	10	AC123880	AC123880 Mus muscu
c 986	47.6	2.8	228947	2	AC111430	AC111430 Rattus no
c 987	47.6	2.8	229283	2	AC095445	AC095445 Rattus no
c 988	47.6	2.8	234199	2	AC098172	AC098172 Rattus no
c 989	47.6	2.8	236508	2	AC094222	AC094222 Rattus no
990	47.6	2.8	236988	2	AC134658	AC134658 Rattus no
c 991	47.6	2.8	239847	2	AC128434	AC128434 Rattus no
992	47.6	2.8	250578	2	AC094142	AC094142 Rattus no
993	47.6	2.8	250713	2	AC103517	AC103517 Rattus no
994	47.6	2.8	259028	2	AC103238	AC103238 Rattus no
995	47.6	2.8	270695	10	AC102542	AC102542 Mus muscu
c 996	47.6	2.8	270808	2	AC102459	AC102459 Mus muscu
997	47.6	2.8	285324	2	AC119574	AC119574 Rattus no
c 998	47.6	2.8	289369	2	BX842563	BX842563 Mus muscu
c 999	47.6	2.8	313499	2	AC119366	AC119366 Rattus no
1000	47.6	2.8	327876	2	AC095476	AC095476 Rattus no
c1001	47.4	2.8	362	11	AU027029	AU027029 Rattus no
c1002	47.4	2.8	625	11	BV030001	BV030001 S208P6392
1003	47.4	2.8	1434	4	AY075023	AY075023 Bos tauru
1004	47.4	2.8	2403	9	AK093753	AK093753 Homo sapi
c1005	47.4	2.8	3001	3	AF192530	AF192530 Drosophil
c1006	47.4	2.8	58326	2	AC108383	AC108383 Pan trogl
1007	47.4	2.8	85836	2	AC108384	AC108384 Pan trogl
1008	47.4	2.8	110000	2	AC112799_1	Continuation (2 of
1009	47.4	2.8	110000	2	AC112804_0	AC112804 Rattus no
c1010	47.4	2.8	110000	2	AC120731_0	AC120731 Rattus no
1011	47.4	2.8	110000	2	AC130947_1	Continuation (2 of
1012	47.4	2.8	110000	2	AC130947_2	Continuation (3 of
c1013	47.4	2.8	111402	10	AP003154	AP003154 Mus muscu
1014	47.4	2.8	114419	10	AL670838	AL670838 Mouse DNA
c1015	47.4	2.8	123110	4	CR385029	CR385029 Opossum D
c1016	47.4	2.8	143147	2	AC141204	AC141204 Rattus no
1017	47.4	2.8	146907	2	AC141031	AC141031 Rattus no
1018	47.4	2.8	150821	2	CR384071	CR384071 Danio rer
1019	47.4	2.8	152363	2	AC135813	AC135813 Rattus no
c1020	47.4	2.8	156444	10	AP003153	AP003153 Mus muscu
1021	47.4	2.8	158822	2	AC136174	AC136174 Rattus no
1022	47.4	2.8	160321	10	AL772321	AL772321 Mouse DNA
c1023	47.4	2.8	162676	10	AC123032	AC123032 Mus muscu
c1024	47.4	2.8	163917	10	AC118689	AC118689 Mus muscu
c1025	47.4	2.8	169201	10	AC123676	AC123676 Mus muscu
c1026	47.4	2.8	169930	2	AC102142	AC102142 Mus muscu
1027	47.4	2.8	172798	2	AC129231	AC129231 Rattus no
1028	47.4	2.8	173283	2	AC112405	AC112405 Rattus no
c1029	47.4	2.8	178519	2	AC124086	AC124086 Mus muscu
1030	47.4	2.8	178820	2	AC142164	AC142164 Rattus no
c1031	47.4	2.8	180007	2	AC132933	AC132933 Mus muscu
c1032	47.4	2.8	182547	10	AC116599	AC116599 Mus muscu
1033	47.4	2.8	183774	2	AC102150	AC102150 Mus muscu
1034	47.4	2.8	185532	10	AC121883	AC121883 Mus muscu
c1035	47.4	2.8	186807	10	AC121592	AC121592 Mus muscu
c1036	47.4	2.8	191106	10	AC131521	AC131521 Rattus no
c1037	47.4	2.8	192682	10	AC107769	AC107769 Mus muscu
c1038	47.4	2.8	194619	2	AC112595	AC112595 Rattus no
c1039	47.4	2.8	195234	2	AC141878	AC141878 Mus muscu
c1040	47.4	2.8	195290	2	AC105798	AC105798 Rattus no
1041	47.4	2.8	202237	10	AC114825	AC114825 Mus muscu
1042	47.4	2.8	207283	2	AC102501	AC102501 Mus muscu
c1043	47.4	2.8	207471	10	AC122249	AC122249 Mus muscu
1044	47.4	2.8	211697	10	AC122296	AC122296 Mus muscu
c1045	47.4	2.8	211758	10	AC133890	AC133890 Mus muscu
1046	47.4	2.8	214026	2	AC111389	AC111389 Rattus no
c1047	47.4	2.8	217690	10	AC126722	AC126722 Rattus no
1048	47.4	2.8	220602	10	AC091248	AC091248 Mus muscu
1049	47.4	2.8	220624	10	AC124598	AC124598 Mus muscu
c1050	47.4	2.8	220629	10	AC113125	AC113125 Mus muscu
1051	47.4	2.8	221449	2	AC111952	AC111952 Rattus no
c1052	47.4	2.8	223030	10	AL669948	AL669948 Mouse DNA
1053	47.4	2.8	223297	2	AC120669	AC120669 Rattus no
1054	47.4	2.8	223469	2	AC095140	AC095140 Rattus no
c1055	47.4	2.8	225448	2	AC123134	AC123134 Rattus no
c1056	47.4	2.8	225868	10	AC098743	AC098743 Mus muscu
1057	47.4	2.8	225992	2	AC097157	AC097157 Rattus no
1058	47.4	2.8	227067	2	AC140391	AC140391 Mus muscu
c1059	47.4	2.8	227646	2	AC125687	AC125687 Rattus no
1060	47.4	2.8	228302	2	AC109973	AC109973 Rattus no
1061	47.4	2.8	228787	2	AC111884	AC111884 Rattus no
c1062	47.4	2.8	230129	2	AC123085	AC123085 Rattus no
1063	47.4	2.8	232670	2	AC129149	AC129149 Rattus no
1064	47.4	2.8	235904	2	AC102729	AC102729 Mus muscu
c1065	47.4	2.8	237193	2	AC108555	AC108555 Rattus no
c1066	47.4	2.8	238812	2	AC111727	AC111727 Rattus no
1067	47.4	2.8	239100	2	AC105455	AC105455 Rattus no
1068	47.4	2.8	239821	10	AC069308	AC069308 Mus muscu
c1069	47.4	2.8	240977	2	AC109437	AC109437 Rattus no
1070	47.4	2.8	242540	2	AC040927	AC040927 Mus muscu
c1071	47.4	2.8	242559	2	AC135156	AC135156 Rattus no
1072	47.4	2.8	244742	2	AC125663	AC125663 Rattus no
1073	47.4	2.8	245299	2	AC113130	AC113130 Mus muscu
1074	47.4	2.8	247544	2	AC092741	AC092741 Mus muscu
1075	47.4	2.8	247925	2	AC131480	AC131480 Rattus no
1076	47.4	2.8	248558	2	AC110320	AC110320 Rattus no
c1077	47.4	2.8	248965	2	AC113215	AC113215 Rattus no
c1078	47.4	2.8	249430	2	AC136568	AC136568 Rattus no
c1079	47.4	2.8	251443	2	AC096251	AC096251 Rattus no
1080	47.4	2.8	251643	2	AC125859	AC125859 Rattus no
c1081	47.4	2.8	254231	2	AC117976	AC117976 Rattus no
c1082	47.4	2.8	256391	2	AC107557	AC107557 Rattus no
1083	47.4	2.8	260082	2	AC130175	AC130175 Rattus no
1084	47.4	2.8	263209	2	AC106130	AC106130 Rattus no
c1085	47.4	2.8	264459	2	AC132720	AC132720 Rattus no
1086	47.4	2.8	265074	2	AC103024	AC103024 Rattus no
c1087	47.4	2.8	266371	2	AC020619	AC020619 Mus muscu
c1088	47.4	2.8	266726	2	AC112860	AC112860 Rattus no
1089	47.4	2.8	267500	2	AC107000	AC107000 Rattus no
c1090	47.4	2.8	269993	2	AC118497	AC118497 Rattus no
1091	47.4	2.8	272363	2	AC128458	AC128458 Rattus no
c1092	47.4	2.8	276162	2	AC094610	AC094610 Rattus no
c1093	47.4	2.8	279020	2	AC109535	AC109535 Rattus no
c1094	47.4	2.8	287427	2	AC106914	AC106914 Rattus no
c1095	47.4	2.8	299793	2	AC099284	AC099284 Rattus no
1096	47.4	2.8	315861	2	AC109931	AC109931 Rattus no
1097	47.4	2.8	329976	2	AC127764	AC127764 Rattus no
1098	47.4	2.8	337486	2	AC114544	AC114544 Mus muscu
1099	47.2	2.8	449	8	AF409168	AF409168 Pseudotsu
c1100	47.2	2.8	1229	9	BC062736	BC062736 Homo sapi
1101	47.2	2.8	2000	6	AX655393	AX655393 Sequence
1102	47.2	2.8	13040	10	AF453571	AF453571 Mus muscu
c1103	47.2	2.8	63798	2	AC124310	AC124310 Homo sapi
c1104	47.2	2.8	84604	10	AL645763	AL645763 Mouse DNA
1105	47.2	2.8	87667	10	AL845546	AL845546 Mouse DNA
c1106	47.2	2.8	93273	9	AC004084	AC004084 Homo sapi
c1107	47.2	2.8	98999	2	AC142052	AC142052 Rattus no
1108	47.2	2.8	107344	2	AC127799_3	Continuation (4 of
1109	47.2	2.8	110000	2	AC103663_1	Continuation (2 of
c1110	47.2	2.8	112401	9	AL606462	AL606462 Human DNA
1111	47.2	2.8	115863	9	HS268D13	AL023513 Human DNA
c1112	47.2	2.8	121869	10	AL831739	AL831739 Mouse DNA
1113	47.2	2.8	130451	10	AC121877	AC121877 Mus muscu
c1114	47.2	2.8	136268	10	AC068496	AC068496 Mus muscu

1115	47.2	2.8	139452	10	AL954675	AL954675 Mouse DNA
1116	47.2	2.8	147257	10	AC116279	AC116279 Rattus no
c1117	47.2	2.8	157430	10	AC127678	AC127678 Mus muscu
1118	47.2	2.8	159042	10	AC112163	AC112163 Mus Muscu
c1119	47.2	2.8	160764	10	RN120J22	BX511205 Rattus no
c1120	47.2	2.8	163429	2	AC114473	AC114473 Mus muscu
1121	47.2	2.8	163546	2	AC103547	AC103547 Rattus no
c1122	47.2	2.8	163690	2	AC131509	AC131509 Strongylo
1123	47.2	2.8	164291	9	AC021351	AC021351 Homo sapi
1124	47.2	2.8	164612	10	AC124697	AC124697 Mus muscu
1125	47.2	2.8	165309	2	BX936424	BX936424 Danio rer
c1126	47.2	2.8	169199	2	AC109292	AC109292 Mus muscu
1127	47.2	2.8	170807	9	AC124307	AC124307 Homo sapi
1128	47.2	2.8	171224	2	AC091600	AC091600 Homo sapi
1129	47.2	2.8	172157	2	AC125832	AC125832 Rattus no
1130	47.2	2.8	175036	9	AC068069	AC068069 Homo sapi
c1131	47.2	2.8	178968	9	AP006274	AP006274 Papio ham
1132	47.2	2.8	179661	2	AC134788	AC134788 Mus muscu
1133	47.2	2.8	185384	10	AL645643	AL645643 Mouse DNA
c1134	47.2	2.8	187353	10	AC124723	AC124723 Mus muscu
c1135	47.2	2.8	187920	10	AC115933	AC115933 Mus muscu
c1136	47.2	2.8	192715	10	AL929556	AL929556 Mouse DNA
c1137	47.2	2.8	192856	10	AC110559	AC110559 Mus muscu
1138	47.2	2.8	194335	10	AC144934	AC144934 Mus muscu
1139	47.2	2.8	194973	2	AC102522	AC102522 Mus muscu
c1140	47.2	2.8	196490	10	AC126038	AC126038 Mus muscu
c1141	47.2	2.8	196545	9	AC113390	AC113390 Homo sapi
c1142	47.2	2.8	200247	10	AC131100	AC131100 Mus muscu
1143	47.2	2.8	200605	10	AC129314	AC129314 Mus muscu
c1144	47.2	2.8	202240	2	AC110232	AC110232 Mus muscu
1145	47.2	2.8	202920	10	AL929441	AL929441 Mouse DNA
1146	47.2	2.8	202996	2	AC109272	AC109272 Mus muscu
1147	47.2	2.8	203122	2	AC102612	AC102612 Mus muscu
c1148	47.2	2.8	204251	10	AC108430	AC108430 Mus muscu
c1149	47.2	2.8	206123	2	AC151732	AC151732 Mus muscu
1150	47.2	2.8	208125	2	AC132953	AC132953 Mus muscu
1151	47.2	2.8	208277	2	AC108910	AC108910 Mus muscu
c1152	47.2	2.8	211657	10	AC123605	AC123605 Mus muscu
1153	47.2	2.8	212506	2	AC079516	AC079516 Mus muscu
c1154	47.2	2.8	213482	10	AC073883	AC073883 Mus muscu
1155	47.2	2.8	214331	2	AL732312	AL732312 Mus muscu
1156	47.2	2.8	215688	2	AC130266	AC130266 Rattus no
c1157	47.2	2.8	216915	2	AC125580	AC125580 Rattus no
c1158	47.2	2.8	217207	2	AC073511	AC073511 Mus muscu
1159	47.2	2.8	217873	9	HUAC004382	AC004382 Homo sapi
1160	47.2	2.8	218644	9	AC147079	AC147079 Pan trogl
1161	47.2	2.8	218679	2	AC136584	AC136584 Rattus no
c1162	47.2	2.8	218980	10	AC117201	AC117201 Mus muscu
1163	47.2	2.8	219266	2	AC130080	AC130080 Rattus no
1164	47.2	2.8	221374	10	AL604043	AL604043 Mouse DNA
c1165	47.2	2.8	222482	2	AC103664	AC103664 Mus muscu
c1166	47.2	2.8	222938	2	AC137160	AC137160 Rattus no
1167	47.2	2.8	223687	2	AC121373	AC121373 Rattus no
1168	47.2	2.8	225395	2	AC130267	AC130267 Rattus no
c1169	47.2	2.8	225992	2	AC097157	AC097157 Rattus no
1170	47.2	2.8	226287	2	AC123086	AC123086 Rattus no
c1171	47.2	2.8	226956	10	AC095558	AC095558 Rattus no
1172	47.2	2.8	228391	10	AL596331	AL596331 Mouse DNA
c1173	47.2	2.8	228689	2	AC137396	AC137396 Rattus no
1174	47.2	2.8	229287	2	AC107509	AC107509 Rattus no
1175	47.2	2.8	230941	2	AC130937	AC130937 Rattus no
c1176	47.2	2.8	231950	2	AC094759	AC094759 Rattus no
c1177	47.2	2.8	234973	10	AC122850	AC122850 Mus muscu
1178	47.2	2.8	235509	10	AC091523	AC091523 Mus muscu
c1179	47.2	2.8	238327	2	AC151718	AC151718 Mus muscu
1180	47.2	2.8	238352	2	AC103276	AC103276 Rattus no
c1181	47.2	2.8	239078	2	AC095928	AC095928 Rattus no
1182	47.2	2.8	239758	10	AL591495	AL591495 Mouse DNA
c1183	47.2	2.8	240292	2	AC103236	AC103236 Rattus no
c1184	47.2	2.8	241789	10	AC102545	AC102545 Mus muscu
c1185	47.2	2.8	242845	2	AC126976	AC126976 Rattus no
c1186	47.2	2.8	243616	2	AC119711	AC119711 Rattus no
c1187	47.2	2.8	243849	2	AC094959	AC094959 Rattus no
c1188	47.2	2.8	244185	2	AC123496	AC123496 Rattus no
c1189	47.2	2.8	246190	2	AC095515	AC095515 Rattus no
c1190	47.2	2.8	247530	2	AC129707	AC129707 Rattus no
c1191	47.2	2.8	248784	2	AC113885	AC113885 Rattus no
c1192	47.2	2.8	249025	2	AC131475	AC131475 Rattus no
1193	47.2	2.8	250362	2	AC117724	AC117724 Mus muscu
1194	47.2	2.8	251286	2	AC125835	AC125835 Rattus no
1195	47.2	2.8	252095	10	AC122187	AC122187 Mus muscu
c1196	47.2	2.8	252326	2	AC094630	AC094630 Rattus no
1197	47.2	2.8	254217	2	AC114075	AC114075 Rattus no
1198	47.2	2.8	254832	2	AC095698	AC095698 Rattus no
c1199	47.2	2.8	257596	2	AC093408	AC093408 Mus muscu
1200	47.2	2.8	257999	2	AC107256	AC107256 Rattus no
c1201	47.2	2.8	263599	2	AC109366	AC109366 Rattus no
1202	47.2	2.8	264016	2	AC114508	AC114508 Rattus no
c1203	47.2	2.8	271162	2	CR405715	CR405715 Danio rer
c1204	47.2	2.8	271233	2	AC096597	AC096597 Rattus no
1205	47.2	2.8	275443	2	AC096407	AC096407 Rattus no
1206	47	2.8	897	3	AF395662	AF395662 Aedes aeg
1207	47	2.8	69346	10	AL671997	AL671997 Mouse DNA
1208	47	2.8	78062	10	AL844572	AL844572 Mouse DNA
c1209	47	2.8	98653	10	AL731664	AL731664 Mouse DNA
c1210	47	2.8	106465	9	HSJ765F13	AL109853 Human DNA
1211	47	2.8	135194	10	AC147368	AC147368 Mus muscu
1212	47	2.8	150986	10	AL645587	AL645587 Mouse DNA
1213	47	2.8	151238	2	AC149989	AC149989 Strongylo
c1214	47	2.8	153722	2	AC127961	AC127961 Rattus no
1215	47	2.8	163257	2	AC140048	AC140048 Mus muscu
1216	47	2.8	166330	2	AC109216	AC109216 Mus muscu
c1217	47	2.8	169310	10	AC119259	AC119259 Mus muscu
c1218	47	2.8	176348	2	AC140956	AC140956 Didelphis
1219	47	2.8	180887	10	AC106833	AC106833 Mus muscu
1220	47	2.8	182454	2	AC133586	AC133586 Mus muscu
c1221	47	2.8	183065	2	AC119970	AC119970 Mus muscu
1222	47	2.8	183761	2	AC120450	AC120450 Rattus no
c1223	47	2.8	184441	2	AC128306	AC128306 Rattus no
c1224	47	2.8	188914	9	AC019118	AC019118 Homo sapi
1225	47	2.8	190317	2	AC137848	AC137848 Mus muscu
c1226	47	2.8	192179	2	AC097365	AC097365 Mus muscu
1227	47	2.8	192365	2	AC139891	AC139891 Rattus no
1228	47	2.8	193775	2	AC123129	AC123129 Rattus no
c1229	47	2.8	195563	10	AC123708	AC123708 Mus muscu
1230	47	2.8	197720	10	AC121791	AC121791 Mus muscu
1231	47	2.8	200746	10	AC117222	AC117222 Mus muscu
1232	47	2.8	201004	2	AC132280	AC132280 Mus muscu
1233	47	2.8	205372	2	AC117090	AC117090 Rattus no
c1234	47	2.8	208734	10	AC102675	AC102675 Mus muscu
1235	47	2.8	210450	2	AC128567	AC128567 Rattus no
1236	47	2.8	211348	2	BX927237	BX927237 Danio rer
c1237	47	2.8	211550	9	AC073912	AC073912 Homo sapi
1238	47	2.8	214225	2	AC105581	AC105581 Rattus no
c1239	47	2.8	220751	2	AC094649	AC094649 Rattus no
1240	47	2.8	220805	2	AC118515	AC118515 Rattus no
c1241	47	2.8	222040	2	AC098532	AC098532 Rattus no
c1242	47	2.8	222348	2	AC084067	AC084067 Mus muscu
1243	47	2.8	224704	2	AC129619	AC129619 Rattus no
1244	47	2.8	225342	2	AC132766	AC132766 Rattus no
1245	47	2.8	225777	10	AC108527	AC108527 Rattus no
1246	47	2.8	233905	2	AC120465	AC120465 Rattus no
1247	47	2.8	235061	2	AC107257	AC107257 Rattus no
1248	47	2.8	235792	2	AC094908	AC094908 Rattus no
c1249	47	2.8	236697	2	AC127845	AC127845 Rattus no
c1250	47	2.8	238488	2	AC103134	AC103134 Rattus no
c1251	47	2.8	239624	2	AC103130	AC103130 Rattus no
1252	47	2.8	245038	2	AC117335	AC117335 Rattus no
c1253	47	2.8	245536	10	AC093320	AC093320 Mus muscu
1254	47	2.8	245892	2	AC096984	AC096984 Rattus no
1255	47	2.8	245961	2	AC094708	AC094708 Rattus no
c1256	47	2.8	246367	2	AC130871	AC130871 Rattus no
1257	47	2.8	246415	2	AC116379	AC116379 Mus muscu
1258	47	2.8	247017	2	AC110624	AC110624 Rattus no
c1259	47	2.8	252054	2	AC097119	AC097119 Rattus no
c1260	47	2.8	252215	2	AC095632	AC095632 Rattus no

c1261	47	2.8	252257	2	AC096047	AC096047 Rattus no
c1262	47	2.8	256974	2	AC103221	AC103221 Rattus no
c1263	47	2.8	258545	2	AC114056	AC114056 Rattus no
c1264	47	2.8	264501	2	AC136579	AC136579 Rattus no
1265	47	2.8	265412	2	AC103143	AC103143 Rattus no
1266	47	2.8	274560	2	AC099390	AC099390 Rattus no
c1267	47	2.8	276710	2	AC129823	AC129823 Rattus no
c1268	47	2.8	279449	2	AC126636	AC126636 Rattus no
1269	46.8	2.8	28194	2	AC145126	AC145126 Homo sapi
1270	46.8	2.8	33106	10	AL928961	AL928961 Mouse DNA
c1271	46.8	2.8	62067	2	AC120018	AC120018 Mus muscu
1272	46.8	2.8	65972	2	AC109317	AC109317 Homo sapi
c1273	46.8	2.8	65972	2	AC109317	AC109317 Homo sapi
1274	46.8	2.8	93626	2	AC147411	AC147411 Homo sapi
c1275	46.8	2.8	93626	2	AC147411	AC147411 Homo sapi
c1276	46.8	2.8	110000	2	AC094316_0	AC094316 Rattus no
1277	46.8	2.8	118689	2	AC141123	AC141123 Rattus no
1278	46.8	2.8	120935	10	AC127276	AC127276 Mus muscu
c1279	46.8	2.8	144746	2	AC116867	AC116867 Mus muscu
1280	46.8	2.8	151507	2	BX936397	BX936397 Danio rer
1281	46.8	2.8	152405	10	AC125318	AC125318 Mus muscu
c1282	46.8	2.8	153001	10	AC147183	AC147183 Mus muscu
1283	46.8	2.8	153350	2	AC108402	AC108402 Mus muscu
1284	46.8	2.8	155270	10	AC130837	AC130837 Mus muscu
1285	46.8	2.8	155843	2	AC102690	AC102690 Mus muscu
1286	46.8	2.8	157160	10	AC131979	AC131979 Mus muscu
c1287	46.8	2.8	159972	2	AC121554	AC121554 Mus muscu
c1288	46.8	2.8	164394	9	AC008706	AC008706 Homo sapi
1289	46.8	2.8	167417	9	AC011505	AC011505 Homo sapi
c1290	46.8	2.8	171631	2	AC118741	AC118741 Mus muscu
1291	46.8	2.8	172224	2	AC102679	AC102679 Mus muscu
1292	46.8	2.8	174534	2	AC132279	AC132279 Mus muscu
1293	46.8	2.8	174638	10	AL670290	AL670290 Mouse DNA
c1294	46.8	2.8	175625	2	AC068475	AC068475 Homo sapi
c1295	46.8	2.8	179906	2	AC119683	AC119683 Rattus no
c1296	46.8	2.8	182248	10	AL606915	AL606915 Mouse DNA
c1297	46.8	2.8	182873	2	AC126192	AC126192 Rattus no
c1298	46.8	2.8	182990	2	AC141383	AC141383 Rattus no
c1299	46.8	2.8	184363	2	AC117762	AC117762 Mus muscu
c1300	46.8	2.8	185319	10	AC147233	AC147233 Mus muscu
1301	46.8	2.8	186306	2	AC134641	AC134641 Rattus no
1302	46.8	2.8	189912	2	AC102434	AC102434 Mus muscu
c1303	46.8	2.8	191100	10	AC139377	AC139377 Mus muscu
c1304	46.8	2.8	194641	10	AC124107	AC124107 Mus muscu
c1305	46.8	2.8	195356	10	AC113495	AC113495 Mus muscu
c1306	46.8	2.8	201040	9	AC009503	AC009503 Homo sapi
1307	46.8	2.8	202103	2	AC121195	AC121195 Rattus no
1308	46.8	2.8	206695	2	AC091466	AC091466 Mus muscu
1309	46.8	2.8	212825	2	AC110735	AC110735 Mus muscu
c1310	46.8	2.8	216878	10	AC147109	AC147109 Mus muscu
c1311	46.8	2.8	220036	2	AC135494	AC135494 Rattus no
1312	46.8	2.8	221362	2	AC134084	AC134084 Rattus no
1313	46.8	2.8	222403	2	AC110851	AC110851 Rattus no
1314	46.8	2.8	222901	2	AC115788	AC115788 Mus muscu
c1315	46.8	2.8	223383	2	AC115332	AC115332 Rattus no
1316	46.8	2.8	223631	2	AC151531	AC151531 Mus muscu
1317	46.8	2.8	224213	10	AC147051	AC147051 Mus muscu
c1318	46.8	2.8	227299	10	AC138722	AC138722 Mus muscu
c1319	46.8	2.8	227607	10	AC120570	AC120570 Rattus no
c1320	46.8	2.8	228869	10	BX470109	BX470109 Mouse DNA
1321	46.8	2.8	230672	10	AL772397	AL772397 Mouse DNA
c1322	46.8	2.8	231980	2	AC094305	AC094305 Rattus no
c1323	46.8	2.8	232320	10	AC127314	AC127314 Mus muscu
c1324	46.8	2.8	236007	2	AC114426	AC114426 Mus muscu
1325	46.8	2.8	237065	2	AC128999	AC128999 Rattus no
1326	46.8	2.8	244974	2	AC097706	AC097706 Rattus no
c1327	46.8	2.8	245569	2	AC113818	AC113818 Rattus no
c1328	46.8	2.8	247196	2	AC073822	AC073822 Mus muscu
c1329	46.8	2.8	249737	2	AC094359	AC094359 Rattus no
c1330	46.8	2.8	250080	2	AC095289	AC095289 Rattus no
1331	46.8	2.8	250570	2	AC134011	AC134011 Rattus no
c1332	46.8	2.8	251636	2	AC096818	AC096818 Rattus no
c1333	46.8	2.8	251990	2	AC128457	AC128457 Rattus no
c1334	46.8	2.8	261198	2	AC106528	AC106528 Rattus no
1335	46.8	2.8	268098	2	AC133387	AC133387 Rattus no
1336	46.8	2.8	285107	2	AC126970	AC126970 Rattus no
c1337	46.8	2.8	307931	2	AC094673	AC094673 Rattus no
1338	46.8	2.8	316024	2	AC108988	AC108988 Rattus no
1339	46.6	2.7	323	6	CQ469739	CQ469739 Sequence
1340	46.6	2.7	324	6	CQ478907	CQ478907 Sequence
c1341	46.6	2.7	2000	6	AX655393	AX655393 Sequence
c1342	46.6	2.7	101619	2	AC136537	AC136537 Rattus no
1343	46.6	2.7	101790	10	BX649280	BX649280 Mouse DNA
c1344	46.6	2.7	110000	2	AC123006_0	AC123006 Rattus no
c1345	46.6	2.7	110996	10	AL672210	AL672210 Mouse DNA
1346	46.6	2.7	129225	9	AC026765	AC026765 Homo sapi
1347	46.6	2.7	139318	2	AC146998	AC146998 Arbacia p
c1348	46.6	2.7	140476	10	AC116659	AC116659 Mus muscu
1349	46.6	2.7	149000	2	AC120842	AC120842 Mus muscu
1350	46.6	2.7	156019	2	AC138609	AC138609 Mus muscu
c1351	46.6	2.7	160781	2	AC128871	AC128871 Rattus no
c1352	46.6	2.7	162782	2	AC120655	AC120655 Rattus no
1353	46.6	2.7	163511	2	AC120155	AC120155 Mus muscu
c1354	46.6	2.7	163915	2	AC140236	AC140236 Mus muscu
1355	46.6	2.7	168555	2	AC139992	AC139992 Rattus no
1356	46.6	2.7	170902	2	AC112422	AC112422 Rattus no
1357	46.6	2.7	173219	2	BX897738	BX897738 Danio rer
c1358	46.6	2.7	173277	2	AC148175	AC148175 Mus muscu
c1359	46.6	2.7	173926	2	MM454K24	AL160232 Mus muscu
1360	46.6	2.7	176349	2	AC122679	AC122679 Rattus no
1361	46.6	2.7	176778	10	AL845336	AL845336 Mouse DNA
c1362	46.6	2.7	176816	2	AC113472	AC113472 Mus muscu
1363	46.6	2.7	179176	2	AC137151	AC137151 Mus muscu
1364	46.6	2.7	179362	10	AC115355	AC115355 Mus muscu
1365	46.6	2.7	180691	2	AC123266	AC123266 Rattus no
1366	46.6	2.7	180823	2	AC095385	AC095385 Rattus no
c1367	46.6	2.7	183519	2	BX000533	BX000533 Mus muscu
c1368	46.6	2.7	183918	10	AC122376	AC122376 Mus muscu
1369	46.6	2.7	184879	2	AC139470	AC139470 Homo sapi
c1370	46.6	2.7	187458	2	AC116882	AC116882 Mus muscu
1371	46.6	2.7	189616	10	AC124480	AC124480 Mus muscu
c1372	46.6	2.7	190290	2	AC102381	AC102381 Mus muscu
1373	46.6	2.7	192439	2	AC101790	AC101790 Mus muscu
c1374	46.6	2.7	194719	2	AC118423	AC118423 Rattus no
c1375	46.6	2.7	195020	2	AC116762	AC116762 Mus muscu
c1376	46.6	2.7	195384	10	AC112149	AC112149 Mus muscu
c1377	46.6	2.7	195519	10	AL672297	AL672297 Mouse DNA
c1378	46.6	2.7	198721	10	AC123844	AC123844 Mus muscu
1379	46.6	2.7	198813	10	AC146616	AC146616 Mus muscu
1380	46.6	2.7	200559	2	AC123506	AC123506 Rattus no
c1381	46.6	2.7	203288	2	AC134811	AC134811 Rattus no
c1382	46.6	2.7	206373	10	AC147565	AC147565 Mus muscu
c1383	46.6	2.7	207026	2	BX927300	BX927300 Danio rer
1384	46.6	2.7	209656	2	AC124665	AC124665 Mus muscu
c1385	46.6	2.7	209782	10	AL603905	AL603905 Mouse DNA
c1386	46.6	2.7	212079	2	AC134605	AC134605 Mus muscu
1387	46.6	2.7	213090	10	AL691427	AL691427 Mouse DNA
c1388	46.6	2.7	213124	2	AC117157	AC117157 Rattus no
c1389	46.6	2.7	214712	10	AC126932	AC126932 Mus muscu
1390	46.6	2.7	215119	2	AC098082	AC098082 Rattus no
1391	46.6	2.7	216036	10	AC117118	AC117118 Rattus no
c1392	46.6	2.7	216615	2	AC128550	AC128550 Rattus no
c1393	46.6	2.7	217434	2	AC133239	AC133239 Rattus no
1394	46.6	2.7	218835	2	AC128468	AC128468 Rattus no
1395	46.6	2.7	219340	10	AL844881	AL844881 Mouse DNA
c1396	46.6	2.7	220669	2	AC123017	AC123017 Rattus no
1397	46.6	2.7	221071	2	AC138221	AC138221 Mus muscu
c1398	46.6	2.7	223152	2	AC114994	AC114994 Mus muscu
1399	46.6	2.7	227842	2	AC123257	AC123257 Rattus no
c1400	46.6	2.7	229563	10	AC024957	AC024957 Mus muscu
c1401	46.6	2.7	230082	2	AC110303	AC110303 Rattus no
1402	46.6	2.7	230877	2	AC105583	AC105583 Rattus no
c1403	46.6	2.7	231311	2	AC132966	AC132966 Rattus no
c1404	46.6	2.7	234158	10	AC124201	AC124201 Mus muscu
1405	46.6	2.7	234398	2	AC122223	AC122223 Mus muscu
1406	46.6	2.7	234897	2	AC130527	AC130527 Mus muscu

c1407	46.6	2.7	236244	10	AC121481	AC121481 Rattus no
1408	46.6	2.7	237032	2	AC132519	AC132519 Rattus no
c1409	46.6	2.7	237720	2	AC094774	AC094774 Rattus no
c1410	46.6	2.7	238675	2	AC095962	AC095962 Rattus no
1411	46.6	2.7	239671	2	AC095570	AC095570 Rattus no
1412	46.6	2.7	243351	2	AC119616	AC119616 Rattus no
1413	46.6	2.7	243487	2	AC094582	AC094582 Rattus no
c1414	46.6	2.7	249412	2	AC095097	AC095097 Rattus no
1415	46.6	2.7	249793	2	AC117104	AC117104 Rattus no
c1416	46.6	2.7	251960	2	AC107279	AC107279 Rattus no
c1417	46.6	2.7	252851	2	AC135094	AC135094 Rattus no
c1418	46.6	2.7	255036	10	AC118206	AC118206 Mus muscu
1419	46.6	2.7	257760	2	AC126638	AC126638 Rattus no
c1420	46.6	2.7	258158	2	BX957297	BX957297 Danio rer
c1421	46.6	2.7	258357	2	AC095993	AC095993 Rattus no
c1422	46.6	2.7	264461	2	AC113717	AC113717 Rattus no
1423	46.6	2.7	265982	2	AC117115	AC117115 Rattus no
1424	46.6	2.7	267290	2	AC098041	AC098041 Rattus no
1425	46.6	2.7	267357	2	AC115424	AC115424 Rattus no
1426	46.6	2.7	270086	2	AC128132	AC128132 Rattus no
1427	46.6	2.7	272630	2	AC094183	AC094183 Rattus no
c1428	46.6	2.7	275900	2	AC123150	AC123150 Rattus no
c1429	46.4	2.7	657	11	AF343846	AF343846 Oryza sat
1430	46.4	2.7	2043	10	RATQLIKEB	L16013 Rattus norv
1431	46.4	2.7	2863	10	RNTHY1G	X03152 Rattus norv
1432	46.4	2.7	2863	10	RNTHYCSG	X02002 Rat thy-1 g
1433	46.4	2.7	4131	5	AY070261	AY070261 Danio rer
c1434	46.4	2.7	6800	10	MUSIGMD	K02138 Mus musculu
1435	46.4	2.7	37719	10	BX294108	BX294108 Mouse DNA
1436	46.4	2.7	56013	10	AL773581	AL773581 Mouse DNA
1437	46.4	2.7	69446	2	AC137105	AC137105 Mus muscu
1438	46.4	2.7	73503	10	AL645603	AL645603 Mouse DNA
c1439	46.4	2.7	77999	5	BX510353	BX510353 Zebrafish
c1440	46.4	2.7	98792	10	AL844517	AL844517 Mouse DNA
c1441	46.4	2.7	105726	10	AF037352	AF037352 Mus muscu
1442	46.4	2.7	110000	2	AC095556_3	Continuation (4 of
c1443	46.4	2.7	110000	2	AC098243_2	Continuation (3 of
c1444	46.4	2.7	110000	2	AC112473_1	Continuation (2 of
1445	46.4	2.7	110000	2	AC026388_1	Continuation (2 of
c1446	46.4	2.7	119555	9	BX004827	BX004827 Human DNA
c1447	46.4	2.7	123943	10	AL592547	AL592547 Mouse DNA
1448	46.4	2.7	140266	10	AC124406	AC124406 Mus muscu
c1449	46.4	2.7	148100	2	AC102683	AC102683 Mus muscu
1450	46.4	2.7	154907	2	AC116793	AC116793 Mus muscu
c1451	46.4	2.7	155221	2	AC145688	AC145688 Pan trogl
c1452	46.4	2.7	157494	10	AL606512	AL606512 Mouse DNA
1453	46.4	2.7	158740	10	AC133497	AC133497 Mus muscu
c1454	46.4	2.7	161787	10	AL645484	AL645484 Mouse DNA
c1455	46.4	2.7	167409	10	AC121982	AC121982 Mus muscu
1456	46.4	2.7	167899	2	AC149965	AC149965 Strongylo
c1457	46.4	2.7	168404	2	AC103366	AC103366 Mus muscu
c1458	46.4	2.7	169623	2	AC120645	AC120645 Rattus no
1459	46.4	2.7	170826	2	AC110902	AC110902 Mus muscu
1460	46.4	2.7	171209	10	AC132622	AC132622 Mus muscu
1461	46.4	2.7	173924	10	AC133496	AC133496 Mus muscu
1462	46.4	2.7	174507	10	AC132955	AC132955 Mus muscu
1463	46.4	2.7	174711	9	AC026639	AC026639 Homo sapi
c1464	46.4	2.7	176731	2	AC137555	AC137555 Mus muscu
1465	46.4	2.7	178416	10	AC140840	AC140840 Mus muscu
c1466	46.4	2.7	178446	10	AC124488	AC124488 Mus muscu
c1467	46.4	2.7	179453	10	AC119893	AC119893 Mus muscu
c1468	46.4	2.7	181034	2	AC135486	AC135486 Rattus no
c1469	46.4	2.7	181136	2	AC132839	AC132839 Mus muscu
1470	46.4	2.7	181548	10	AC116326	AC116326 Mus muscu
c1471	46.4	2.7	181603	2	AC119873	AC119873 Mus muscu
1472	46.4	2.7	181895	2	AC117068	AC117068 Rattus no
c1473	46.4	2.7	182122	2	AC104194	AC104194 Mus muscu
1474	46.4	2.7	187751	10	AC127690	AC127690 Mus muscu
c1475	46.4	2.7	188514	10	AC132374	AC132374 Mus muscu
1476	46.4	2.7	190017	2	AC107782	AC107782 Mus muscu
1477	46.4	2.7	191809	10	AC117615	AC117615 Mus muscu
1478	46.4	2.7	194185	10	BX470110	BX470110 Mouse DNA
1479	46.4	2.7	194609	2	AC013775	AC013775 Mus muscu
c1480	46.4	2.7	197448	2	AC129841	AC129841 Rattus no
c1481	46.4	2.7	199946	10	AC105071	AC105071 Mus muscu
c1482	46.4	2.7	199963	2	AC115782	AC115782 Mus muscu
1483	46.4	2.7	201381	2	AC110394	AC110394 Rattus no
c1484	46.4	2.7	202551	10	AL954710	AL954710 Mouse DNA
1485	46.4	2.7	203891	10	AC122395	AC122395 Mus muscu
c1486	46.4	2.7	203946	2	AC069465	AC069465 Mus muscu
1487	46.4	2.7	208023	2	AC115493	AC115493 Rattus no
c1488	46.4	2.7	209230	10	AC121574	AC121574 Mus muscu
1489	46.4	2.7	210145	2	AC114314	AC114314 Homo sapi
c1490	46.4	2.7	210911	2	AC115265	AC115265 Rattus no
1491	46.4	2.7	212129	2	AC139817	AC139817 Homo sapi
1492	46.4	2.7	212445	10	AC108419	AC108419 Mus muscu
1493	46.4	2.7	212792	2	AC109173	AC109173 Mus muscu
c1494	46.4	2.7	213521	2	AC137161	AC137161 Rattus no
c1495	46.4	2.7	213593	2	AC131402	AC131402 Rattus no
1496	46.4	2.7	215351	10	AL844212	AL844212 Mouse DNA
1497	46.4	2.7	215731	2	AC136554	AC136554 Rattus no
c1498	46.4	2.7	215876	2	AC108551	AC108551 Rattus no
c1499	46.4	2.7	217352	10	AL645784	AL645784 Mouse DNA
c1500	46.4	2.7	218632	2	AC138335	AC138335 Mus muscu

ALIGNMENTS

```
RESULT 1
AX092342
LOCUS       AX092342                1701 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 73 from Patent WO0116318.
ACCESSION   AX092342
VERSION     AX092342.1  GI:13444485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0116318-A 73 08-MAR-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1701
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     unsure          1528
                     /note="unknown base"
ORIGIN

  Query Match           99.9%;  Score 1700;  DB 6;  Length 1701;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1701;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
```

```
Qy       241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
Db       241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300

Qy       301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
Db       301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360

Qy       361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
Db       361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420

Qy       421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
Db       421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480

Qy       481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
Db       481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540

Qy       541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
Db       541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600

Qy       601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
Db       601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660

Qy       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
Db       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720

Qy       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
Db       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780

Qy       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
Db       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840

Qy       841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
Db       841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900

Qy       901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
Db       901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960

Qy       961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
Db       961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020

Qy      1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
Db      1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080

Qy      1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
Db      1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140

Qy      1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
Db      1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200

Qy      1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
Db      1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260

Qy      1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
Db      1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320

Qy      1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
Db      1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380

Qy      1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
Db      1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440

Qy      1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
Db      1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500

Qy      1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
Db      1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560

Qy      1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
Db      1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620

Qy      1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
Db      1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680

Qy      1681 GAAATTAAAGTTTCTGACTTT 1701
Db      1681 GAAATTAAAGTTTCTGACTTT 1701
```

RESULT 2
AX376200
LOCUS AX376200 1701 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 267 from Patent WO0168848.
ACCESSION AX376200
VERSION AX376200.1 GI:19170492
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 267 20-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1701
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 99.9%; Score 1700; DB 6; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
Db         1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60

Qy        61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
Db        61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120

Qy       121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
Db       121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180

Qy       181 TCTCTCTCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
```

```
Db        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
```

```
Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
Qy       1681 GAAATTAAAGTTTCTGACTTT 1701
              |||||||||||||||||||||
Db       1681 GAAATTAAAGTTTCTGACTTT 1701
```

RESULT 3
AX697354
LOCUS AX697354 1701 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 422 from Patent WO0078961.
ACCESSION AX697354
VERSION AX697354.1 GI:29498488
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0078961-A 422 28-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1701
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 99.9%; Score 1700; DB 6; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
```

```
Qy       181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
Db       181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240

Qy       241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
Db       241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300

Qy       301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
Db       301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360

Qy       361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
Db       361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420

Qy       421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
Db       421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480

Qy       481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
Db       481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540

Qy       541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
Db       541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600

Qy       601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
Db       601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660

Qy       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
Db       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720

Qy       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
Db       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780

Qy       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
Db       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840

Qy       841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
Db       841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900

Qy       901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
Db       901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960

Qy       961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
Db       961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020

Qy      1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
Db      1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080

Qy      1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
Db      1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140

Qy      1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
Db      1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200

Qy      1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
Db      1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260

Qy      1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
Db      1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320

Qy      1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
Db      1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380

Qy      1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
Db      1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440

Qy      1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
Db      1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500

Qy      1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
Db      1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560

Qy      1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
Db      1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620

Qy      1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
Db      1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680

Qy      1681 GAAATTAAAGTTTCTGACTTT 1701
Db      1681 GAAATTAAAGTTTCTGACTTT 1701
```

```
RESULT 4
AY358689
LOCUS       AY358689               1701 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA62812 CA14 (UNQ690) mRNA, complete cds.
ACCESSION   AY358689
VERSION     AY358689.1  GI:37182499
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1701)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1701)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1701
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA62812"
     gene            1. .1701
                     /locus_tag="UNQ690"
     CDS             271. .1284
                     /locus_tag="UNQ690"
```

/note="PRO1335"
/codon_start=1
/product="CA14"
/protein_id="AAQ89052.1"
/db_xref="GI:37182500"
/translation="MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNA
QSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRK
YVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVL
GILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTT
PPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFA
SFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKSVVFTSAQAT
TEA"

ORIGIN

Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200

Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440

Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500

Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620

Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680

Qy       1681 GAAATTAAAGTTTCTGACTTT 1701
              |||||||||||||||||||||
Db       1681 GAAATTAAAGTTTCTGACTTT 1701
```

RESULT 5
CQ728278
LOCUS CQ728278 1743 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14212 from Patent WO02068579.
ACCESSION CQ728278
VERSION CQ728278.1 GI:42296681
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 14212 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1743
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.8%;  Score 1698.4;  DB 6;  Length 1743;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1699;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 100

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 160

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 220

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 280

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 340

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 400

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 460

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 520

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 580

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 640

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 700

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 760

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 820

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 880

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 940

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 1000

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1060

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1120

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1180

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1240

Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1300

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1360

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1420

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1421 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1480

Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1481 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1540

Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1541 GAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1600

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1660

Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1720

Qy       1681 GAAATTAAAGTTTCTGACTTT 1701
              |||||||||||||||||||||
Db       1721 GAAATTAAAGTTTCTGACTTT 1741


RESULT 6
AB025904
LOCUS       AB025904               1757 bp    mRNA    linear   PRI 31-OCT-1999
DEFINITION  Homo sapiens mRNA for carbonic anhydrase 14, complete cds.
ACCESSION   AB025904
VERSION     AB025904.1  GI:6009639
KEYWORDS    carbonic anhydrase XIV; carbonic anhydrase 14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (sites)
  AUTHORS   Fujikawa-Adachi,K., Nishimori,I., Taguchi,T. and Onishi,S.
  TITLE     Human carbonic anhydrase XIV (CA14): cDNA cloning, mRNA expression,
            and mapping to chromosome 1
  JOURNAL   Genomics 61 (1), 74-81 (1999)
  MEDLINE   99443874
   PUBMED   10512682
REFERENCE   2  (bases 1 to 1757)
  AUTHORS   Fujikawa-Adachi,K. and Nishimori,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1999) Kiyomi Fujikawa-Adachi, Kochi Medical
            School, First Department of Internal Medicine; Kohasu, Nankoku,
            Kochi 783-8505, Japan (E-mail:adachik@kochi-ms.ac.jp,
            Tel:81-888-80-2338, Fax:81-888-80-2338)
FEATURES             Location/Qualifiers
     source          1. .1757
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q21"
     CDS             310. .1323
                     /codon_start=1
                     /product="carbonic anhydrase 14"
                     /protein_id="BAA85002.1"
                     /db_xref="GI:6009640"
                     /translation="MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNA
                     QSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRK
                     YVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVL
                     GILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTT
                     PPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFA
                     SFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKSVVFTSAQAT
                     TEA"
ORIGIN

  Query Match           99.8%;  Score 1696.8;  DB 9;  Length 1757;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1698;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 99

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 159

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GACAGCAAGAAAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 219

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 279

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 339

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 399

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 459

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 519

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 579

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 639

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 699

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 759

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 819

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 879

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 939

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 999

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1059

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1119

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1179

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1239

Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1299

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1359

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1419

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1420 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1479

Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1480 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1539

Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1540 GAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1599

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1600 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1659
```

```
Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1660 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1719

Qy       1681 GAAATTAAAGTTTCTGACTTT 1701
             |||||||||||||||||||||
Db       1720 GAAATTAAAGTTTCTGACTTT 1740


RESULT 7
CQ782700
LOCUS       CQ782700                1771 bp    DNA     linear   PAT 17-MAR-2004
DEFINITION  Sequence 2840 from Patent EP1396543.
ACCESSION   CQ782700
VERSION     CQ782700.1  GI:45502643
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primers for synthesizing full length cDNA clones and their use
  JOURNAL   Patent: EP 1396543-A 2840 10-MAR-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .1771
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             356. .1369
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAF85934.1"
                     /db_xref="GI:45502644"
                     /translation="MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNA
                     QSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRK
                     YVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVL
                     GILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTT
                     PPCYQSVLWTAFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFA
                     SFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKSVVFTSAQAT
                     TEA"
ORIGIN

  Query Match             98.8%;  Score 1680.2;  DB 6;  Length 1771;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1682;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 145

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 205

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 265

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 325

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 385

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 445

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 505

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 565

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 625

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 685

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        686 CACTGGGGTCAGAAAGGATCCCCAGGTGGGTCAGAACACCAGATCAACAGTGAAGCCACA 745

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 805

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 865

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 925

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 985

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        986 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGCTTTT 1045

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1105

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1165

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1225

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1285

Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1345

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1405

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1465

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1466 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1525
```

```
Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1585

Qy       1501 GAAATCGCTGTGTTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1586 GAAATCGCTGTGTTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1645

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1705

Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1765

Qy       1681 GAAATT 1686
             ||||||
Db       1766 GAAATT 1771


RESULT 8
BD127270
LOCUS       BD127270               1771 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD127270
VERSION     BD127270.1  GI:23222215
KEYWORDS    JP 2002017375-A/2701.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1771)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 2701 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017375-A/2701
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                    Location/Qualifiers
            FT   CDS             (356). .(1366).
FEATURES            Location/Qualifiers
     source         1. .1771
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN

  Query Match           98.8%;  Score 1680.2;  DB 6;  Length 1771;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1682;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 145

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        146 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 205

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 265

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 TCTCTCTCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 325

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 385

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 445

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 505

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 565

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 625

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 685

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        686 CACTGGGGTCAGAAAGGATCCCCAGGTGGGTCAGAACACCAGATCAACAGTGAAGCCACA 745

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 805

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 865

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 925

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 985

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        986 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGCTTTT 1045

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1105

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1165

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1225

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1285
```

```
Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1345

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1405

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1465

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1466 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1525

Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1585

Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1586 GAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1645

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1705

Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1765

Qy       1681 GAAATT 1686
             ||||||
Db       1766 GAAATT 1771
```

RESULT 9
AK074765

```
LOCUS       AK074765                1771 bp    mRNA    linear   PRI 03-SEP-2002
DEFINITION  Homo sapiens cDNA FLJ90284 fis, clone NT2RP1000613, weakly similar
            to CARBONIC ANHYDRASE VI (EC 4.2.1.1).
ACCESSION   AK074765
VERSION     AK074765.1  GI:22760421
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
            Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
            Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
            Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
            Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
            Ninomiya,K.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1771)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction:
            Institute of Medical Science, University of Tokyo, Laboratory of
            Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
            sequencing and clone selection: Helix Research Institute (supported
            by Japan Key Technology Center etc.).
FEATURES            Location/Qualifiers
     source         1. .1771
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="NT2RP1000613"
                    /cell_line="NT2"
                    /cell_type="teratocarcinoma"
                    /clone_lib="NT2RP1"
                    /note="cloning vector: pUC19FL3~mRNA from NT2 neuronal
                    precursor cells after 48-hours retinoic acid (RA)
                    induction"
     CDS            356. .1369
                    /note="unnamed protein product"
                    /codon_start=1
                    /protein_id="BAC11191.1"
                    /db_xref="GI:22760422"
                    /translation="MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNA
                    QSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRK
                    YVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVL
                    GILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTT
                    PPCYQSVLWTAFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFA
                    SFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKSVVFTSAQAT
                    TEA"
ORIGIN
```

```
  Query Match             98.8%;  Score 1680.2;  DB 9;  Length 1771;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1682;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 145

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 205

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 265

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 325

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 385

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 445

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 505

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 565

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 625

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 685

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        686 CACTGGGGTCAGAAAGGATCCCCAGGTGGGTCAGAACACCAGATCAACAGTGAAGCCACA 745
```

```
Qy       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       746 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 805

Qy       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       806 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 865

Qy       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       866 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 925

Qy       841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       926 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 985

Qy       901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       986 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGCTTTT 1045

Qy       961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1046 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1105

Qy      1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1106 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1165

Qy      1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1166 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1225

Qy      1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1226 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1285

Qy      1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1286 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1345

Qy      1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1346 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1405

Qy      1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1406 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1465

Qy      1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      1466 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1525

Qy      1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1526 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1585

Qy      1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      1586 GAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1645

Qy      1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1646 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1705

Qy      1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1706 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1765

Qy      1681 GAAATT 1686
            ||||||
Db      1766 GAAATT 1771
```

```
RESULT 10
BC034412
LOCUS       BC034412               1767 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens carbonic anhydrase XIV, mRNA (cDNA clone MGC:34392
            IMAGE:5175251), complete cds.
ACCESSION   BC034412
VERSION     BC034412.1  GI:21706778
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1767)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1767)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 51 Row: l Column: 20
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6912283.
FEATURES             Location/Qualifiers
     source          1. .1767
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:34392 IMAGE:5175251"
                     /tissue_type="Brain, Lung, Testis, adult, pooled whole"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .1767
```

```
                     /gene="CA14"
                     /db_xref="LocusID:23632"
                     /db_xref="MIM:604832"
     CDS             241. .1254
                     /gene="CA14"
                     /codon_start=1
                     /product="carbonic anhydrase XIV, precursor"
                     /protein_id="AAH34412.1"
                     /db_xref="GI:21706779"
                     /db_xref="LocusID:23632"
                     /db_xref="MIM:604832"
                     /translation="MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNA
                     QSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRK
                     YVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVL
                     GILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTT
                     PPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFA
                     SFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKSVVFTSAQAT
                     TEA"
ORIGIN

  Query Match            98.1%;  Score 1668.4;  DB 9;  Length 1767;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1669;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         31 CAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACA 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACA 60

Qy         91 CCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACT 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACT 120

Qy        151 CACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCT 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCT 180

Qy        211 GCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACT 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACT 240

Qy        271 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 300

Qy        331 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 360

Qy        391 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 420

Qy        451 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 480

Qy        511 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 540

Qy        571 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 600

Qy        631 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 660

Qy        691 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 720

Qy        751 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 780

Qy        811 TTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAG 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAG 840

Qy        871 CTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT 900

Qy        931 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAG 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAG 960

Qy        991 CTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTA 1050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTA 1020

Qy       1051 CAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAA 1110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAA 1080

Qy       1111 GCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGC 1170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGC 1140

Qy       1171 TGTCTCTGCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTG 1230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGTCTCTGCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTG 1200

Qy       1231 GAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCT 1290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCT 1260

Qy       1291 TCTCAGATACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATG 1350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TCTCAGATACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATG 1320

Qy       1351 GGGTGTAGGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTG 1410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGGTGTAGGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTG 1380

Qy       1411 GACATCTCTTAGAGAGGAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTC 1470
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GACATCTCCTAGAGAGGAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTC 1440

Qy       1471 AGCCTCTCCAAACATGTAGGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCA 1530
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1441 AGCCTCTCCAAACATGTAGGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGAACA 1500

Qy       1531 AACTCTGTTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACT 1590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AACTCTGTTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACT 1560

Qy       1591 TTTATGGCCCTTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTT 1650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTTATGGCCCTTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTT 1620

Qy       1651 GAAGTTGTATATTTTTGATCAATATATTTGGAAATTAAAGTTTCTGACTTT 1701
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAAGTTGTATATTTTTGATCAATATATTTGGAAATTAAAGTTTCTGACTTT 1671


RESULT 11
AX574386
LOCUS       AX574386               1657 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 19 from Patent WO02064795.
ACCESSION   AX574386
VERSION     AX574386.1  GI:27551721
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sanjanwala,M.M., Lu,Y., Lee,E.A., Hafalia,A.J., Warren,B.A.,
            Baughn,M.R., Tang,T.Y., Yue,H., Yao,M.G., Lee,S., Thornton,M.,
            Walia,N.K., Xu,Y., Tran,U.K., Lal,P.G., Lu,D.A., Swarnaker,A.,
            Jones,K.A. and Ring,H.Z.
  TITLE     Enzymes
  JOURNAL   Patent: WO 02064795-A 19 22-AUG-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1657
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 2706884CB1"
ORIGIN

  Query Match             87.9%;  Score 1496;  DB 6;  Length 1657;
  Best Local Similarity   94.5%;  Pred. No. 0;
  Matches 1607;  Conservative    0;  Mismatches    6;  Indels   88;  Gaps    2;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 95

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 155

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 215

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 275

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 335

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 395

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 455

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 515

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 575

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 635

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        636 CACTGGGGTCAGAAAGGATCCCCAGGTGGGTCAGAACACCAGATCAACAGTGAAGCCACA 695

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        696 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGCTT 755

Qy        721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 815

Qy        781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 875

Qy        841 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 ACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC 935

Qy        901 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 CGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTT 995

Qy        961 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 TATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCC 1055

Qy       1021 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 ACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAAT 1115

Qy       1081 CAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATG 1140
              |||||||||||||||||||||||||||||   ||||||||||||||||||
Db       1116 CAGCGCATGGTCTTTGCTTCTTTCATCCA---AGGATCCTCGTATACCACA--------- 1163

Qy       1141 CTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTC 1200

Db       1164 ------------------------------------------------------------ 1163

Qy       1201 ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1260
                                    |||||||||||| ||||||||||||||||||||||||||||
Db       1164 ----------------GGAAGAAGAGGCTTGAAAACCGAAAGAGTGTGGTCTTCACCTCA 1207

Qy       1261 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCC 1267

Qy       1321 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 CTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAG 1327

Qy       1381 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGC 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 GAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGGC 1387

Qy       1441 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 TGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG 1447

Qy       1501 GAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1560
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1448 GAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGGG 1507

Qy       1561 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 ATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGG 1567

Qy       1621 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTG 1627

Qy       1681 GAAATTAAAGTTTCTGACTTT 1701
              |||||||||||||||||||||
Db       1628 GAAATTAAAGTTTCTGACTTT 1648


RESULT 12
AX593027
LOCUS       AX593027               1673 bp    DNA     linear   PAT 30-AUG-2003
DEFINITION  Sequence 4 from Patent WO0073509.
ACCESSION   AX593027
VERSION     AX593027.1  GI:28374491
KEYWORDS    .
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
            Bratcher,S.R., Dufour,G.E., Cohen,H.J., Rosen,B.H., Chalup,M.S.,
            Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B., Panzer,S.R.,
            Roseberry,A.M., Wright,R.J. and Daniels,S.E.
  TITLE     Molecules for diagnostics and therapeutics
  JOURNAL   Patent: WO 0073509-A 4 07-DEC-2000;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1673
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 277927.2"
ORIGIN

  Query Match             87.4%;  Score 1486.6;  DB 6;  Length 1673;
  Best Local Similarity   94.5%;  Pred. No. 0;
  Matches 1608;  Conservative    0;  Mismatches    5;  Indels   89;  Gaps    3;

Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db.        36 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 95

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 155

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 215

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 275

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 335

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        336 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAAGGCCCACATGGTCAG 395

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 455

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 515

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 575

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 635

Qy        601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        636 CACTGGGGTCAGAAAGGATCCCCATGTGGGTCAGAACACCAGATCAACAGTGAAGCCACA 695

Qy        661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGC- 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        696 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 755

Qy        720 TGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAA 815

Qy        780 GAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAA 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 GAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAA 875

Qy        840 GACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 GACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTT 935

Qy        900 CCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 CCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTT 995

Qy        960 TTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 TTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTC 1055

Qy       1020 CACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 CACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1115

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
              ||||||||||||||||||||||||||||||   ||||||||||||||||||
Db       1116 TCAGCGCATGGTCTTTGCTTCTTTCATCCA---AGGATCCTCGTATACCACA-------- 1164

Qy       1140 GCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTT 1199

Db       1165 ---------------------------------------------------------- 1164

Qy       1200 CATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTC 1259
                              ||||||||||||||||||||||||||||||||||||||||||||
Db       1165 ----------------GGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTC 1207

Qy       1260 AGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTC 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 AGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTC 1267

Qy       1320 CCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTA 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 CCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTA 1327

Qy       1380 GGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGG 1439
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1328 GGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAGG 1387

Qy       1440 CTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGA 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1388 CTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGA 1447

Qy       1500 GGAAATCGCTGTGTTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTGG 1559
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1448 GGAAATCGCTGTGTTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTGG 1507

Qy       1560 GATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCG 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 GATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCG 1567

Qy       1620 GGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTT 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTT 1627

Qy       1680 GGAAATTAAAGTTTCTGACTTT 1701
              |||||||||||||||||||||||
Db       1628 GGAAATTAAAGTTTCTGACTTT 1649


RESULT 13
BD205641
LOCUS       BD205641               1537 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  97 human secreted proteins.
ACCESSION   BD205641
```

```
VERSION     BD205641.1  GI:33015411
KEYWORDS    JP 2002533058-A/18.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1537)
  AUTHORS   Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
            Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
            Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
  TITLE     97 human secreted proteins
  JOURNAL   Patent: JP 2002533058-A 18 08-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533058-A/18
            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
            12-MAY-1998 US    60/085105,12-MAY-1998 US    60/085180 PR
            18-MAY-1998 US    60/085927,18-MAY-1998 US    60/085906 PR
            18-MAY-1998 US    60/085924,18-MAY-1998 US    60/085922 PR
            18-MAY-1998 US    60/085923,18-MAY-1998 US    60/085921 PR
            18-MAY-1998 US    60/085925,18-MAY-1998 US    60/085928 PR
            18-MAY-1998 US    60/085920
            PI   STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
            CC   97 human secreted proteins.
            FH   Key             Location/Qualifiers
            FT   source          1. .1537
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .1537
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             70.6%;  Score 1201.4;  DB 6;  Length 1537;
  Best Local Similarity   86.4%;  Pred. No. 0;
  Matches 1437;  Conservative    0;  Mismatches    2;  Indels  225;  Gaps    1;

Qy         38 GCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATC 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATC 125

Qy         98 CCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCA 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCA 185

Qy        158 GGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTC 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTC 245

Qy        218 CTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGT 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGT 305

Qy        278 TCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGA 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGA 365

Qy        338 CGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACA 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACA 425

Qy        398 ATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTG 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTG 485

Qy        458 CTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATG 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATG 545

Qy        518 GCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAAT 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAAT 605

Qy        578 ATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAAC 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAAC 665

Qy        638 ACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATT 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATT 725

Qy        698 CCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCC 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCC 785

Qy        758 TAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATG 817
              ||||||
Db        786 TAATTG---------------------------------------------------- 791

Qy        818 AAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCC 877

Db        792 ---------------------------------------------------------- 791

Qy        878 CCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACC 937

Db        792 ---------------------------------------------------------- 791

Qy        938 AGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAA 997
                                                                 ||||||||
Db        792 ----------------------------------------------------AGCTGGAAA 800

Qy        998 AGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACT 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 AGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACT 860

Qy       1058 ACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGAT 1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 ACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGAT 920

Qy       1118 CCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCT 1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 CCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCT 980

Qy       1178 GCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACC 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 GCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACC 1040

Qy       1238 GAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGA 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1041 GAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGA 1100

Qy       1298 TACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTA 1357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1101 TACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTA 1160

Qy       1358 GGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCT 1417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1161 GGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCT 1220

Qy       1418 CTTAGAGAGGAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCT 1477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1221 CCTAGAGAGGAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCT 1280
```

```
Qy       1478 CCAAACATGTAGGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTG 1537
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1281 CCAAACATGTAGGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGAACAAACTCTG 1340

Qy       1538 TTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGG 1597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1341 TTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGG 1400

Qy       1598 CCCTTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTG 1657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1401 CCCTTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTG 1460

Qy       1658 TATATTTTTGATCAATATATTTGGAAATTAAAGTTTCTGACTTT 1701
             |||||||||||||||||||||||||||||||||||||||||||||
Db       1461 TATATTTTTGATCAATATATTTGGAAATTAAAGTTTCTGACTTT 1504
```

RESULT 14
AL451074
LOCUS AL451074 188217 bp DNA linear PRI 22-AUG-2001
DEFINITION Human DNA sequence from clone RP11-466F5 on chromosome 1, complete sequence.
ACCESSION AL451074
VERSION AL451074.13 GI:15384634
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 188217)
AUTHORS Martin,S.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Aug 31, 2001 this sequence version replaced gi:13872396.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-466F5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-466F5 The true left end of clone RP11-525G13 is at 121279 in this sequence. The true right end of clone RP11-306I1 is at 86674 in this sequence.
FEATURES Location/Qualifiers
source 1. .188217
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-466F5"
/clone_lib="RPCI-11.2"
misc_feature 75412. .75457
/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
misc_feature 75559. .75579
/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
ORIGIN

Query Match 49.5%; Score 842.6; DB 9; Length 188217;
Best Local Similarity 71.0%; Pred. No. 1.8e-263;
Matches 1423; Conservative 0; Mismatches 250; Indels 331; Gaps 10;

```
Qy          1 GAGACTGCAGAGGGAGATAA-AGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGG 59
              |||||||| ||||  |  || |||||| |   | ||| ||||||||||||||| |||||
Db      60903 GAGACTGCCGAGGAGGTGAAGAGAGAGGGCTGAGAGAAGCAGCAAGAGATTTGTTCTGGG 60962

Qy         60 GATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAG 119
              || |||||||||| | |||||||||||| | | |||||| ||||| ||||||||||||
Db      60963 GACCCAGAAACCCACGGTACCCTACTGAAAATCAAATCCCTTGGAAACCCACAGAGACAG 61022

Qy        120 AGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCT 179
                ||  || ||    | ||| |   |    || |     | ||| ||| ||  ||||||
Db      61023 CAGCAAAAAAAGGGATAAAGACACTCAACACCAGGAACTCACCTCTCTCTCTGCCTCTCT 61082

Qy        180 CTCTCTCTCACTC----------------------------------------CTCCCTCCCT 202
              | |  |||| |||                                        |||||   ||
Db      61083 CCCCGTCTCTCTCTCTCTGCCTCTCTCCCCGTCTCTCTCTCTCTGCCTCTCTCCCCGTCT 61142

Qy        203 CTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCT 262
              |||||||||||||| ||||||| |||||||  |||| ||||||||||||||  |||||||||
Db      61143 CTCTCTCTGCCTGCCCTAGTCATCTAGTCTCCAAACTCCCAGTCCCCTGTGCCCCTTCCT 61202

Qy        263 GGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATG 322
              |||| || |||||||||| |  |||||||| |||||||||||||||||||||||||||| |
Db      61203 GGGATACCATGTTGTTCTTCATCCTCCTGCTAGAGGTGATTTGGATCCTGGCTGCAGACG 61262

Qy        323 GGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA--TTGGCCAGCCTCTTA 380
              |||||||||||||| |||||| |||||||| |||||||||   |||||||||| |||
Db      61263 AGGGTCAACACTGGACATATGAGTGCCCACATAGTCAGGACCACTGTGGCCAGCCTTTTA 61322

Qy        381 CCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATT 440
              |||||||||||||||||| | ||||| ||| |||||| | ||||||||||||||||| |
Db      61323 CCCTGAGTGTGGAAACAATACACAGTCCCCCTTCGATATCCGGACAGACAGTGTGACAAT 61382

Qy        441 TGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTT 500
              ||||||| |  || |||||||| |||||||| |||||||||| ||||||||| ||||||||
Db      61383 TGACCCTTAGATGACTGCTCTACAGCCCCATGGATATGACCGGCCTGGCACTGAGCCTTT 61442

Qy        501 GGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGG 560
              |||||||||| ||| || ||||||| ||||| |||||||||||||||||||||||| ||
Db      61443 AGACCTGCACAAGAATAGCTACACAGTACAACTGTCTCTGCCCTCTACCCTGTATCTAGG 61502

Qy        561 TGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC 620
              ||||||| || |||||||||||||| ||||||| |||||||||||||||||  | ||||
Db      61503 TGGACTTTCCAGAAAATATGTAGCTACCCAGCTACACCTGCACTGGGGTCAG-GATGATC 61561

Qy        621 CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGT 680
              ||||||||| |||||||||||||||||||||||||||| |||| ||||||||||  |
Db      61562 CCCAGGGGGCTCAGAACACCAGATCAACAGTGAAGCCACAGTTGCCGAGCTCCACATCAT 61621

Qy        681 ACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCT 740
              || ||||| || |||||||| ||| |||||||||||||| ||| ||||||||||||||||
Db      61622 ACGTTATGGCTGTGATTCCTGTGATAGCTTGAGTGAGGCCGCTCAGAGGCCTCAGGGCCT 61681

Qy        741 GGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATA---------------- 784
              | |||||||||||||||||||||||||||| ||||||||||||||
Db      61682 GACTGTCCTGGGCATCCTAATTGAGGTGAGTGAGACTAAGAATATAGCTTATGCCAGCCT 61741

Qy        785 ------------------------------------------------------------ 784

Db      61742 GGCCAACATGGTGAAACCCCGTCTCTATTAAAAATACAAAAATTAGCTGGGTGTGGTAGT 61801
```

```
Qy        785 ------------------------------------------------------------ 784

Db      61802 GGGCACCTGTAATCCCAGCTTACCCGGGAGACTGAGGTAGGAGAAGAATCACTTGAACCT 61861

Qy        785 ------------------------------------------------------------ 784

Db      61862 GGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTCCAGCCTGGGCAACAGA 61921

Qy        785 ---------------------------------------TAGCTTATGAACACATTCTGA 805
                                                    ||||||||||||||||||||
Db      61922 GCGAGACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAATGTAGCTTATGAACACATTCTGG 61981

Qy        806 GTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAA 865
              ||||||||||||||| ||| |||||||||||||||||||||||||---------------| 
Db      61982 GTCACTTGCATGAAATCAAGCATAAAGATCAGAAGACCTCAGTG---------------A 62026

Qy        866 GAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTC 925
              |||||||||||||| |||||| ||||||| |||||  |||||| ||||||||||||||| 
Db      62027 GAGAGCTGCTCCCCCGACAGCTAGGGCAGTTCTTCCTTTACAATAGCTCGCTCACAACTT 62086

Qy        926 CCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGG 985
              ||||||| ||  |||| |||| ||||||||||||    |  |||| |||||||||||||| 
Db      62087 CCCCTTGTTAGTAGAGGGTGCCCTGGACAGTTTTCAGTCCAAGGGCCCAGATTTCAATGG 62146

Qy        986 AACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTC 1045
              ||| |||||||||||||||| |||||||||||||||||||||| |||||| ||| | | 
Db      62147 AACGGCTGGAAAAGCTTCAGGAGACATTGTTCTCCACAGAAGAGGGGCCCTCCAAG-TCC 62205

Qy       1046 TGGTACAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCA 1105
              || |||||||||| || ||| |||||||||||| |||| ||| |||||||| ||||| 
Db      62206 TGATACAGAACTACTGATCCCCTCAGCCTCTCAACCAGC-AATGACCTTTGCTTTTTTCA 62264

Qy       1106 TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGG 1165
              ||||    ||||||| |||| | |||||||||||||||| || |||||||||||||||| 
Db      62265 TCCAGATGGGATCCTTGTATCCTACAGGTGAAATGCTGAGCCTTGGTGTAGGAATCTTGG 62324

Qy       1166 TTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGA 1225
              |||||| |||||| ||||| |||||  |||  ||||| ||||||| | ||| ||| |||| 
Db      62325 TTGGCTCTCTCTGACTTCTGCTGGCCATTTTCTTCATGGCTAGAAGGCTTCAGAACAAGA 62384

Qy       1226 GGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAA 1285
              |||||||||| |  ||||| |||||| |||||||||||  |||||| |||||||||||||| 
Db      62385 GGCTGGAAAATCAGAAGAGCGTGGTCATCACCTCAGCATGAGCCACCACTGAGGCATAAA 62444

Qy       1286 TTCCTTCTCAGATACCATGGATGTGGATGACTTCCCTTCATGCCTA-------------- 1331
               ||| ||| ||||||| ||||| |||||| |||||| || |||||
Db      62445 CTCCCTCTTAGATACCTTGGATATGGATGCCTTCCCCTCGTGCCTCCAGAGGTGCTTTCC 62504

Qy       1332 -------------------TCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAA 1372
                                 ||||| | |||||||||||||||| |||  |||||| |||
Db      62505 CCTCATGTCTCACCACCCCTCAGGGAACCTCTAAAATGGGGTGCAGGGACTGGCCGGAAT 62564

Qy       1373 CACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGG 1432
              ||||||||||||||| ||   | |||||    |     |   |||||||| |||| 
Db      62565 TACTGTAGGAGTAGTAGGCGCTTCTCCTCTGGAC-----ATCCCCTGCAGAGAGGTATGG 62619

Qy       1433 ACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAG 1492
              ||||||||| |||||| |||||||||| |||||||||||||| ||| ||||||||||||| 
Db      62620 ACCCAGGCTCTCATTCAAGGAAGAACAGCAGAGCCTTCAGCCCCTCAAAACATGTAGGAG 62679

Qy       1493 GAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGA 1552
              || || |||  ||| |||||||||| |||||||  |||||| |||||||||  |||||| 
Db      62680 GAGATCAGGGCATCCCTGTGTTGTTAGTGCAGAGGACAAACTGTGTTTAGTTTTAGGGGA 62739

Qy       1553 AGTTTGGGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATA 1612
              |||||||||| |||||||||||||| |||  ||||| |||||| ||||||||||||||| 
Db      62740 AGTTTGGGATGTACCCCAAAGTCCTCCACCATCTCACCTTTATGTCCCTTTCCCTAGATA 62799

Qy       1613 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAA 1672
              || ||| ||||||| |||||||| |||||||||||||||  ||| |||||||||| |||| 
Db      62800 TATTGCAGGATCTCCCCTTAGGAGAAAGAGTTGCTGTTGGGGTTATATATTTTTGCTCAA 62859

Qy       1673 TATATTTGGAAATTAAAGTTTCTG 1696
              |||||||||| ||||||||||| 
Db      62860 CATATTTGGAAACTAAAGTTTCTG 62883
```

```
RESULT 15
AC064827
LOCUS       AC064827              203959 bp    DNA     linear   HTG 24-AUG-2000
DEFINITION  Homo sapiens chromosome 1 clone RP11-306I1, WORKING DRAFT SEQUENCE,
            46 unordered pieces.
ACCESSION   AC064827
VERSION     AC064827.2  GI:9887807
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 203959)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 203959)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Aug 24, 2000 this sequence version replaced gi:7637352.

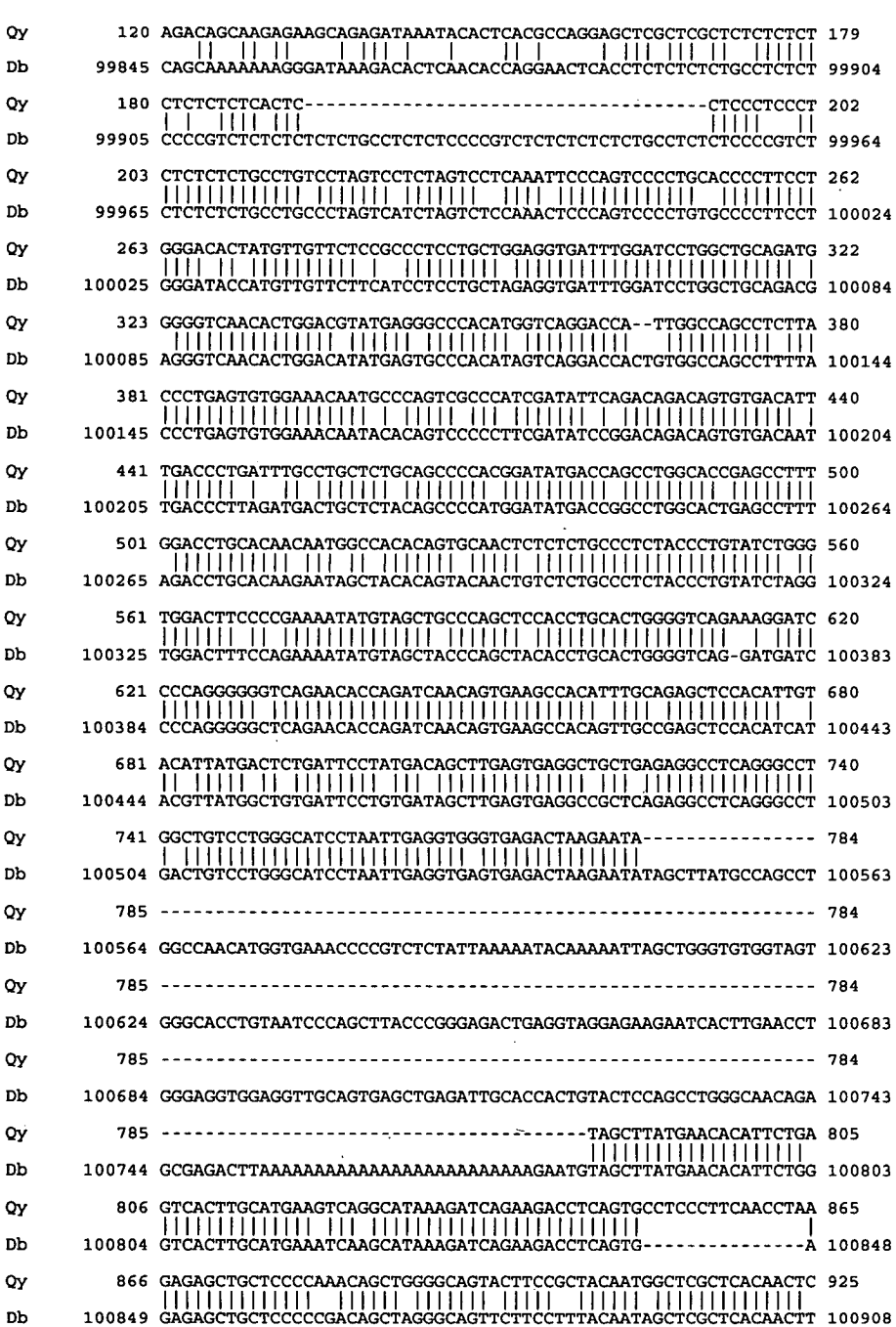
            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0306I01
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 184768 bases at least Q40
            Consensus quality: 189866 bases at least Q30
            Consensus quality: 192333 bases at least Q20
            Insert size: 193000; agarose-fp
            Insert size: 199459; sum-of-contigs
            Quality coverage: 3.45 in Q20 bases; agarose-fp
            Quality coverage: 3.42 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 46 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1438: contig of 1438 bp in length
            *     1439     1538: gap of unknown length
            *     1539     3665: contig of 2127 bp in length
            *     3666     3765: gap of unknown length
            *     3766     6090: contig of 2325 bp in length
            *     6091     6190: gap of unknown length
            *     6191     8063: contig of 1873 bp in length
            *     8064     8163: gap of unknown length
            *     8164     9769: contig of 1606 bp in length
            *     9770     9869: gap of unknown length
            *     9870    12111: contig of 2242 bp in length
            *    12112    12211: gap of unknown length
            *    12212    14650: contig of 2439 bp in length
            *    14651    14750: gap of unknown length
            *    14751    16668: contig of 1918 bp in length
            *    16669    16768: gap of unknown length
```

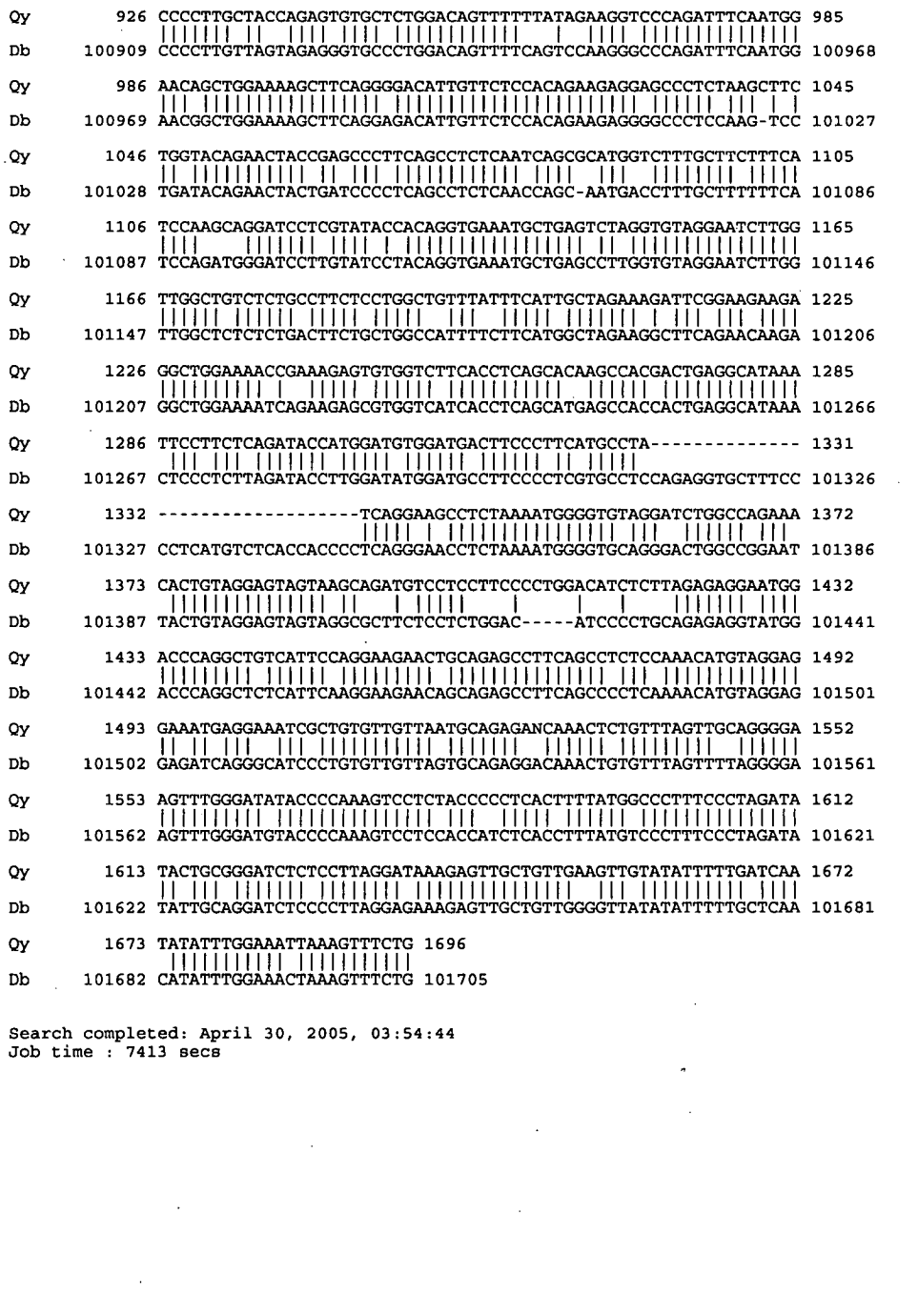
```
*    16769    19004: contig of 2236 bp in length
*    19005    19104: gap of unknown length
*    19105    21792: contig of 2688 bp in length
*    21793    21892: gap of unknown length
*    21893    23341: contig of 1449 bp in length
*    23342    23441: gap of unknown length
*    23442    26485: contig of 3044 bp in length
*    26486    26585: gap of unknown length
*    26586    28702: contig of 2117 bp in length
*    28703    28802: gap of unknown length
*    28803    31393: contig of 2591 bp in length
*    31394    31493: gap of unknown length
*    31494    33777: contig of 2284 bp in length
*    33778    33877: gap of unknown length
*    33878    36707: contig of 2830 bp in length
*    36708    36807: gap of unknown length
*    36808    40396: contig of 3589 bp in length
*    40397    40496: gap of unknown length
*    40497    44511: contig of 4015 bp in length
*    44512    44611: gap of unknown length
*    44612    48500: contig of 3889 bp in length
*    48501    48600: gap of unknown length
*    48601    52724: contig of 4124 bp in length
*    52725    52824: gap of unknown length
*    52825    57081: contig of 4257 bp in length
*    57082    57181: gap of unknown length
*    57182    61751: contig of 4570 bp in length
*    61752    61851: gap of unknown length
*    61852    65499: contig of 3648 bp in length
*    65500    65599: gap of unknown length
*    65600    68468: contig of 2869 bp in length
*    68469    68568: gap of unknown length
*    68569    72801: contig of 4233 bp in length
*    72802    72901: gap of unknown length
*    72902    76766: contig of 3865 bp in length
*    76767    76866: gap of unknown length
*    76867    82497: contig of 5631 bp in length
*    82498    82597: gap of unknown length
*    82598    87024: contig of 4427 bp in length
*    87025    87124: gap of unknown length
*    87125    91086: contig of 3962 bp in length
*    91087    91186: gap of unknown length
*    91187    96104: contig of 4918 bp in length
*    96105    96204: gap of unknown length
*    96205   102630: contig of 6426 bp in length
*   102631   102730: gap of unknown length
*   102731   108961: contig of 6231 bp in length
*   108962   109061: gap of unknown length
*   109062   115347: contig of 6286 bp in length
*   115348   115447: gap of unknown length
*   115448   121828: contig of 6381 bp in length
*   121829   121928: gap of unknown length
*   121929   127815: contig of 5887 bp in length
*   127816   127915: gap of unknown length
*   127916   135093: contig of 7178 bp in length
*   135094   135193: gap of unknown length
*   135194   144907: contig of 9714 bp in length
*   144908   145007: gap of unknown length
*   145008   153321: contig of 8314 bp in length
*   153322   153421: gap of unknown length
*   153422   162203: contig of 8782 bp in length
*   162204   162303: gap of unknown length
*   162304   171228: contig of 8925 bp in length
*   171229   171328: gap of unknown length
*   171329   183897: contig of 12569 bp in length
*   183898   183997: gap of unknown length
*   183998   185516: contig of 1519 bp in length
*   185517   185616: gap of unknown length
*   185617   197902: contig of 12286 bp in length
*   197903   198002: gap of unknown length
*   198003   199893: contig of 1891 bp in length
*   199894   199993: gap of unknown length
*   199994   201952: contig of 1959 bp in length
*   201953   202052: gap of unknown length
*   202053   203959: contig of 1907 bp in length.
FEATURES             Location/Qualifiers
     source          1. .203959
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-306I1"
     misc_feature    1. .1438
                     /note="assembly_name:Contig10"
     misc_feature    1539. .3665
                     /note="assembly_name:Contig11"
     misc_feature    3766. .6090
                     /note="assembly_name:Contig12"
     misc_feature    6191. .8063
                     /note="assembly_name:Contig13"
     misc_feature    8164. .9769
                     /note="assembly_name:Contig14"
     misc_feature    9870. .12111
                     /note="assembly_name:Contig15"
     misc_feature    12212. .14650
                     /note="assembly_name:Contig16"
     misc_feature    14751. .16668
                     /note="assembly_name:Contig17"
     misc_feature    16769. .19004
                     /note="assembly_name:Contig18"
     misc_feature    19105. .21792
                     /note="assembly_name:Contig19"
     misc_feature    21893. .23341
                     /note="assembly_name:Contig2"
     misc_feature    23442. .26485
                     /note="assembly_name:Contig20"
     misc_feature    26586. .28702
                     /note="assembly_name:Contig21"
     misc_feature    28803. .31393
                     /note="assembly_name:Contig22"
     misc_feature    31494. .33777
                     /note="assembly_name:Contig23"
     misc_feature    33878. .36707
                     /note="assembly_name:Contig24"
     misc_feature    36808. .40396
                     /note="assembly_name:Contig25"
     misc_feature    40497. .44511
                     /note="assembly_name:Contig26"
     misc_feature    44612. .48500
                     /note="assembly_name:Contig27"
     misc_feature    48601. .52724
                     /note="assembly_name:Contig28"
     misc_feature    52825. .57081
                     /note="assembly_name:Contig29"
     misc_feature    57182. .61751
                     /note="assembly_name:Contig30"
     misc_feature    61852. .65499
                     /note="assembly_name:Contig31"
     misc_feature    65600. .68468
                     /note="assembly_name:Contig32"
     misc_feature    68569. .72801
                     /note="assembly_name:Contig33"
     misc_feature    72902. .76766
                     /note="assembly_name:Contig34"

  Query Match             49.5%;  Score 842.6;  DB 2;  Length 203959;
  Best Local Similarity   71.0%;  Pred. No. 1.9e-263;
  Matches 1423;  Conservative    0;  Mismatches  250;  Indels  331;  Gaps   10;

Qy          1 GAGACTGCAGAGGGAGATAA-AGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGG 59
              |||||||| ||||  |  || ||||||  |   | ||| ||||||||||||||| |||||
Db      99725 GAGACTGCCGAGGAGGTGAAGAGAGAGGGCTGAGAGAAGCAGCAAGAGATTTGTTCTGGG 99784

Qy         60 GATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAG 119
              || |||||||||||  | ||||||||||||  | | ||||||  |||||  ||||||||||||
Db      99785 GACCCAGAAACCCACGGTACCCTACTGAAAATCAAATCCCTTGGAAACCCACAGAGACAG 99844
```





Search completed: April 30, 2005, 03:54:44
Job time : 7413 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Run on: April 29, 2005, 22:58:46 ; Search time 892 Seconds
(without alignments)
11288.655 Million cell updates/sec
Title: US-10-063-583-73
Perfect score: 1701
Sequence: 1 gagactgcagagggagataa.....aaattaaagtttctgacttt 1701
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAA37142 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA sequence SEQ ID NO:422.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 3; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID AAF54501 standard; DNA; 1701 BP.
DE Primer #119 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAS46058 standard; cDNA; 1701 BP.
DE Human DNA encoding PRO polypeptide sequence #134.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4
ID AAF92094 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 5
ID ABS74414 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 6; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ACA89508 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ACA73518 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID ACA05833 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID ACA66667 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO protein #134.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID ACA91200 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACD81577 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ACF20242 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 13
ID ACF19628 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACD21916 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACF13081 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.

PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ACD25184 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACF00233 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACA60399 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA72290 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACD04814 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ACD18275 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ACD08282 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACA88716 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACA70158 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ACD12380 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ACC74295 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ACD15923 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ACD25491 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ACD17968 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ACC88255 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ACD21609 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ACD18676 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ACA58846 standard; cDNA; 1701 BP.
DE cDNA encoding human secreted polypeptide PRO1335.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ABX98286 standard; cDNA; 1701 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 267.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ACD14037 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032117-A1.
PD 13-FEB-2003.

Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ACD09817 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ACC88562 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ACD21302 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ABX75674 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1335.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ACA64022 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #37.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ABX97877 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ACA97353 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ACA57816 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACD14344 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ACC91127 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ACC88869 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ACD07066 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ACA67517 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ACC81572 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ACA91286 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #37.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ACC89176 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ACC86532 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ACC89790 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ACC92969 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ACA72597 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003022295-A1.
PD 30-JAN-2003.

```
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 56
ID   ACA89115 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003022297-A1.
PD   30-JAN-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 57
ID   ACA69851 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003032105-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 58
ID   ACA96994 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003032123-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 59
ID   ACA90990 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003032108-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 60
ID   ACA70772 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003032111-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 61
ID   ACA95282 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 62
ID   ACC86225 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003027263-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 63
ID   ACD45185 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane polypeptide PRO1335 cDNA.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 64
ID   ACC90097 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003027271-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 65
ID   ACD12705 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003036125-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 66
ID   ACF19935 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003040068-A1.
PD   27-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 67
ID   ABX76879 standard; cDNA; 1701 BP.
DE   Human PRO polynucleotide #134.
PN   US2003027280-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 68
ID   ACA73211 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003022300-A1.
PD   30-JAN-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 69
ID   ACA68754 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003036136-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 70
ID   ACA74598 standard; cDNA; 1701 BP.
DE   cDNA encoding human PRO polypeptide #134.
PN   US2003036138-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 71
ID   ACA70465 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003032109-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 72
ID   ACD14651 standard; cDNA; 1701 BP.
DE   Human PRO polynucleotide #134.
PN   US2003040066-A1.
PD   27-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 73
ID   ACA93733 standard; cDNA; 1701 BP.
DE   Human cDNA encoding secreted/transmembrane protein PRO1335.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 74
ID   ACA68323 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003032104-A1.
PD   13-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 75
ID   ABX98788 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003036157-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 8;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 76
```

ID ACA67307 standard; cDNA; 1701 BP.
DE cDNA encoding human secreted polypeptide PRO1335.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ACC81265 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ACA95589 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ACD04507 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ACC87948 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ACF12610 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ACH66280 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ACA96325 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ACA65099 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ACA73825 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ACA74237 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ACA96632 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ACD10738 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ACC91434 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ACD02769 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ACC87334 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ACC85918 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ACA65406 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ACA94223 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ACA97967 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ACA91469 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.

PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ACA90683 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ACD16230 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ACD17391 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ACC92048 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ACD02334 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ACA74905 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ACA91776 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ACA89325 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ACA71420 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ACC90820 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ACA65830 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO protein #134.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ACA68962 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ACA94975 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ACD16537 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ACD15616 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ACA98484 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ABX16719 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein #134.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 8; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ACA63409 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #37.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ACA97660 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ACA99109 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.

PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ACC91741 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ACD11152 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ACD15002 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ACD11766 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ACC95895 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ACF16458 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ACF02576 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ACF02883 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ACF21470 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ACF10154 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ACF78047 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ACD46752 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ACD49515 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ACF28282 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ACD88972 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ACD84367 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ACD99141 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADA78019 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135

ID ACF48883 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ACD09203 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ACF11996 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ACF41230 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ACF15844 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ACF16151 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ADB17130 standard; cDNA; 1701 BP.
DE Human cDNA clone (SeqID 73) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ACD31978 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ACF18786 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ACF09233 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ACF78354 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ACF51953 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ACF26440 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ACF24233 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ACF63544 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ACF50418 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ACH07889 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ACF13695 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ACD41621 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 154
ID ACF32034 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ACF23312 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ACF40002 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ACD45524 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ACF53181 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ACF27361 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ACF45199 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ACF29817 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ACD89893 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ACD84674 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ACD98834 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ACF77126 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ACF76819 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ACF49804 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ACF50111 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ACD09510 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ACD08589 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ACH03612 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane polypeptide PRO 1335 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ACF12303 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 173
ID ACC94811 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ACD22530 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ACF15230 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ACC97325 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ACC92355 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ACF14002 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ACF14309 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ACF09540 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ACD68540 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ACD45831 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ACD47980 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ACD67711 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ACF25519 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ACF29203 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ACD84981 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ACD84060 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ACD88051 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ACF30738 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ACF32341 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104555-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ACH12001 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ACH12308 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADA19935 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ACD40700 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADB17318 standard; cDNA; 1701 BP.
DE Human cDNA clone (SeqID 73) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ACF18172 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ACF08619 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ACF31420 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ACF52260 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ACD50129 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ACF38832 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ACF26747 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ACF24847 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ACF46427 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ACF27975 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ACD89279 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ACF63851 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ACF60491 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 210
ID ACH12615 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ACH10038 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ACD03893 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ACD10431 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ACD12073 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ACF42458 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ACF18479 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ACF02269 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ACF21777 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ACF10461 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ACF33913 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ACF44875 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ACD90507 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ACD91120 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ACF30431 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ACD87130 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ACF60184 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ACF46734 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ACF75591 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 229
ID ADA79811 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ACF17251 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ACF23005 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ACF08005 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ACF08312 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ACF40616 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ACF53795 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ACD47059 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ACF47962 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ACF47348 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ACF46120 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ACD86209 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ACF52567 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ACF52874 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ACF64867 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ACF76512 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ACF61412 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ACF61719 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ACD30750 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;

```
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 248
ID   ACD31671 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003054454-A1.
PD   20-MAR-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 249
ID   ACD32592 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003054477-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 250
ID   ADA20107 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 251
ID   ACD82126 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane polypeptide PRO 1335 cDNA.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 252
ID   ACF17558 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003054460-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 253
ID   ACF07391 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003049753-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 254
ID   ACF20549 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003049763-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 255
ID   ACF20856 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 256
ID   ACF21163 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 257
ID   ACD47673 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003068700-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 258
ID   ACF47655 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003068736-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 259
ID   ACF53488 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003068679-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 260
ID   ACD86823 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003068767-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 261
ID   ACH05071 standard; cDNA; 1701 BP.
DE   cDNA encoding human PRO polypeptide #134.
PN   US2003073182-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 262
ID   ACF44568 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 263
ID   ADA81538 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 264
ID   ACD22223 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003027276-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 265
ID   ACD24570 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003044920-A1.
PD   06-MAR-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 266
ID   ACD39773 standard; cDNA; 1701 BP.
DE   cDNA encoding human PRO polypeptide #134.
PN   US2003027265-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 9;  Length 1701;
```

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ACD40080 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ACF13388 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ACF03190 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ACF78661 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ACF11382 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ACF50725 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ACF34220 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ACD46445 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ACD48287 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ACF27668 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ACF24540 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ACD85595 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ACD90200 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ACD83753 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ACF49190 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ACH07275 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ACH07582 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ACH08196 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ACH11387 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049766-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ACH11694 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ACH10345 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ACF01348 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ACF40923 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ACD24263 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ACD31364 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ACF17865 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ACF32648 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ACF40309 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ACF48269 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ACF38218 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ACF25154 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ACF27054 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ACF29510 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ACD87744 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ACF76205 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ACF49497 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ACF43954 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ACH06299 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ACH06606 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ADA83336 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ACC92662 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ACC93276 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ACF19321 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ACD13012 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ACF06470 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ACC94504 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ACC97932 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ACC94197 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ACF42151 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ACD31057 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ACD43086 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ACD43393 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ACF14923 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ACF01655 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ACF31727 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ACD67404 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ACD48594 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ACD48901 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ACF51339 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ACF54102 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ACF25826 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ACF39139 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ACF28896 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ACD90813 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ACD86516 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ACH05378 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ACF65174 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ADB20379 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ACF43647 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ACH09117 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ACH09424 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ADA78631 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ACF09847 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ADA00404 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane polypeptide PRO 1335 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ACF51032 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ACF23926 standard; cDNA; 1701 BP.

DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ACD88358 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ACH09731 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ACH10652 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ACD11459 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ACC96509 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ACH04642 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ACC98539 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ACF41844 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ACF16765 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ACD32285 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ACD30443 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ACD41314 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ACF07698 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ACF31113 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ACF77433 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ACF11075 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ACF32955 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ACF26133 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ACD83446 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.

PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ACF23619 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ACF43033 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ACF43340 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ACH05992 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ACH08810 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ACC90404 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ACF10768 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ACC93583 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ACC96202 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ACD24877 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ACF01962 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ACF22084 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ACF22698 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ACF08926 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ACF33262 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ACF54716 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ACF48576 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ACD47366 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380

ID ACD49208 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID ACF37911 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ACF30124 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 383
ID ACD87437 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ACF62026 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ACH10959 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ACD10124 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ACD16849 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ACC99146 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ACF00540 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ACD41007 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ACF14616 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ACF22391 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ACF78968 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ACD68186 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ACF11689 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ACF51646 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ACF33569 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ACD49822 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 399
ID ACF37604 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ACF28589 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ACD88665 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ACF75284 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 403
ID ACF61105 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 404
ID ACF44261 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 405
ID ACH08503 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ACC93890 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 407
ID ACD20995 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 408
ID ACF06777 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 409
ID ACD20688 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 410
ID ACD22837 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 411
ID ACF41537 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 412
ID ACF07084 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 413
ID ACF77740 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 414
ID ACD46138 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 415
ID ACF47041 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 416
ID ACF54409 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ACF45813 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 418

ID ACF45506 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ACF38525 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ACD89586 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ACD85288 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ACD85902 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ACF75898 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ACF60798 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ACH05685 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ADA82702 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ADB85646 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ACF55944 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 99.9%; Score 1700; DB 9; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ACF55330 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ADB86010 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ACF56251 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ACF56558 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ADB68325 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ADB68132 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 435
ID ACF55637 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ACF55023 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003068771-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 437
ID ADB90949 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ADC07029 standard; cDNA; 1701 BP.
DE Human PRO1335 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 439
ID ADC18291 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #121.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 440
ID ADC17208 standard; cDNA; 1701 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 73).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ADC14906 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ADC52401 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ADD05740 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ADD70937 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ADD40014 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ADD70460 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID ADD36077 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ADD38581 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ADD39537 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID ADD39060 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ADD40491 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID ADE50712 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID ADE20324 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ADE50235 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ADE21793 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ADF30218 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ADF56111 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ADG01078 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ADG08631 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
ID ADG02735 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID ADG01442 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID ADF95617 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID ADF95252 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID ADG12432 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ADH24105 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ADH34131 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ADH29964 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID ADH23935 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID ADH09092 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ADG85339 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADH24615 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ADH37471 standard; cDNA; 1701 BP.
DE Human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473

ID ADH02060 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID ADH37641 standard; cDNA; 1701 BP.
DE Human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID ADG85679 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADH24275 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID ADH38569 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 478
ID ADG83690 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 479
ID ADH29498 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 480
ID ADH27614 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 481
ID ADH37811 standard; cDNA; 1701 BP.
DE Human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 482
ID ADH37988 standard; cDNA; 1701 BP.
DE Human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 483
ID ADH57408 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 484
ID ADH53550 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 485
ID ADH53720 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 486
ID ADH52056 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 487
ID ADH49911 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 488
ID ADI25421 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 489
ID ADH90214 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 490
ID ADI25591 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 491
ID ADH97765 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.

PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 492
ID ADH99615 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 493
ID ADI03613 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 494
ID ADI11970 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 495
ID ADH90044 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 496
ID ADH98445 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADI11120 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 498
ID ADI11630 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADH98275 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADH98615 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADH98105 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ABX78661 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ACA75633 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID ACA71113 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505
ID ACC87641 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ACC87027 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ACD04200 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ACA69531 standard; cDNA; 1701 BP.
DE cDNA encoding human PRO polypeptide #134.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ACA90376 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ACC89483 standard; cDNA; 1701 BP.
DE Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN US2003027264-A1.
PD 06-FEB-2003.

```
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 511
ID   ACA98274 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003036144-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 512
ID   ACA93916 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003036149-A1.
PD   20-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 513
ID   ACD15309 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003044923-A1.
PD   06-MAR-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 514
ID   ACD08896 standard; cDNA; 1701 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #134.
PN   US2003040062-A1.
PD   27-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 515
ID   ACC96816 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003040056-A1.
PD   27-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 516
ID   ACF15537 standard; cDNA; 1701 BP.
DE   Human secreted polypeptide PRO1335-encoding cDNA, SEQ ID NO:267.
PN   US2003044926-A1.
PD   06-MAR-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 517
ID   ACA72904 standard; cDNA; 1701 BP.
DE   Human PRO polynucleotide #134.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 518
ID   ACD03076 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003013153-A1.
PD   16-JAN-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 519
ID   ACD01891 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003017544-A1.
PD   23-JAN-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 520
ID   ACA92083 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003027277-A1.
PD   06-FEB-2003.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 521
ID   ADI05093 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 522
ID   ADI03443 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 523
ID   ADI04838 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 524
ID   ADH78292 standard; cDNA; 1701 BP.
DE   Human PRO polynucleotide #37.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 525
ID   ADI19636 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 526
ID   ADH90384 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 527
ID   ADI03103 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 528
ID   ADH77952 standard; cDNA; 1701 BP.
DE   Human PRO polynucleotide #37.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 529
ID   ADH97935 standard; cDNA; 1701 BP.
DE   Novel human secreted and transmembrane protein PRO1335 cDNA.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             99.9%;  Score 1700;  DB 10;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 0;
RESULT 530
```

ID ADI01320 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ADI02015 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ADI03273 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 533
ID ADI11460 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 534
ID ADI02362 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 535
ID ADI11800 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 536
ID ADI05437 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 537
ID ADH79509 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 538
ID ADI19466 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 539
ID ADI05267 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 540
ID ADH79679 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 541
ID ADI01505 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 542
ID ADI01675 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 543
ID ADI01845 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 544
ID ADH79849 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 545
ID ADI04667 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 546
ID ADI02803 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 547
ID ADH78122 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 548
ID ADI25761 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.

PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 549
ID ADI25931 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 550
ID ADK65443 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 551
ID ADH98785 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 552
ID ADH80026 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 10; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 553
ID ADL32873 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 11; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 554
ID ADM30407 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 11; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 555
ID ADL93757 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 11; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 556
ID ADC52211 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 557
ID ADE74404 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 558
ID ADE75016 standard; cDNA; 1701 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #134.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 559
ID ADE96795 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 560
ID ADF26106 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 561
ID ADF25005 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 562
ID ADF29741 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 563
ID ADE97272 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 564
ID ADF96229 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 565
ID ADG04500 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 566
ID ADG00660 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 567
ID ADH06643 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 568
ID ADH06473 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 569
ID ADG68894 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 570
ID ADH27784 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 571
ID ADH25125 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 572
ID ADH33757 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 573
ID ADG82916 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 574
ID ADH03310 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 575
ID ADH02400 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 576
ID ADH08007 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 577
ID ADG69404 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 578
ID ADH39225 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 579
ID ADH04264 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 580
ID ADH03787 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADH26197 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 582
ID ADG83965 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 583
ID ADG85509 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADH06303 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADH30133 standard; cDNA; 1701 BP.

DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADH24445 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADH33166 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADG69574 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADH07837 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADG85849 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADH39395 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADH33587 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADH33927 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADH01137 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADG69744 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADH02230 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADG69234 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADG86019 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADH24955 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600
ID ADH39572 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADH02570 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
ID ADG69064 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 603
ID ADH07667 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180850-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 604
ID ADG86189 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 605
ID ADH24785 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 606
ID ADH25833 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 607
ID ADH38399 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 608
ID ADH57238 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 609
ID ADH52225 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 610
ID ADH04741 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 611
ID ADH49592 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 612
ID ADH90554 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 613
ID ADI11290 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 614
ID ADH98955 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 615
ID ADI02185 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 616
ID ADH61742 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 617
ID ADH90724 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 618
ID ADJ54905 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 619
ID ADJ98599 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 620
ID ADJ98769 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 621
ID ADH78928 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 622
ID ADJ99162 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 623
ID ADJ99332 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 624
ID ADJ98950 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 625
ID ADH79098 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 626
ID ADK00958 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 627
ID ADK14479 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADJ64676 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #134.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADM31572 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADM36619 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADM40424 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADM80928 standard; cDNA; 1701 BP.
DE Human PRO polynucleotide #37.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADL94941 standard; cDNA; 1701 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1335.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADN38032 standard; cDNA; 1701 BP.
DE Novel human secreted and transmembrane protein PRO1335 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1700; DB 12; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID AAK94241 standard; cDNA; 1771 BP.
DE Human full-length cDNA, SEQ ID NO: 2840.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 98.8%; Score 1680.2; DB 4; Length 1771;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 636
ID ADL30807 standard; cDNA; 1771 BP.
DE Full length human cDNA clone SeqID 2840.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 98.8%; Score 1680.2; DB 12; Length 1771;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 637
ID ADD12606 standard; cDNA; 1735 BP.
DE Human ENZM-9 encoding cDNA SEQ ID NO:66.
PN WO2003072729-A2.
PD 04-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 89.7%; Score 1526; DB 10; Length 1735;
Best Local Similarity 94.5%; Pred. No. 0;
RESULT 638
ID ACN41903 standard; cDNA; 2201 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:778.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 88.1%; Score 1498; DB 13; Length 2201;
Best Local Similarity 94.3%; Pred. No. 0;
RESULT 639
ID ABK91319 standard; cDNA; 1657 BP.
DE cDNA encoding novel human enzyme, NZMS-8, Incyte 27068847CB1.
PN WO200264795-A2.
PD 22-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 87.9%; Score 1496; DB 6; Length 1657;
Best Local Similarity 94.5%; Pred. No. 0;

RESULT 640
ID AAC91304 standard; cDNA; 1673 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 4.
PN WO200073509-A2.
PD 07-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 87.4%; Score 1486.6; DB 4; Length 1673;
Best Local Similarity 94.5%; Pred. No. 0;
RESULT 641
ID AAZ65258 standard; DNA; 1537 BP.
DE Human secreted protein gene 9.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.6%; Score 1201.4; DB 3; Length 1537;
Best Local Similarity 86.4%; Pred. No. 0;
RESULT 642
ID ADA40114 standard; cDNA; 1537 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.6%; Score 1201.4; DB 8; Length 1537;
Best Local Similarity 86.4%; Pred. No. 0;
RESULT 643
ID ADC73682 standard; DNA; 1537 BP.
DE Human secreted protein-related DNA - SEQ ID 315.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.6%; Score 1201.4; DB 10; Length 1537;
Best Local Similarity 86.4%; Pred. No. 0;
RESULT 644
ID ADE11647 standard; cDNA; 1537 BP.
DE Human secreted polypeptide cDNA #9.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 70.6%; Score 1201.4; DB 10; Length 1537;
Best Local Similarity 86.4%; Pred. No. 0;
RESULT 645
ID ADA56286 standard; DNA; 1537 BP.
DE Gene encoding human secreted protein #465.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.6%; Score 1201.4; DB 10; Length 1537;
Best Local Similarity 86.4%; Pred. No. 0;
RESULT 646
ID ABL90091 standard; cDNA; 1434 BP.
DE Human polynucleotide SEQ ID NO 653.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 68.9%; Score 1172.8; DB 6; Length 1434;
Best Local Similarity 86.1%; Pred. No. 0;
RESULT 647
ID ADR21623 standard; cDNA; 1430 BP.
DE Human enzyme ENZM-5 encoding cDNA SEQ ID NO:44.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 62.2%; Score 1058.4; DB 13; Length 1430;
Best Local Similarity 81.7%; Pred. No. 0;
RESULT 648
ID AAS30168 standard; cDNA; 999 BP.
DE DNA encoding renal and cardiovascular-associated protein, Seq ID 14.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 56.1%; Score 954.8; DB 4; Length 999;
Best Local Similarity 99.2%; Pred. No. 4.2e-284;
RESULT 649
ID ACD01423 standard; cDNA; 999 BP.
DE Human polynucleotide #4.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 56.1%; Score 954.8; DB 8; Length 999;
Best Local Similarity 99.2%; Pred. No. 4.2e-284;
RESULT 650
ID ADR21643 standard; cDNA; 1295 BP.
DE Human enzyme ENZM-25 encoding cDNA SEQ ID NO:64.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 52.8%; Score 898.4; DB 13; Length 1295;
Best Local Similarity 79.3%; Pred. No. 1.4e-266;
RESULT 651
ID ADL90253 standard; DNA; 939 BP.
DE Human enzyme, ENZM-17 coding sequence, SEQ ID 63.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 50.8%; Score 863.4; DB 12; Length 939;
Best Local Similarity 99.3%; Pred. No. 7.8e-256;
RESULT 652
ID ADB85169 standard; DNA; 1624 BP.
DE Mouse carbonic anhydrase XIV gene SEQ ID NO:50.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 46.8%; Score 795.6; DB 10; Length 1624;
Best Local Similarity 83.2%; Pred. No. 1e-234;
RESULT 653
ID ADL90251 standard; DNA; 947 BP.
DE Human enzyme, ENZM-15 coding sequence, SEQ ID 61.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 42.6%; Score 724.2; DB 12; Length 947;
Best Local Similarity 92.0%; Pred. No. 9.5e-213;
RESULT 654
ID AAK91822 standard; cDNA; 865 BP.
DE Human cDNA 5'-end sequence, SEQ ID NO: 282.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 40.0%; Score 679.8; DB 4; Length 865;
Best Local Similarity 93.7%; Pred. No. 5e-199;
RESULT 655
ID AAK93221 standard; cDNA; 865 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 1681.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 40.0%; Score 679.8; DB 4; Length 865;
Best Local Similarity 93.7%; Pred. No. 5e-199;
RESULT 656

ID ADL28249 standard; cDNA; 865 BP.
DE 5' end of a human cDNA molecule SeqID 282.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.0%; Score 679.8; DB 12; Length 865;
Best Local Similarity 93.7%; Pred. No. 5e-199;
RESULT 657
ID ADL29648 standard; cDNA; 865 BP.
DE 5' end of a representative human cDNA cluster SeqID 1681.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.0%; Score 679.8; DB 12; Length 865;
Best Local Similarity 93.7%; Pred. No. 5e-199;
RESULT 658
ID AAS41754 standard; DNA; 11470 BP.
DE Genomic sequence #70 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.4%; Score 482.4; DB 4; Length 11470;
Best Local Similarity 99.6%; Pred. No. 2.9e-137;
RESULT 659
ID AAS41755 standard; DNA; 2912 BP.
DE Genomic sequence #71 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.8%; Score 456.2; DB 4; Length 2912;
Best Local Similarity 98.8%; Pred. No. 1.6e-129;
RESULT 660
ID AAS30216 standard; cDNA; 561 BP.
DE DNA encoding renal and cardiovascular-associated protein, Seq ID 62.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.7%; Score 420.6; DB 4; Length 561;
Best Local Similarity 85.4%; Pred. No. 6.3e-119;
RESULT 661
ID AAS40941 standard; cDNA; 561 BP.
DE cDNA encoding novel human enzyme polypeptide #157.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.7%; Score 420.6; DB 4; Length 561;
Best Local Similarity 85.4%; Pred. No. 6.3e-119;
RESULT 662
ID ACD01471 standard; cDNA; 561 BP.
DE Human polynucleotide #52.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 24.7%; Score 420.6; DB 8; Length 561;
Best Local Similarity 85.4%; Pred. No. 6.3e-119;
RESULT 663
ID ACH47461 standard; cDNA; 406 BP.
DE Human infant brain cDNA #1524.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 23.6%; Score 401.2; DB 9; Length 406;
Best Local Similarity 99.3%; Pred. No. 5.3e-113;
RESULT 664
ID ABL78464 standard; cDNA; 458 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1442.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 15.7%; Score 267.8; DB 6; Length 458;
Best Local Similarity 81.3%; Pred. No. 1.1e-71;
RESULT 665
ID ABX88688 standard; cDNA; 297 BP.
DE Corn ear-derived polynucleotide (cpd) #7148.
PN US6476212-B1.
PD 05-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.1%; Score 222.2; DB 10; Length 297;
Best Local Similarity 87.9%; Pred. No. 1.1e-57;
RESULT 666
ID AAT15448 standard; cDNA; 1104 BP.
DE Lung cancer specific antigen HCAVIII pre-protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.6%; Score 213.6; DB 2; Length 1104;
Best Local Similarity 53.9%; Pred. No. 1.1e-54;
RESULT 667
ID AAA50665 standard; cDNA; 1104 BP.
DE Non-small cell lung carcinoma cell antigen LCGA cDNA.
PN US6117981-A.
PD 12-SEP-2000.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.6%; Score 213.6; DB 3; Length 1104;
Best Local Similarity 53.9%; Pred. No. 1.1e-54;
RESULT 668
ID AAD06839 standard; cDNA; 1104 BP.
DE Human cell surface glycoprotein antigen LCGA cDNA.
PN US6242204-B1.
PD 05-JUN-2001.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.6%; Score 213.6; DB 5; Length 1104;
Best Local Similarity 53.9%; Pred. No. 1.1e-54;
RESULT 669
ID AAT15452 standard; cDNA; 2134 BP.
DE Lung cancer specific antigen HCAVIII pre-protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.6%; Score 213.6; DB 2; Length 2134;
Best Local Similarity 53.9%; Pred. No. 1.6e-54;
RESULT 670
ID AAH57508 standard; cDNA; 2704 BP.
DE Human kidney cell specific cDNA sequence SEQ ID NO:348.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.6%; Score 213.6; DB 4; Length 2704;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 671
ID AAL50829 standard; DNA; 2771 BP.
DE Human cancer status prediction method-related DNA sequence #21.
PN WO200272828-A1.
PD 19-SEP-2002.
PA (DNAC-) DNA CHIP RES INC.
PA (HISF) HITACHI SOFTWARE ENG CO LTD.
Query Match 12.6%; Score 213.6; DB 6; Length 2771;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 672
ID ACA64890 standard; DNA; 2771 BP.
DE Human CA12 DNA corresponding to AF037335.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 12.6%; Score 213.6; DB 8; Length 2771;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 673
ID ADQ20404 standard; DNA; 2771 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3224.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.6%; Score 213.6; DB 12; Length 2771;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 674
ID ACC72716 standard; cDNA; 2775 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:55.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.6%; Score 213.6; DB 10; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 675
ID ADN38977 standard; cDNA; 2775 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:295.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.6%; Score 213.6; DB 11; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 676
ID ADJ75076 standard; DNA; 2775 BP.
DE Marker gene SEQ ID NO:328.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 12.6%; Score 213.6; DB 12; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 677
ID ADL61163 standard; DNA; 2775 BP.
DE Human protein tyrosine kinase biomarker carbonic anhydrase XII DNA.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.6%; Score 213.6; DB 12; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 678
ID ADR24714 standard; DNA; 2775 BP.
DE Breast cancer prognosis marker #575.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 12.6%; Score 213.6; DB 13; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 679
ID ACN39820 standard; cDNA; 2775 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326004, SEQ ID NO:4203.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 213.6; DB 13; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.9e-54;
RESULT 680
ID ADL63522 standard; DNA; 3171 BP.
DE Human ovarian cancer DNA marker #21734.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 12.6%; Score 213.6; DB 5; Length 3171;
Best Local Similarity 53.9%; Pred. No. 2.1e-54;
RESULT 681
ID ADP07265 standard; DNA; 3992 BP.
DE Human CA XII DNA.
PN DE10255104-A1.
PD 11-MAR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 12.6%; Score 213.6; DB 12; Length 3992;
Best Local Similarity 53.9%; Pred. No. 2.4e-54;
RESULT 682
ID ACC72717 standard; cDNA; 1718 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:56.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.4%; Score 211.6; DB 10; Length 1718;
Best Local Similarity 54.4%; Pred. No. 6e-54;
RESULT 683
ID AAT47747 standard; cDNA; 2679 BP.
DE Renal cancer antigen HOM-RCC 3.1.3 cDNA clone SK313.
PN WO9640209-A1.
PD 19-DEC-1996.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 12.4%; Score 211; DB 2; Length 2679;
Best Local Similarity 53.6%; Pred. No. 1.2e-53;
RESULT 684
ID AAV04266 standard; cDNA; 2679 BP.
DE Renal cell carcinoma antigen clone HOM-RCC-3.1.3.
PN WO9748721-A1.
PD 24-DEC-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 12.4%; Score 211; DB 2; Length 2679;
Best Local Similarity 53.6%; Pred. No. 1.2e-53;
RESULT 685
ID AAT15451 standard; cDNA; 822 BP.
DE Lung cancer specific antigen HCAVIII truncated protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.1%; Score 206; DB 2; Length 822;
Best Local Similarity 55.0%; Pred. No. 2.1e-52;
RESULT 686
ID AAT15454 standard; cDNA; 986 BP.
DE HCAVIII phosphorylation-modified (S302G) protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.1%; Score 206; DB 2; Length 986;
Best Local Similarity 55.0%; Pred. No. 2.3e-52;
RESULT 687
ID AAT15449 standard; cDNA; 986 BP.
DE Lung cancer specific antigen HCAVIII mature protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.1%; Score 206; DB 2; Length 986;
Best Local Similarity 55.0%; Pred. No. 2.3e-52;
RESULT 688
ID AAT15450 standard; cDNA; 813 BP.
DE Lung cancer specific antigen HCAVIII truncated protein cDNA.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 12.1%; Score 205.2; DB 2; Length 813;
Best Local Similarity 55.2%; Pred. No. 3.7e-52;
RESULT 689
ID AAT47752 standard; cDNA; 1190 BP.
DE Renal cancer antigen HOM-RCC 3.1.3 gene translated region.
PN WO9640209-A1.
PD 19-DEC-1996.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 11.9%; Score 203; DB 2; Length 1190;
Best Local Similarity 54.4%; Pred. No. 2.2e-51;
RESULT 690
ID ADQ24404 standard; DNA; 3151 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7224.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 11.9%; Score 202.4; DB 12; Length 3151;
Best Local Similarity 53.1%; Pred. No. 6.1e-51;
RESULT 691
ID AAV04265 standard; cDNA; 1190 BP.
DE Renal cell carcinoma antigen clone HOM-RCC-313.
PN WO9748721-A1.
PD 24-DEC-1997.

PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 11.8%; Score 201.4; DB 2; Length 1190;
Best Local Similarity 54.3%; Pred. No. 6.9e-51;
RESULT 692
ID ADR21634 standard; cDNA; 1857 BP.
DE Human enzyme ENZM-16 encoding cDNA SEQ ID NO:55.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.3%; Score 158.2; DB 13; Length 1857;
Best Local Similarity 51.3%; Pred. No. 2.1e-37;
RESULT 693
ID ADM02846 standard; cDNA; 2556 BP.
DE Human cDNA of the invention SEQ ID NO:1531.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.6%; Score 146; DB 11; Length 2556;
Best Local Similarity 55.4%; Pred. No. 1.5e-33;
RESULT 694
ID ADO35568 standard; DNA; 1496 BP.
DE Novel mouse gene sequence #241.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 7.7%; Score 131; DB 12; Length 1496;
Best Local Similarity 87.7%; Pred. No. 4.9e-29;
RESULT 695
ID ADL70159 standard; cDNA; 1089 BP.
DE Human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 7.4%; Score 125.2; DB 12; Length 1089;
Best Local Similarity 50.6%; Pred. No. 2.5e-27;
RESULT 696
ID ADL70155 standard; cDNA; 1380 BP.
DE Human carbonic anhydrase isozyme CA IX coding sequence.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 7.0%; Score 118.4; DB 12; Length 1380;
Best Local Similarity 50.6%; Pred. No. 3.7e-25;
RESULT 697
ID ADP54000 standard; DNA; 1392 BP.
DE Human carbonic anhydrase IX coding sequence.
PN WO2004048544-A2.
PD 10-JUN-2004.
PA (FARB) BAYER HEALTHCARE.
PA (VIRO-) INST VIROLOGY.
PA (SUPU/) SUPURAN C.
PA (SCOZ/) SCOZZAFAVA A.
Query Match 7.0%; Score 118.4; DB 12; Length 1392;
Best Local Similarity 50.6%; Pred. No. 3.7e-25;
RESULT 698
ID ADS73098 standard; cDNA; 1519 BP.
DE Human kidney tumour specific cDNA, SEQ ID 1695.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.0%; Score 118.4; DB 7; Length 1519;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 699
ID AAT09186 standard; cDNA; 1522 BP.
DE MuTu putative oncogene MN cDNA.
PN WO9534650-A2.
PD 21-DEC-1995.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 2; Length 1522;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 700
ID AAA16540 standard; cDNA; 1522 BP.
DE Human MN protein encoding cDNA SEQ ID NO:1.
PN US6027887-A.
PD 22-FEB-2000.
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 3; Length 1522;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 701
ID AAA52459 standard; cDNA; 1522 BP.
DE Human MN cDNA.
PN WO200024913-A2.
PD 04-MAY-2000.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 3; Length 1522;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 702
ID ADG31413 standard; cDNA; 1522 BP.
DE Human MN cDNA SeqID 1.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 12; Length 1522;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 703
ID ADK41803 standard; DNA; 1522 BP.
DE Human MN gene sequence SeqID1.
PN WO2004005348-A1.
PD 15-JAN-2004.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 12; Length 1522;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 704
ID ABL64779 standard; DNA; 1552 BP.
DE Lung cancer related gene sequence SEQ ID NO:3116.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 7.0%; Score 118.4; DB 6; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 705
ID ABL62179 standard; DNA; 1552 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:516.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 7.0%; Score 118.4; DB 6; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 706
ID ABL65416 standard; DNA; 1552 BP.
DE Lung cancer related gene sequence SEQ ID NO:3753.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 7.0%; Score 118.4; DB 6; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 707
ID ABL68346 standard; DNA; 1552 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6683.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 7.0%; Score 118.4; DB 6; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 708
ID ABX76385 standard; DNA; 1552 BP.
DE Lung cancer-associated polynucleotide #249.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.0%; Score 118.4; DB 8; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;

RESULT 709
ID ABX76124 standard; DNA; 1552 BP.
DE Lung cancer-associated polynucleotide #1.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.0%; Score 118.4; DB 8; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 710
ID ADG89343 standard; DNA; 1552 BP.
DE Cancer detection method related gene #6.
PN WO2003078662-A1.
PD 25-SEP-2003.
PA (GENO-) GENOMIC HEALTH INC.
Query Match 7.0%; Score 118.4; DB 10; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 711
ID ACC72730 standard; cDNA; 1552 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:69.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.0%; Score 118.4; DB 10; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 712
ID ABZ77284 standard; cDNA; 1552 BP.
DE Nucleotide sequence of human CA9 polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 7.0%; Score 118.4; DB 10; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 713
ID ADN39704 standard; cDNA; 1552 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C76.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.0%; Score 118.4; DB 11; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 714
ID ADN38987 standard; cDNA; 1552 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:305.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.0%; Score 118.4; DB 11; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 715
ID ADG31472 standard; cDNA; 1552 BP.
DE Human Car9 cDNA used to design RT-PCR primers SeqID 70.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 7.0%; Score 118.4; DB 12; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 716
ID ADQ17643 standard; DNA; 1552 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 460.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.0%; Score 118.4; DB 12; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 717
ID ADQ29645 standard; DNA; 1552 BP.
DE Human colorectal cancer-associated protein coding sequence #67.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 118.4; DB 12; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 718
ID ADQ87399 standard; cDNA; 1552 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4276.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 7.0%; Score 118.4; DB 13; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 719
ID ADR24713 standard; DNA; 1552 BP.
DE Breast cancer prognosis marker #574.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 7.0%; Score 118.4; DB 13; Length 1552;
Best Local Similarity 50.6%; Pred. No. 3.9e-25;
RESULT 720
ID ADQ22315 standard; DNA; 1658 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5135.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.0%; Score 118.4; DB 12; Length 1658;
Best Local Similarity 50.6%; Pred. No. 4.1e-25;
RESULT 721
ID AAH26551 standard; cDNA; 1833 BP.
DE DNA encoding G250-GM-CSF fusion protein.
PN WO200160317-A2.
PD 23-AUG-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.0%; Score 118.4; DB 4; Length 1833;
Best Local Similarity 50.6%; Pred. No. 4.4e-25;
RESULT 722
ID ADQ22975 standard; DNA; 6687 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5795.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.9%; Score 117.2; DB 12; Length 6687;
Best Local Similarity 49.4%; Pred. No. 2.2e-24;
RESULT 723
ID AAQ71842 standard; cDNA; 4338 BP.
DE Human RPTP-gamma.
PN WO9418309-A1.
PD 18-AUG-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 6.8%; Score 115.6; DB 2; Length 4338;
Best Local Similarity 49.3%; Pred. No. 5.4e-24;
RESULT 724
ID ADG31474 standard; cDNA; 1965 BP.
DE Murine carbonic anhydrase (MN/ CA9) cDNA SeqID 79.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 6.6%; Score 111.8; DB 12; Length 1965;
Best Local Similarity 50.7%; Pred. No. 5e-23;
RESULT 725
ID ACD94155 standard; cDNA; 510 BP.
DE Human colon cancer cell expressed cDNA #2567.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 6.0%; Score 102.2; DB 10; Length 510;
Best Local Similarity 56.3%; Pred. No. 2.1e-20;
RESULT 726
ID ADJ95127 standard; DNA; 1006 BP.

DE Novel NOVX gene sequence #178.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.5%; Score 94.4; DB 10; Length 1006;
Best Local Similarity 51.3%; Pred. No. 8.1e-18;
RESULT 727
ID ADN04268 standard; cDNA; 1316 BP.
DE Antipsoriatic cDNA sequence #334.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 91.2; DB 12; Length 1316;
Best Local Similarity 51.0%; Pred. No. 9.4e-17;
RESULT 728
ID AAQ48456 standard; cDNA; 1397 BP.
DE MN cDNA clone.
PN WO9318152-A1.
PD 16-SEP-1993.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 5.3%; Score 90.8; DB 2; Length 1397;
Best Local Similarity 50.0%; Pred. No. 1.3e-16;
RESULT 729
ID ABT33350 standard; DNA; 828 BP.
DE NOVX DNA sequence SEQ ID No 15.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.0%; Score 85; DB 8; Length 828;
Best Local Similarity 51.6%; Pred. No. 5.9e-15;
RESULT 730
ID ADH41590 standard; DNA; 828 BP.
DE Novel human nucleic acid NOV13a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.0%; Score 85; DB 12; Length 828;
Best Local Similarity 51.6%; Pred. No. 5.9e-15;
RESULT 731
ID AAC32435 standard; cDNA; 145 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 36510.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.8%; Score 82.4; DB 3; Length 145;
Best Local Similarity 98.8%; Pred. No. 1.3e-14;
RESULT 732
ID ABT33351 standard; DNA; 833 BP.
DE NOVX DNA sequence SEQ ID No 17.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 81.8; DB 8; Length 833;
Best Local Similarity 51.2%; Pred. No. 5.8e-14;
RESULT 733
ID ADH41594 standard; DNA; 833 BP.
DE Novel human nucleic acid NOV13c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 81.8; DB 12; Length 833;
Best Local Similarity 51.2%; Pred. No. 5.8e-14;
RESULT 734
ID AAD41388 standard; cDNA; 1023 BP.
DE Human NZMS-1 cDNA.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.8%; Score 81.8; DB 6; Length 1023;
Best Local Similarity 51.2%; Pred. No. 6.5e-14;
RESULT 735
ID ADM01954 standard; cDNA; 3564 BP.
DE Human cDNA of the invention SEQ ID NO:639.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 81.8; DB 11; Length 3564;
Best Local Similarity 51.2%; Pred. No. 1.4e-13;
RESULT 736
ID ADQ88165 standard; DNA; 3564 BP.
DE Human 85553 DNA encodes a carbonic anhydrase protein.
PN WO2004063340-A2.
PD 29-JUL-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.8%; Score 81.8; DB 13; Length 3564;
Best Local Similarity 51.2%; Pred. No. 1.4e-13;
RESULT 737
ID AAF22342 standard; cDNA; 688 BP.
DE Human secreted protein gene 27 SEQ ID NO:37.
PN WO200061748-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 80.2; DB 3; Length 688;
Best Local Similarity 50.9%; Pred. No. 1.6e-13;
RESULT 738
ID ADG31473 standard; DNA; 586 BP.
DE Human MN DNA fragment amplified by RT-PCR SeqID 73.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 4.7%; Score 79.8; DB 12; Length 586;
Best Local Similarity 51.8%; Pred. No. 1.9e-13;
RESULT 739
ID ADH41592 standard; DNA; 784 BP.
DE Novel human nucleic acid NOV13b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 76.8; DB 12; Length 784;
Best Local Similarity 50.9%; Pred. No. 2e-12;
RESULT 740
ID ACN41593 standard; cDNA; 1810 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:468.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.4%; Score 75.6; DB 13; Length 1810;
Best Local Similarity 49.6%; Pred. No. 7.6e-12;
RESULT 741
ID AAH83009 standard; cDNA; 408 BP.
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:633.
PN WO200151513-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.3%; Score 73.8; DB 5; Length 408;
Best Local Similarity 57.4%; Pred. No. 1.1e-11;
RESULT 742
ID ADB56954 standard; DNA; 483 BP.
DE Toxicity-related gene, SEQ ID 1980.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 4.3%; Score 73.6; DB 10; Length 483;
Best Local Similarity 73.0%; Pred. No. 1.4e-11;
RESULT 743
ID AAH82505 standard; cDNA; 521 BP.
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:129.
PN WO200151513-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.3%; Score 73.2; DB 5; Length 521;
Best Local Similarity 57.4%; Pred. No. 2e-11;
RESULT 744
ID ABI99672 standard; cDNA; 1067 BP.

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:707.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 4.2%; Score 72; DB 6; Length 1067;
Best Local Similarity 50.4%; Pred. No. 7.2e-11;
RESULT 745
ID AAH82742 standard; cDNA; 418 BP.
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:366.
PN WO200151513-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 70; DB 5; Length 418;
Best Local Similarity 56.5%; Pred. No. 1.7e-10;
RESULT 746
ID ADS72100 standard; cDNA; 296 BP.
DE Human kidney tumour specific cDNA, SEQ ID 697.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 69.8; DB 7; Length 296;
Best Local Similarity 56.9%; Pred. No. 1.6e-10;
RESULT 747
ID ADL70161 standard; cDNA; 978 BP.
DE Glu-tagged human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 4.1%; Score 69.2; DB 12; Length 978;
Best Local Similarity 50.8%; Pred. No. 5e-10;
RESULT 748
ID ADB79880 standard; DNA; 6801 BP.
DE Rat phosphacan coding sequence, SEQ ID 120.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 4.0%; Score 68.2; DB 10; Length 6801;
Best Local Similarity 46.1%; Pred. No. 3.3e-09;
RESULT 749
ID ADO31207 standard; DNA; 6801 BP.
DE Rat phosphacan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 4.0%; Score 68.2; DB 12; Length 6801;
Best Local Similarity 46.1%; Pred. No. 3.3e-09;
RESULT 750
ID ADL70163 standard; cDNA; 978 BP.
DE Glu-tagged human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 4.0%; Score 67.8; DB 12; Length 978;
Best Local Similarity 47.8%; Pred. No. 1.4e-09;
RESULT 751
ID ADJ95125 standard; DNA; 1136 BP.
DE Novel NOVX gene sequence #177.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 67.8; DB 10; Length 1136;
Best Local Similarity 50.5%; Pred. No. 1.5e-09;
RESULT 752
ID AAS30989 standard; cDNA; 1248 BP.
DE Human diagnostic and therapeutic polynucleotide (DITHP) #4.
PN WO200162927-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.0%; Score 67.6; DB 4; Length 1248;
Best Local Similarity 50.2%; Pred. No. 1.8e-09;
RESULT 753
ID AAS24167 standard; cDNA; 304 BP.
DE Human ovarian PCR-subtracted cDNA library clone #348.
PN WO200157207-A2.
PD 09-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 66.6; DB 4; Length 304;
Best Local Similarity 56.0%; Pred. No. 1.6e-09;
RESULT 754
ID ADJ56205 standard; cDNA; 1508 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 11.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Query Match 3.9%; Score 66.4; DB 10; Length 1508;
Best Local Similarity 49.6%; Pred. No. 4.8e-09;
RESULT 755
ID ADG32995 standard; DNA; 1164 BP.
DE Human DNA differentially expressed in patients with SLE SeqID319.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 3.8%; Score 65.2; DB 10; Length 1164;
Best Local Similarity 48.8%; Pred. No. 9.7e-09;
RESULT 756
ID AAS24411 standard; cDNA; 297 BP.
DE Human ovarian PCR-subtracted cDNA library clone #592.
PN WO200157207-A2.
PD 09-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.8%; Score 64.4; DB 4; Length 297;
Best Local Similarity 56.0%; Pred. No. 7.5e-09;
RESULT 757
ID ADL90244 standard; DNA; 716 BP.
DE Human enzyme, ENZM-8 coding sequence, SEQ ID 54.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 64.4; DB 12; Length 716;
Best Local Similarity 49.8%; Pred. No. 1.3e-08;
RESULT 758
ID ABA97691 standard; DNA; 911 BP.
DE Human lyase HLYA-1 encoding cDNA.
PN WO200200840-A2.
PD 03-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.8%; Score 63.8; DB 6; Length 911;
Best Local Similarity 50.1%; Pred. No. 2.3e-08;
RESULT 759
ID ACN41592 standard; cDNA; 1527 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:467.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 63.8; DB 13; Length 1527;
Best Local Similarity 48.6%; Pred. No. 3.1e-08;
RESULT 760
ID ACN41594 standard; cDNA; 1802 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:469.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 63.8; DB 13; Length 1802;
Best Local Similarity 48.6%; Pred. No. 3.4e-08;
RESULT 761
ID ABX34690 standard; cDNA; 2094 BP.
DE Human mddt cDNA SEQ ID 251.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.8%; Score 63.8; DB 8; Length 2094;
Best Local Similarity 50.1%; Pred. No. 3.7e-08;
RESULT 762

ID ACN41599 standard; cDNA; 1433 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:474.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 63.6; DB 13; Length 1433;
Best Local Similarity 52.9%; Pred. No. 3.4e-08;
RESULT 763
ID ACN41598 standard; cDNA; 1438 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:473.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 63.6; DB 13; Length 1438;
Best Local Similarity 52.9%; Pred. No. 3.4e-08;
RESULT 764
ID ACN41596 standard; cDNA; 1708 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:471.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 63.6; DB 13; Length 1708;
Best Local Similarity 52.9%; Pred. No. 3.8e-08;
RESULT 765
ID ACN41595 standard; cDNA; 1713 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:470.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 63.6; DB 13; Length 1713;
Best Local Similarity 52.9%; Pred. No. 3.8e-08;
RESULT 766
ID ABK63770 standard; cDNA; 1201 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1677.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 63.4; DB 6; Length 1201;
Best Local Similarity 48.6%; Pred. No. 3.6e-08;
RESULT 767
ID ADB58364 standard; DNA; 1201 BP.
DE Toxicity-related gene, SEQ ID 3390.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 63.4; DB 10; Length 1201;
Best Local Similarity 48.6%; Pred. No. 3.6e-08;
RESULT 768
ID ADB52938 standard; DNA; 1201 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3480.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 63.4; DB 10; Length 1201;
Best Local Similarity 48.6%; Pred. No. 3.6e-08;
RESULT 769
ID ADJ76009 standard; DNA; 6887 BP.
DE Marker gene SEQ ID NO:1261.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.7%; Score 63.4; DB 12; Length 6887;
Best Local Similarity 45.6%; Pred. No. 1e-07;
RESULT 770
ID ADO31209 standard; DNA; 6887 BP.
DE Mouse phosphacan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 3.7%; Score 63.4; DB 12; Length 6887;
Best Local Similarity 45.6%; Pred. No. 1e-07;
RESULT 771
ID AAH82384 standard; cDNA; 434 BP.
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:8.
PN WO200151513-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.7%; Score 62.2; DB 5; Length 434;
Best Local Similarity 57.1%; Pred. No. 4.5e-08;
RESULT 772
ID ABN36392 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:9140.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 3.5%; Score 59; DB 6; Length 60;
Best Local Similarity 98.3%; Pred. No. 1.4e-07;
RESULT 773
ID AAS23827 standard; cDNA; 305 BP.
DE Human ovarian PCR-subtracted cDNA library clone #8.
PN WO200157207-A2.
PD 09-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.5%; Score 58.8; DB 4; Length 305;
Best Local Similarity 56.6%; Pred. No. 4.1e-07;
RESULT 774
ID AAF64764 standard; cDNA; 417 BP.
DE Novel human polynucleotide, SEQ ID NO: 520.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 58.8; DB 5; Length 417;
Best Local Similarity 52.4%; Pred. No. 5e-07;
RESULT 775
ID ABK63769 standard; cDNA; 988 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1676.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 58.8; DB 6; Length 988;
Best Local Similarity 50.0%; Pred. No. 8.4e-07;
RESULT 776
ID ADB58363 standard; DNA; 988 BP.
DE Toxicity-related gene, SEQ ID 3389.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.5%; Score 58.8; DB 10; Length 988;
Best Local Similarity 50.0%; Pred. No. 8.4e-07;
RESULT 777
ID AAH33294 standard; cDNA; 1233 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:350.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 58.4; DB 4; Length 1233;
Best Local Similarity 48.1%; Pred. No. 1.3e-06;
RESULT 778
ID ADA10961 standard; cDNA; 1244 BP.
DE Human cDNA differentially expressed in colon cancer #54.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 3.4%; Score 58.4; DB 9; Length 1244;
Best Local Similarity 48.1%; Pred. No. 1.3e-06;
RESULT 779
ID ADG47984 standard; DNA; 1244 BP.
DE Human carbonic anhydrase I (CAI) gene.
PN US2003101002-A1.
PD 29-MAY-2003.
PA (BART/) BARTHA G T.
PA (WALK/) WALKER M.
Query Match 3.4%; Score 58.4; DB 12; Length 1244;
Best Local Similarity 48.1%; Pred. No. 1.3e-06;

RESULT 780
ID AAL43637 standard; DNA; 2785 BP.
DE Human carbonic anhydrase I (Cln115) colon specific gene.
PN US2002042088-A1.
PD 11-APR-2002.
PA (MACI/) MACINA R A.
PA (PIDE/) PIDERIT A.
PA (SUNY/) SUN Y.
Query Match 3.4%; Score 58.4; DB 6; Length 2785;
Best Local Similarity 48.1%; Pred. No. 2.1e-06;
RESULT 781
ID ADG39671 standard; cDNA; 2785 BP.
DE Human cDNA #31 of gene differentially expressed in colorectal cancer.
PN US2003186302-A1.
PD 02-OCT-2003.
PA (WANG/) WANG Y.
Query Match 3.4%; Score 58.4; DB 12; Length 2785;
Best Local Similarity 48.1%; Pred. No. 2.1e-06;
RESULT 782
ID ADG39720 standard; cDNA; 2785 BP.
DE Human cDNA #31 of gene differentially expressed in colorectal cancer.
PN US2003186303-A1.
PD 02-OCT-2003.
PA (WANG/) WANG Y.
Query Match 3.4%; Score 58.4; DB 12; Length 2785;
Best Local Similarity 48.1%; Pred. No. 2.1e-06;
RESULT 783
ID AAD59160 standard; cDNA; 2826 BP.
DE Human carbonic anhydrase I (CAI) cDNA.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.
Query Match 3.4%; Score 58.4; DB 10; Length 2826;
Best Local Similarity 48.1%; Pred. No. 2.1e-06;
RESULT 784
ID ABA92275 standard; DNA; 1266 BP.
DE Streptavidin-carbonic anhydrase III (SAV-CAIII) fusion DNA.
PN WO200216943-A2.
PD 28-FEB-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 3.3%; Score 56; DB 6; Length 1266;
Best Local Similarity 49.8%; Pred. No. 7.2e-06;
RESULT 785
ID ADM66956 standard; DNA; 1743 BP.
DE Human adipocyte specific carbonic anhydrase III DNA SeqID 90.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Query Match 3.3%; Score 56; DB 12; Length 1743;
Best Local Similarity 49.8%; Pred. No. 8.7e-06;
RESULT 786
ID AAH57384 standard; cDNA; 1765 BP.
DE Human skeletal muscle cell specific cDNA sequence SEQ ID NO:224.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.3%; Score 56; DB 4; Length 1765;
Best Local Similarity 49.8%; Pred. No. 8.7e-06;
RESULT 787
ID ABQ93292 standard; cDNA; 2286 BP.
DE Human cDNA SEQ ID NO 5.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 56; DB 6; Length 2286;
Best Local Similarity 49.8%; Pred. No. 1e-05;
RESULT 788
ID ADQ18303 standard; DNA; 2357 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1121.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 56; DB 12; Length 2357;
Best Local Similarity 49.8%; Pred. No. 1e-05;
RESULT 789
ID AAS77142 standard; cDNA; 1084 BP.
DE DNA encoding novel human diagnostic protein #12946.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 54.6; DB 5; Length 1084;
Best Local Similarity 48.9%; Pred. No. 1.8e-05;
RESULT 790
ID AAQ67283 standard; cDNA; 6924 BP.
DE Human RPTP-beta.
PN WO9418308-A1.
PD 18-AUG-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 3.2%; Score 53.8; DB 2; Length 6924;
Best Local Similarity 45.1%; Pred. No. 9.5e-05;
RESULT 791
ID ADC51431 standard; DNA; 321 BP.
DE Ovine carbonate dehydratase gene SEQ ID NO:7.
PN JP2002306172-A.
PD 22-OCT-2002.
PA (KANF) KANEKA CORP.
Query Match 3.2%; Score 53.6; DB 10; Length 321;
Best Local Similarity 53.1%; Pred. No. 1.7e-05;
RESULT 792
ID ACH49863 standard; cDNA; 423 BP.
DE Human leukocyte cDNA #1457.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.1%; Score 53; DB 9; Length 423;
Best Local Similarity 55.0%; Pred. No. 3.1e-05;
RESULT 793
ID ADL90255 standard; DNA; 635 BP.
DE Human enzyme, ENZM-19 coding sequence, SEQ ID 65.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.1%; Score 53; DB 12; Length 635;
Best Local Similarity 55.0%; Pred. No. 4e-05;
RESULT 794
ID ADP71487 standard; DNA; 568 BP.
DE Renal toxin progression gene marker #76.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.1%; Score 52.6; DB 12; Length 568;
Best Local Similarity 52.5%; Pred. No. 5e-05;
RESULT 795
ID ADQ50263 standard; DNA; 579 BP.
DE Novel canine microarray-related DNA sequence SeqID1565.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 3.1%; Score 52.4; DB 13; Length 579;
Best Local Similarity 52.4%; Pred. No. 5.8e-05;
RESULT 796
ID ABN53472 standard; DNA; 65 BP.
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:26220.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 3.1%; Score 52.2; DB 6; Length 65;
Best Local Similarity 87.7%; Pred. No. 1.8e-05;
RESULT 797
ID AAD48126 standard; DNA; 3091 BP.

DE Human protein tyrosine phosphatase zeta SM1 variant DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 3.1%; Score 52.2; DB 8; Length 3091;
Best Local Similarity 44.9%; Pred. No. 0.00018;
RESULT 798
ID ADN39729 standard; cDNA; 3340 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C101.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 3340;
Best Local Similarity 44.9%; Pred. No. 0.00019;
RESULT 799
ID ADQ18133 standard; DNA; 3350 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 950.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.1%; Score 52.2; DB 12; Length 3350;
Best Local Similarity 44.9%; Pred. No. 0.00019;
RESULT 800
ID ADN39731 standard; cDNA; 4220 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C103.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 4220;
Best Local Similarity 44.9%; Pred. No. 0.00022;
RESULT 801
ID ADN39724 standard; cDNA; 4347 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C96.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 4347;
Best Local Similarity 44.9%; Pred. No. 0.00023;
RESULT 802
ID ABX76418 standard; DNA; 5343 BP.
DE Lung cancer-associated polynucleotide #282.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5343;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 803
ID ABX76219 standard; DNA; 5343 BP.
DE Lung cancer-associated polynucleotide #88.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5343;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 804
ID ADN39057 standard; cDNA; 5343 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:375.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 5343;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 805
ID ABX76417 standard; DNA; 5367 BP.
DE Lung cancer-associated polynucleotide #281.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5367;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 806
ID ABX76218 standard; DNA; 5367 BP.
DE Lung cancer-associated polynucleotide #87.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5367;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 807
ID ADN39055 standard; cDNA; 5367 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:373.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 5367;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 808
ID ADN39726 standard; cDNA; 5367 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C98.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 5367;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 809
ID ABX76420 standard; DNA; 5481 BP.
DE Lung cancer-associated polynucleotide #284.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5481;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 810
ID ABX76221 standard; DNA; 5481 BP.
DE Lung cancer-associated polynucleotide #90.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 5481;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 811
ID ADN39728 standard; cDNA; 5481 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C100.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 5481;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 812
ID ADN39061 standard; cDNA; 5481 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:379.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 5481;
Best Local Similarity 44.9%; Pred. No. 0.00026;
RESULT 813
ID ABL66502 standard; DNA; 7941 BP.
DE Lung cancer related gene sequence SEQ ID NO:4839.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.1%; Score 52.2; DB 6; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 814
ID ABX76421 standard; DNA; 7941 BP.
DE Lung cancer-associated polynucleotide #285.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 815
ID AAD48125 standard; DNA; 7941 BP.
DE Human PTPRZ1 DNA.
PN WO200276510-A1.

PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 3.1%; Score 52.2; DB 8; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 816
ID ACC72641 standard; cDNA; 7941 BP.
DE Human protein tyrosine phosphatase receptor-type z polypeptide 1 cDNA.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 10; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 817
ID ADN39063 standard; cDNA; 7941 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:381.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 818
ID ADJ75139 standard; DNA; 7941 BP.
DE Marker gene SEQ ID NO:391.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 3.1%; Score 52.2; DB 12; Length 7941;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 819
ID ABX76217 standard; DNA; 7944 BP.
DE Lung cancer-associated polynucleotide #86.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 7944;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 820
ID ABX76416 standard; DNA; 7944 BP.
DE Lung cancer-associated polynucleotide #280.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 8; Length 7944;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 821
ID ADN39725 standard; cDNA; 7944 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C97.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 7944;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 822
ID ADN39053 standard; cDNA; 7944 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:371.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.1%; Score 52.2; DB 11; Length 7944;
Best Local Similarity 44.9%; Pred. No. 0.00032;
RESULT 823
ID AAD48127 standard; DNA; 8058 BP.
DE Human protein tyrosine phosphatase zeta SM2 variant DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 3.1%; Score 52.2; DB 8; Length 8058;
Best Local Similarity 44.9%; Pred. No. 0.00033;
RESULT 824
ID AAH73240 standard; cDNA; 8146 BP.
DE Human cervical cancer marker nucleic acid 4514.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 52.2; DB 4; Length 8146;
Best Local Similarity 44.9%; Pred. No. 0.00033;
RESULT 825
ID ADQ22702 standard; DNA; 8292 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5522.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.1%; Score 52.2; DB 12; Length 8292;
Best Local Similarity 44.9%; Pred. No. 0.00033;
RESULT 826
ID ACH37537 standard; cDNA; 478 BP.
DE Human endothelial cell cDNA #5670.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.1%; Score 52; DB 9; Length 478;
Best Local Similarity 67.6%; Pred. No. 6.9e-05;
RESULT 827
ID AAF65774 standard; cDNA; 398 BP.
DE Novel human polynucleotide, SEQ ID NO: 1530.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 51.8; DB 5; Length 398;
Best Local Similarity 52.6%; Pred. No. 7.1e-05;
RESULT 828
ID ACN41600 standard; cDNA; 1430 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:475.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.0%; Score 51.8; DB 13; Length 1430;
Best Local Similarity 51.0%; Pred. No. 0.00015;
RESULT 829
ID ACN41597 standard; cDNA; 1705 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:472.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.0%; Score 51.8; DB 13; Length 1705;
Best Local Similarity 51.0%; Pred. No. 0.00017;
RESULT 830
ID ABT07619 standard; cDNA; 3670 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 98.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 3.0%; Score 51.8; DB 6; Length 3670;
Best Local Similarity 49.1%; Pred. No. 0.00027;
RESULT 831
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.0%; Score 51.8; DB 11; Length 128668;
Best Local Similarity 54.5%; Pred. No. 0.0023;
RESULT 832
ID AAC00298 standard; cDNA; 408 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 296.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.0%; Score 51.4; DB 3; Length 408;
Best Local Similarity 54.6%; Pred. No. 9.6e-05;
RESULT 833

ID ADJ44746 standard; cDNA; 981 BP.
DE Plant cDNA #5746.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 50.8; DB 12; Length 981;
Best Local Similarity 55.7%; Pred. No. 0.00025;
RESULT 834
ID ABS59531 standard; cDNA; 1104 BP.
DE Human cDNA, designated SEC10.
PN WO200255705-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.0%; Score 50.8; DB 6; Length 1104;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 835
ID ABZ22559 standard; cDNA; 1104 BP.
DE Human carbonic anhydrase IV encoding cDNA SEQ ID NO:12.
PN WO2002100336-A2.
PD 19-DEC-2002.
PA (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Query Match 3.0%; Score 50.8; DB 8; Length 1104;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 836
ID ADB75223 standard; cDNA; 1104 BP.
DE Prostate cancer marker cDNA.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.0%; Score 50.8; DB 10; Length 1104;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 837
ID ADL56809 standard; cDNA; 1104 BP.
DE Human SECX cDNA #10.
PN US2003215449-A1.
PD 20-NOV-2003.
PA (MEZE/) MEZES P D.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGHS C.
PA (SPYT/) SPYTEK K A.
PA (DIPI/) DIPIPPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYM/) PEYMAN J A.
PA (ELLE/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
PA (VOSS/) VOSS E Z.
PA (MILL/) MILLER C E.
Query Match 3.0%; Score 50.8; DB 12; Length 1104;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 838
ID ADO28596 standard; cDNA; 1104 BP.
DE Human CAH4 encoding cDNA SEQ ID NO:25.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.0%; Score 50.8; DB 12; Length 1104;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 839
ID ABL61831 standard; DNA; 1105 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:168.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.0%; Score 50.8; DB 6; Length 1105;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 840
ID ABL65919 standard; DNA; 1105 BP.
DE Lung cancer related gene sequence SEQ ID NO:4256.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.0%; Score 50.8; DB 6; Length 1105;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 841
ID ABK84097 standard; cDNA; 1105 BP.
DE Human cDNA differentially expressed in granulocytic cells #668.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 50.8; DB 6; Length 1105;
Best Local Similarity 48.4%; Pred. No. 0.00027;
RESULT 842
ID ADA10949 standard; cDNA; 1237 BP.
DE Human cDNA differentially expressed in colon cancer #45.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 3.0%; Score 50.8; DB 9; Length 1237;
Best Local Similarity 48.4%; Pred. No. 0.00029;
RESULT 843
ID ABT09359 standard; DNA; 683 BP.
DE Phase-1 Rat CT gene SEQ ID No 447.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.0%; Score 50.6; DB 6; Length 683;
Best Local Similarity 50.8%; Pred. No. 0.00023;
RESULT 844
ID ADG30858 standard; DNA; 683 BP.
DE Liver toxicity predictive DNA 38.
PN WO2003085083-A2.
PD 16-OCT-2003.
PA (PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.
Query Match 3.0%; Score 50.6; DB 10; Length 683;
Best Local Similarity 50.8%; Pred. No. 0.00023;
RESULT 845
ID ADG45418 standard; DNA; 683 BP.
DE Liver inflammatory predictive gene related DNA sequence.
PN WO2003095624-A2.
PD 20-NOV-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.0%; Score 50.6; DB 12; Length 683;
Best Local Similarity 50.8%; Pred. No. 0.00023;
RESULT 846
ID ADR91076 standard; cDNA; 683 BP.
DE Spleen necrosis predictive cDNA sequence, SEQ ID No 32.
PN WO2004083402-A2.
PD 30-SEP-2004.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

Query Match 3.0%; Score 50.6; DB 13; Length 683;
Best Local Similarity 50.8%; Pred. No. 0.00023;
RESULT 847
ID ADN39730 standard; cDNA; 4480 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C102.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.0%; Score 50.6; DB 11; Length 4480;
Best Local Similarity 44.8%; Pred. No. 0.00072;
RESULT 848
ID ADC51425 standard; DNA; 261 BP.
DE Ovine carbonate dehydratase cDNA SEQ ID NO:1.
PN JP2002306172-A.
PD 22-OCT-2002.
PA (KANF) KANEKA CORP.
Query Match 3.0%; Score 50.4; DB 10; Length 261;
Best Local Similarity 52.8%; Pred. No. 0.00015;
RESULT 849
ID ABK83564 standard; cDNA; 198161 BP.
DE Human cDNA differentially expressed in granulocytic cells #135.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 50.4; DB 6; Length 198161;
Best Local Similarity 69.0%; Pred. No. 0.0081;
RESULT 850
ID ADQ17348 standard; DNA; 198161 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 165.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.0%; Score 50.4; DB 12; Length 198161;
Best Local Similarity 69.0%; Pred. No. 0.0081;
RESULT 851
ID ADR52701 standard; DNA; 198161 BP.
DE Drug therapy altered expressed gene #52.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.0%; Score 50.4; DB 13; Length 198161;
Best Local Similarity 69.0%; Pred. No. 0.0081;
RESULT 852
ID ADF08271 standard; DNA; 263744 BP.
DE Mouse apoA5 DNA.
PN US2003150003-A1.
PD 07-AUG-2003.
PA (RUBI/) RUBIN E.
PA (PENN/) PENNACCHIO L A.
Query Match 3.0%; Score 50.2; DB 10; Length 263744;
Best Local Similarity 68.3%; Pred. No. 0.011;
RESULT 853
ID ADO39193 standard; cDNA; 1104 BP.
DE Human cDNA encoding novel secreted protein SEC10.
PN US2004018196-A1.
PD 29-JAN-2004.
PA (MEZE/) MEZES P D.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGHS C.
PA (SPYT/) SPYTEK K A.
PA (DIPI/) DIPIPPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYM/) PEYMAN J A.
PA (ELLE/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
Query Match 2.9%; Score 49.8; DB 12; Length 1104;
Best Local Similarity 48.2%; Pred. No. 0.00055;
RESULT 854
ID ADA02519 standard; DNA; 23169 BP.
DE Mouse Nmcy1 carcinoma associated gene, SEQ ID NO:1037.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.9%; Score 49.6; DB 9; Length 23169;
Best Local Similarity 72.7%; Pred. No. 0.0039;
RESULT 855
ID ADB72257 standard; DNA; 23169 BP.
DE Mouse Nmyc1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.9%; Score 49.6; DB 10; Length 23169;
Best Local Similarity 72.7%; Pred. No. 0.0039;
RESULT 856
ID ADE95767 standard; DNA; 23169 BP.
DE Mouse Nmyc1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.9%; Score 49.6; DB 10; Length 23169;
Best Local Similarity 72.7%; Pred. No. 0.0039;
RESULT 857
ID ADQ97640 standard; DNA; 79731 BP.
DE Mouse cancer associated sequence MD10-020, SEQ ID 617.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.9%; Score 49.6; DB 12; Length 79731;
Best Local Similarity 63.3%; Pred. No. 0.0083;
RESULT 858
ID ADQ97433 standard; DNA; 295772 BP.
DE Human cancer associated sequence HD08-047, SEQ ID 410.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.9%; Score 49.4; DB 12; Length 295772;
Best Local Similarity 68.7%; Pred. No. 0.021;
RESULT 859
ID ABD33622 standard; DNA; 125322 BP.
DE Murine cancer-associated (CA) gene MD07-127.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.9%; Score 49.2; DB 13; Length 125322;
Best Local Similarity 70.2%; Pred. No. 0.014;
RESULT 860
ID ABL13349 standard; cDNA; 1439 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34529.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.9%; Score 49; DB 4; Length 1439;
Best Local Similarity 47.7%; Pred. No. 0.0011;
RESULT 861
ID ABL13348 standard; cDNA; 8352 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34526.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.9%; Score 49; DB 4; Length 8352;
Best Local Similarity 47.7%; Pred. No. 0.0033;
RESULT 862
ID ABD33460 standard; DNA; 119057 BP.
DE Murine cancer-associated (CA) gene MD07-088.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.9%; Score 49; DB 13; Length 119057;
Best Local Similarity 56.5%; Pred. No. 0.016;
RESULT 863
ID AAF64493 standard; cDNA; 428 BP.
DE Novel human polynucleotide, SEQ ID NO: 249.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.8; DB 5; Length 428;
Best Local Similarity 55.2%; Pred. No. 0.00063;
RESULT 864
ID ABD33364 standard; DNA; 203132 BP.
DE Murine cancer-associated (CA) gene MD07-067.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.9%; Score 48.6; DB 13; Length 203132;
Best Local Similarity 72.4%; Pred. No. 0.03;
RESULT 865
ID AAF64493 standard; cDNA; 428 BP.
DE Novel human polynucleotide, SEQ ID NO: 249.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.8%; Score 48.4; DB 5; Length 428;
Best Local Similarity 57.5%; Pred. No. 0.00084;
RESULT 866
ID ABX76220 standard; DNA; 5363 BP.
DE Lung cancer-associated polynucleotide #89.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.8%; Score 48.4; DB 8; Length 5363;
Best Local Similarity 51.9%; Pred. No. 0.0038;
RESULT 867
ID ABX76419 standard; DNA; 5363 BP.
DE Lung cancer-associated polynucleotide #283.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.8%; Score 48.4; DB 8; Length 5363;
Best Local Similarity 51.9%; Pred. No. 0.0038;
RESULT 868
ID ADN39059 standard; cDNA; 5363 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:377.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.8%; Score 48.4; DB 11; Length 5363;
Best Local Similarity 51.9%; Pred. No. 0.0038;
RESULT 869
ID ADN39727 standard; cDNA; 5363 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C99.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.8%; Score 48.4; DB 11; Length 5363;
Best Local Similarity 51.9%; Pred. No. 0.0038;
RESULT 870
ID ADQ22835 standard; DNA; 2905 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5655.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.8%; Score 47.4; DB 12; Length 2905;
Best Local Similarity 50.7%; Pred. No. 0.0054;
RESULT 871
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 47.2; DB 8; Length 2000;
Best Local Similarity 9.2%; Pred. No. 0.005;
RESULT 872
ID ABA19436 standard; DNA; 6804 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11767.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 47.2; DB 5; Length 6804;
Best Local Similarity 80.9%; Pred. No. 0.01;
RESULT 873
ID ABA17963 standard; DNA; 32192 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10294.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 47.2; DB 5; Length 32192;
Best Local Similarity 65.6%; Pred. No. 0.026;
RESULT 874
ID ACN44160 standard; DNA; 47745 BP.
DE Mouse genomic sequence mCG15331.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 47.2; DB 11; Length 47745;
Best Local Similarity 59.8%; Pred. No. 0.034;
RESULT 875
ID AAL57580 standard; cDNA; 93273 BP.
DE Human GTPase activating protein-like cDNA.
PN WO2003059148-A2.
PD 24-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
Query Match 2.8%; Score 47.2; DB 9; Length 93273;
Best Local Similarity 80.9%; Pred. No. 0.05;
RESULT 876
ID ADQ19685 standard; DNA; 115863 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2504.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.8%; Score 47.2; DB 12; Length 115863;
Best Local Similarity 72.6%; Pred. No. 0.057;
RESULT 877
ID ACN44148 standard; DNA; 256525 BP.
DE Mouse genomic sequence mCG15044.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 47; DB 11; Length 256525;
Best Local Similarity 52.4%; Pred. No. 0.11;
RESULT 878
ID ADQ24706 standard; DNA; 3079 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7526.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.8%; Score 46.8; DB 12; Length 3079;
Best Local Similarity 57.5%; Pred. No. 0.0086;
RESULT 879
ID ABV01614 standard; cDNA; 323 BP.

DE Human prostate expression marker cDNA 1605.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 46.6; DB 5; Length 323;
Best Local Similarity 68.8%; Pred. No. 0.0026;
RESULT 880
ID ABV10783 standard; cDNA; 324 BP.
DE Human prostate expression marker cDNA 10774.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 46.6; DB 5; Length 324;
Best Local Similarity 68.8%; Pred. No. 0.0026;
RESULT 881
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 46.6; DB 8; Length 2000;
Best Local Similarity 9.6%; Pred. No. 0.0076;
RESULT 882
ID ADQ97602 standard; DNA; 76644 BP.
DE Mouse cancer associated sequence MD10-013, SEQ ID 579.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 46.6; DB 12; Length 76644;
Best Local Similarity 66.3%; Pred. No. 0.068;
RESULT 883
ID ABX35889 standard; cDNA; 453 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1054.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.7%; Score 46.4; DB 8; Length 453;
Best Local Similarity 50.9%; Pred. No. 0.0036;
RESULT 884
ID ABD32594 standard; DNA; 684187 BP.
DE Mouse cancer-associated genomic DNA MD7-220.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 46.4; DB 13; Length 110000;
Best Local Similarity 59.4%; Pred. No. 0.098;
RESULT 885
ID ACN45180 standard; DNA; 185555 BP.
DE Mouse genomic sequence mCG9266.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 46.2; DB 11; Length 185555;
Best Local Similarity 62.6%; Pred. No. 0.15;
RESULT 886
ID ADQ59377 standard; DNA; 225734 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:13.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 46.2; DB 12; Length 225734;
Best Local Similarity 66.7%; Pred. No. 0.17;
RESULT 887
ID ADA70246 standard; DNA; 828 BP.
DE Rice gene, SEQ ID 3569.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 46; DB 8; Length 828;
Best Local Similarity 65.7%; Pred. No. 0.0069;

RESULT 888
ID ACN44224 standard; DNA; 157044 BP.
DE Mouse genomic sequence mCG16088.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 46; DB 11; Length 157044;
Best Local Similarity 60.3%; Pred. No. 0.16;
RESULT 889
ID ABL64977 standard; DNA; 1523 BP.
DE Lung cancer related gene sequence SEQ ID NO:3314.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.7%; Score 45.8; DB 6; Length 1523;
Best Local Similarity 48.4%; Pred. No. 0.011;
RESULT 890
ID ABL62488 standard; DNA; 1523 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:825.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.7%; Score 45.8; DB 6; Length 1523;
Best Local Similarity 48.4%; Pred. No. 0.011;
RESULT 891
ID ABL68606 standard; DNA; 1523 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6943.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.7%; Score 45.8; DB 6; Length 1523;
Best Local Similarity 48.4%; Pred. No. 0.011;
RESULT 892
ID ABN97349 standard; DNA; 1523 BP.
DE Gene #3847 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 45.8; DB 6; Length 1523;
Best Local Similarity 48.4%; Pred. No. 0.011;
RESULT 893
ID ADS73156 standard; cDNA; 1551 BP.
DE Human kidney tumour specific cDNA, SEQ ID 1753.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 45.8; DB 7; Length 1551;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 894
ID ADO24557 standard; cDNA; 1551 BP.
DE Human PRO62628 encoding cDNA SEQ ID NO:196.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 45.8; DB 12; Length 1551;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 895
ID ADR24562 standard; DNA; 1551 BP.
DE Breast cancer prognosis marker #423.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 2.7%; Score 45.8; DB 13; Length 1551;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 896
ID ADP24251 standard; cDNA; 1551 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1429.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 45.8; DB 13; Length 1551;
Best Local Similarity 48.4%; Pred. No. 0.012;

RESULT 897
ID ADQ23525 standard; DNA; 1608 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6345.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 45.8; DB 12; Length 1608;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 898
ID AAC98162 standard; cDNA; 1723 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:172.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.8; DB 3; Length 1723;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 899
ID AAS94944 standard; DNA; 1755 BP.
DE Human DNA sequence #199 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 45.8; DB 6; Length 1755;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 900
ID AAD59159 standard; cDNA; 1755 BP.
DE Human carbonic anhydrase II cDNA.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.
Query Match 2.7%; Score 45.8; DB 10; Length 1755;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 901
ID ADI61756 standard; cDNA; 1755 BP.
DE Human cDNA upregulated in Alzheimer's disease, INCYTE 248306.1.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.7%; Score 45.8; DB 12; Length 1755;
Best Local Similarity 48.4%; Pred. No. 0.012;
RESULT 902
ID ADL63525 standard; DNA; 1886 BP.
DE Human ovarian cancer DNA marker #21737.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 45.8; DB 5; Length 1886;
Best Local Similarity 48.4%; Pred. No. 0.013;
RESULT 903
ID ABK35712 standard; cDNA; 2391 BP.
DE cDNA sequence #103 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.7%; Score 45.8; DB 6; Length 2391;
Best Local Similarity 48.4%; Pred. No. 0.015;
RESULT 904
ID ABV21018 standard; cDNA; 4742 BP.
DE Human prostate expression marker cDNA 21009.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 45.8; DB 5; Length 4742;
Best Local Similarity 69.7%; Pred. No. 0.023;
RESULT 905
ID ABV23634 standard; cDNA; 4742 BP.
DE Human prostate expression marker cDNA 23625.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 45.8; DB 5; Length 4742;
Best Local Similarity 69.7%; Pred. No. 0.023;
RESULT 906
ID ABV29493 standard; cDNA; 4742 BP.
DE Human prostate expression marker cDNA 29484.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 45.8; DB 5; Length 4742;
Best Local Similarity 69.7%; Pred. No. 0.023;
RESULT 907
ID ABV26861 standard; cDNA; 4742 BP.
DE Human prostate expression marker cDNA 26852.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 45.8; DB 5; Length 4742;
Best Local Similarity 69.7%; Pred. No. 0.023;
RESULT 908
ID AAZ23899 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Query Match 2.7%; Score 45.8; DB 2; Length 49999;
Best Local Similarity 76.7%; Pred. No. 0.094;
RESULT 909
ID ABD33568 standard; DNA; 115223 BP.
DE Murine cancer-associated (CA) gene MD07-114.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 45.8; DB 13; Length 115223;
Best Local Similarity 87.7%; Pred. No. 0.15;
RESULT 910
ID ADQ97107 standard; DNA; 121124 BP.
DE Mouse cancer associated sequence MD08-002, SEQ ID 83.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 45.8; DB 12; Length 121124;
Best Local Similarity 59.9%; Pred. No. 0.16;
RESULT 911
ID AAT45889 standard; cDNA; 605 BP.
DE Human colon specific gene CSG10 cDNA partial clone.
PN WO9639419-A1.
PD 12-DEC-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.6; DB 2; Length 605;
Best Local Similarity 48.7%; Pred. No. 0.0076;
RESULT 912
ID AAV16677 standard; cDNA; 605 BP.
DE Polynucleotide sequence of a colon-specific gene.
PN US5733748-A.
PD 31-MAR-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.6; DB 2; Length 605;
Best Local Similarity 48.7%; Pred. No. 0.0076;
RESULT 913
ID ABK15465 standard; cDNA; 605 BP.
DE Human colon specific gene 10 (CSG10) cDNA.
PN US6337195-B1.
PD 08-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.6; DB 6; Length 605;
Best Local Similarity 48.7%; Pred. No. 0.0076;
RESULT 914
ID ABS52546 standard; cDNA; 605 BP.
DE Human colon specific gene (CSG) 11 cDNA.
PN US2002086314-A1.
PD 04-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.6; DB 6; Length 605;
Best Local Similarity 48.7%; Pred. No. 0.0076;
RESULT 915

ID ADQ58735 standard; cDNA; 605 BP.
DE Human colon specific gene #8.
PN US2004132976-A1.
PD 08-JUL-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 45.6; DB 12; Length 605;
Best Local Similarity 48.7%; Pred. No. 0.0076;
RESULT 916
ID AAI86182 standard; cDNA; 254 BP.
DE Human polynucleotide SEQ ID NO 6242.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 45.4; DB 4; Length 254;
Best Local Similarity 70.1%; Pred. No. 0.0052;
RESULT 917
Query Match 2.7%; Score 45.4; DB 8; Length 110000;
Best Local Similarity 58.9%; Pred. No. 0.2;
RESULT 918
ID ADQ59449 standard; DNA; 153740 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:85.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 45.4; DB 12; Length 153740;
Best Local Similarity 61.3%; Pred. No. 0.24;
RESULT 919
ID AAF65716 standard; cDNA; 427 BP.
DE Novel human polynucleotide, SEQ ID NO: 1472.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 45.2; DB 5; Length 427;
Best Local Similarity 52.7%; Pred. No. 0.0082;
RESULT 920
ID ADD29627 standard; mRNA; 1077 BP.
DE Human tumour suppressor mRNA SEQ ID NO:82.
PN WO2003058201-A2.
PD 17-JUL-2003.
PA (QUAR-) QUARK BIOTECH INC.
PA (CLEV-) CLEVELAND CLINIC FOUND.
Query Match 2.7%; Score 45.2; DB 10; Length 1077;
Best Local Similarity 54.9%; Pred. No. 0.014;
RESULT 921
ID ADQ97821 standard; DNA; 49077 BP.
DE Mouse cancer associated sequence MD11-004, SEQ ID 798.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 45.2; DB 12; Length 49077;
Best Local Similarity 71.6%; Pred. No. 0.14;
RESULT 922
ID ACN44280 standard; DNA; 91141 BP.
DE Mouse genomic sequence mCG16959.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 45.2; DB 11; Length 91141;
Best Local Similarity 59.2%; Pred. No. 0.21;
RESULT 923
ID ACN44070 standard; DNA; 344548 BP.
DE Human genomic sequence hCG36954.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 45.2; DB 11; Length 344548;
Best Local Similarity 58.0%; Pred. No. 0.46;
RESULT 924
ID AAA37330 standard; DNA; 45 BP.
DE Human PRO1335 hybridisation probe SEQ ID NO:427.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 925
ID AAF54505 standard; DNA; 45 BP.
DE Primer #121 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 926
ID ACD68544 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #55.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 927
ID ACH04646 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 928
ID ACD68190 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #55.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 929
ID ADC18296 standard; DNA; 45 BP.
DE Human PRO probe #60.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 930
ID ADD70942 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 931
ID ADD40019 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 932
ID ADD70465 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 933
ID ADD38586 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

```
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 934
ID   ADD39542 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003096954-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 935
ID   ADD39065 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003092061-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 936
ID   ADD40496 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003082627-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 937
ID   ADE50717 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003069179-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 938
ID   ADE20329 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003092883-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 939
ID   ADE50240 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003082626-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 940
ID   ADE21798 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003082628-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 941
ID   ADF30223 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003204053-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 942
ID   ADF56116 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003204054-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 943
ID   ADH99620 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003065142-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 944
ID   ADE96800 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003195347-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 945
ID   ADF26111 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003199675-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 946
ID   ADF25010 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003198993-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 947
ID   ADF29746 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003203401-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 948
ID   ADE97277 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003195334-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 949
ID   ADH03315 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003216562-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 950
ID   ADH04269 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003220471-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
RESULT 951
ID   ADH03792 standard; DNA; 45 BP.
DE   Human secreted/transmembrane protein PRO1335 probe.
PN   US2003224478-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             2.6%;  Score 45;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0024;
```

RESULT 952
ID ADH04746 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 953
ID ADH61747 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 954
ID ADL94946 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1335 probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0024;
RESULT 955
ID AAF66094 standard; cDNA; 395 BP.
DE Novel human polynucleotide, SEQ ID NO: 1850.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 45; DB 5; Length 395;
Best Local Similarity 63.3%; Pred. No. 0.009;
RESULT 956
ID AAI89231 standard; cDNA; 472 BP.
DE Human polynucleotide SEQ ID NO 9291.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 45; DB 4; Length 472;
Best Local Similarity 80.2%; Pred. No. 0.01;
RESULT 957
ID AAK68792 standard; DNA; 1820 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23604.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 45; DB 4; Length 1820;
Best Local Similarity 65.3%; Pred. No. 0.023;
RESULT 958
ID AAK68793 standard; DNA; 1820 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23605.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 45; DB 4; Length 1820;
Best Local Similarity 65.3%; Pred. No. 0.023;
RESULT 959
ID AAK68794 standard; DNA; 1820 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23606.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 45; DB 4; Length 1820;
Best Local Similarity 65.3%; Pred. No. 0.023;
RESULT 960
ID AAK65890 standard; DNA; 38771 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20702.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 45; DB 4; Length 38771;
Best Local Similarity 67.7%; Pred. No. 0.14;
RESULT 961
ID ADL15091 standard; DNA; 125729 BP.
DE Human PHKBP1 pseudogene DNA for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 2.6%; Score 45; DB 10; Length 125729;
Best Local Similarity 67.7%; Pred. No. 0.29;
RESULT 962
ID AAH88704 standard; DNA; 160755 BP.
DE Human DNA sequence SEQ ID 544.
PN WO200151659-A2.
PD 19-JUL-2001.
PA (GEST) GENSET.
Query Match 2.6%; Score 45; DB 4; Length 160755;
Best Local Similarity 65.3%; Pred. No. 0.33;
RESULT 963
ID ABQ82329 standard; cDNA; 1108 BP.
DE Human NOV4 encoding cDNA SEQ ID NO:7.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 44.8; DB 6; Length 1108;
Best Local Similarity 54.3%; Pred. No. 0.019;
RESULT 964
ID ACN45048 standard; DNA; 32963 BP.
DE Mouse genomic sequence mCG7264.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.8; DB 11; Length 32963;
Best Local Similarity 69.4%; Pred. No. 0.15;
RESULT 965
Query Match 2.6%; Score 44.8; DB 12; Length 110000;
Best Local Similarity 59.4%; Pred. No. 0.31;
RESULT 966
Query Match 2.6%; Score 44.8; DB 13; Length 110000;
Best Local Similarity 65.3%; Pred. No. 0.31;
RESULT 967
ID AAI16839 standard; DNA; 600 BP.
DE Probe #6772 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 968
ID ABA60650 standard; DNA; 600 BP.
DE Human foetal liver single exon nucleic acid probe #8955.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 969
ID AAI40540 standard; DNA; 600 BP.
DE Probe #9226 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 970
ID ABA28752 standard; DNA; 600 BP.
DE Probe #7218 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 971
ID AAK34823 standard; DNA; 600 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 9380.

PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 972
ID AAK08932 standard; DNA; 600 BP.
DE Human brain expressed single exon probe SEQ ID NO: 8923.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 973
ID ABS34586 standard; DNA; 600 BP.
DE Human liver single exon probe, SEQ ID No 9576.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 4; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 974
ID ABS09368 standard; DNA; 600 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 9359.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.6%; Score 44.6; DB 6; Length 600;
Best Local Similarity 58.8%; Pred. No. 0.015;
RESULT 975
ID ABD33526 standard; DNA; 31312 BP.
DE Murine cancer-associated (CA) gene MD07-104.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 44.6; DB 13; Length 31312;
Best Local Similarity 71.1%; Pred. No. 0.17;
RESULT 976
ID ABS55821 standard; DNA; 69327 BP.
DE Human transporter protein gene.
Query Match 2.6%; Score 44.6; DB 6; Length 69327;
Best Local Similarity 60.2%; Pred. No. 0.27;
RESULT 977
ID ADL15741 standard; DNA; 69327 BP.
DE Novel human transporter genomic DNA.
Query Match 2.6%; Score 44.6; DB 12; Length 69327;
Best Local Similarity 60.2%; Pred. No. 0.27;
RESULT 978
ID ACN45170 standard; DNA; 133955 BP.
DE Human genomic sequence hCG23504.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.6; DB 11; Length 133955;
Best Local Similarity 58.8%; Pred. No. 0.4;
RESULT 979
ID ADA02520 standard; cDNA; 7340 BP.
DE Mouse Nmcy1 carcinoma associated cDNA, SEQ ID NO:1038.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.4; DB 9; Length 7340;
Best Local Similarity 64.7%; Pred. No. 0.08;
RESULT 980
ID ADB72258 standard; mRNA; 7340 BP.
DE Mouse Nmyc1 mRNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.4; DB 10; Length 7340;
Best Local Similarity 64.7%; Pred. No. 0.08;
RESULT 981
ID ADE95768 standard; DNA; 7340 BP.
DE Mouse DNA related to Nmyc1 gene mRNA.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.4; DB 10; Length 7340;
Best Local Similarity 64.7%; Pred. No. 0.08;
RESULT 982
ID ABD32846 standard; DNA; 89873 BP.
DE Mouse cancer-associated genomic DNA MD17-016.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 44.4; DB 13; Length 89873;
Best Local Similarity 65.6%; Pred. No. 0.36;
RESULT 983
ID ACN44070 standard; DNA; 344548 BP.
DE Human genomic sequence hCG36954.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 44.4; DB 11; Length 344548;
Best Local Similarity 67.0%; Pred. No. 0.81;
RESULT 984
ID AAF64628 standard; cDNA; 386 BP.
DE Novel human polynucleotide, SEQ ID NO: 384.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 44.2; DB 5; Length 386;
Best Local Similarity 56.4%; Pred. No. 0.016;
RESULT 985
ID AAF66094 standard; cDNA; 395 BP.
DE Novel human polynucleotide, SEQ ID NO: 1850.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 44.2; DB 5; Length 395;
Best Local Similarity 68.8%; Pred. No. 0.016;
RESULT 986
ID ACN41705 standard; cDNA; 1529 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:580.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.6%; Score 44.2; DB 13; Length 1529;
Best Local Similarity 47.5%; Pred. No. 0.036;
RESULT 987
ID ADA10998 standard; cDNA; 1759 BP.
DE Human cDNA differentially expressed in colon cancer #78.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 2.6%; Score 44.2; DB 9; Length 1759;
Best Local Similarity 48.1%; Pred. No. 0.039;
RESULT 988
ID ACH04029 standard; cDNA; 1759 BP.
DE Human cDNA differentially expressed in lung cancer #234.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 2.6%; Score 44.2; DB 9; Length 1759;
Best Local Similarity 48.1%; Pred. No. 0.039;
RESULT 989
ID ADL12914 standard; cDNA; 1759 BP.
DE Human steroid-induced C3A liver cell cDNA #643.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.6%; Score 44.2; DB 12; Length 1759;
Best Local Similarity 48.1%; Pred. No. 0.039;

RESULT 990
ID ADQ97761 standard; DNA; 71594 BP.
DE Mouse cancer associated sequence MD10-042, SEQ ID 738.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 44.2; DB 12; Length 71594;
Best Local Similarity 59.2%; Pred. No. 0.36;
RESULT 991
ID ABD33020 standard; DNA; 256294 BP.
DE Mouse cancer-associated genomic DNA MD22-007.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 44.2; DB 13; Length 256294;
Best Local Similarity 60.3%; Pred. No. 0.78;
RESULT 992
ID AAI88728 standard; cDNA; 343 BP.
DE Human polynucleotide SEQ ID NO 8788.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 44; DB 4; Length 343;
Best Local Similarity 65.3%; Pred. No. 0.017;
RESULT 993
ID AAF66668 standard; cDNA; 399 BP.
DE Novel human polynucleotide, SEQ ID NO: 2424.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 44; DB 5; Length 399;
Best Local Similarity 61.2%; Pred. No. 0.019;
RESULT 994
ID ADG76389 standard; cDNA; 1635 BP.
DE Human Incyte cDNA encoding an enzyme (SeqID 81).
PN WO2003083082-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.6%; Score 44; DB 10; Length 1635;
Best Local Similarity 47.4%; Pred. No. 0.043;
RESULT 995
ID ADR67061 standard; DNA; 75164 BP.
DE Mouse cancer associated gene genomic sequence SEQ ID NO:107.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 44; DB 13; Length 75164;
Best Local Similarity 58.8%; Pred. No. 0.43;
RESULT 996
Query Match 2.6%; Score 44; DB 13; Length 110000;
Best Local Similarity 70.2%; Pred. No. 0.54;
RESULT 997
Query Match 2.6%; Score 44; DB 13; Length 110000;
Best Local Similarity 77.9%; Pred. No. 0.54;
RESULT 998
ID ADP03002 standard; cDNA; 140152 BP.
DE Human housekeeping gene cDNA #43.
PN JP2004135552-A.
PD 13-MAY-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 2.6%; Score 44; DB 12; Length 140152;
Best Local Similarity 58.3%; Pred. No. 0.63;
RESULT 999
ID ADS88500 standard; cDNA; 140152 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:43.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 2.6%; Score 44; DB 13; Length 140152;
Best Local Similarity 58.3%; Pred. No. 0.63;
RESULT 1000
ID AAF66649 standard; cDNA; 397 BP.
DE Novel human polynucleotide, SEQ ID NO: 2405.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 43.8; DB 5; Length 397;
Best Local Similarity 81.0%; Pred. No. 0.021;
RESULT 1001
ID AAV84140 standard; DNA; 5403 BP.
DE Mouse prothrombinase fgl2 gene.
PN WO9851335-A1.
PD 19-NOV-1998.
PA (LEVY/) LEVY G.
Query Match 2.6%; Score 43.8; DB 2; Length 5403;
Best Local Similarity 81.0%; Pred. No. 0.1;
RESULT 1002
ID AAD64732 standard; DNA; 34637 BP.
DE Mouse carcinoma-associated (CA) gene TBX21.
PN US2003099963-A1.
PD 29-MAY-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.6%; Score 43.8; DB 10; Length 34637;
Best Local Similarity 76.1%; Pred. No. 0.31;
RESULT 1003
ID ADA02645 standard; DNA; 37135 BP.
DE Mouse Tbx21 carcinoma associated gene, SEQ ID NO:1163.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 43.8; DB 9; Length 37135;
Best Local Similarity 76.1%; Pred. No. 0.33;
RESULT 1004
ID ADB72383 standard; DNA; 37135 BP.
DE Mouse Tbx21 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 43.8; DB 10; Length 37135;
Best Local Similarity 76.1%; Pred. No. 0.33;
RESULT 1005
ID ADE95893 standard; DNA; 37135 BP.
DE Mouse Tbx21 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 43.8; DB 10; Length 37135;
Best Local Similarity 76.1%; Pred. No. 0.33;
RESULT 1006
ID ACN43952 standard; DNA; 47856 BP.
DE Mouse genomic sequence mCG11829.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 43.8; DB 11; Length 47856;
Best Local Similarity 69.0%; Pred. No. 0.38;
RESULT 1007
ID AAD58261 standard; DNA; 77287 BP.
DE Murine tumour suppressor gene, Lmt intron 3 DNA.
PN WO2003066869-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 2.6%; Score 43.8; DB 9; Length 77287;
Best Local Similarity 59.1%; Pred. No. 0.51;
RESULT 1008
ID ADQ97980 standard; DNA; 97081 BP.
DE Human cancer associated sequence HD11-034, SEQ ID 957.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 43.8; DB 12; Length 97081;
Best Local Similarity 76.1%; Pred. No. 0.58;
RESULT 1009

Query Match 2.6%; Score 43.8; DB 12; Length 110000;
Best Local Similarity 71.7%; Pred. No. 0.62;
RESULT 1010
ID ADQ97965 standard; DNA; 152096 BP.
DE Mouse cancer associated sequence MD11-032, SEQ ID 942.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 43.8; DB 12; Length 152096;
Best Local Similarity 87.3%; Pred. No. 0.76;
RESULT 1011
ID AAD58258 standard; DNA; 167739 BP.
DE Murine tumour suppressor gene, Lmt reverse complement DNA.
PN WO2003066869-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 2.6%; Score 43.8; DB 9; Length 167739;
Best Local Similarity 59.1%; Pred. No. 0.8;
RESULT 1012
ID ABX11086 standard; DNA; 42999 BP.
DE Human ribosomal RNA (rRNA) gene.
PN US2002160410-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.6%; Score 43.6; DB 8; Length 42999;
Best Local Similarity 46.9%; Pred. No. 0.41;
RESULT 1013
ID ABD32815 standard; DNA; 127678 BP.
DE Mouse cancer-associated genomic DNA MD17-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 43.6; DB 13; Length 127678;
Best Local Similarity 70.6%; Pred. No. 0.79;
RESULT 1014
ID AAL16082 standard; cDNA; 617 BP.
DE Human breast cancer expressed polynucleotide 8539.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 43.4; DB 4; Length 617;
Best Local Similarity 55.9%; Pred. No. 0.037;
RESULT 1015
ID ACN86039 standard; DNA; 1133 BP.
DE Breast cancer related marker, seq id 7189.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.6%; Score 43.4; DB 11; Length 1133;
Best Local Similarity 55.9%; Pred. No. 0.053;
RESULT 1016
ID ABN80241 standard; DNA; 7316 BP.
DE Human chemically modified disease associated gene SEQ ID NO 258.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.6%; Score 43.4; DB 6; Length 7316;
Best Local Similarity 66.7%; Pred. No. 0.16;
RESULT 1017
ID ADR66991 standard; DNA; 21779 BP.
DE Mouse cancer associated gene genomic sequence SEQ ID NO:37.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.6%; Score 43.4; DB 13; Length 21779;
Best Local Similarity 57.4%; Pred. No. 0.31;
RESULT 1018
Query Match 2.6%; Score 43.4; DB 8; Length 110000;
Best Local Similarity 57.4%; Pred. No. 0.83;
RESULT 1019
ID AAF64486 standard; cDNA; 437 BP.
DE Novel human polynucleotide, SEQ ID NO: 242.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 43.2; DB 5; Length 437;
Best Local Similarity 61.6%; Pred. No. 0.035;
RESULT 1020
ID AAF65388 standard; cDNA; 458 BP.
DE Novel human polynucleotide, SEQ ID NO: 1144.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 43.2; DB 5; Length 458;
Best Local Similarity 66.4%; Pred. No. 0.036;
RESULT 1021
ID AAV47615 standard; cDNA; 783 BP.
DE Nucleotide sequence encoding for carbonic anhydrase II protein.
PN WO9836084-A2.
PD 20-AUG-1998.
PA (AGRI-) AGRIC TECHNOLOGIES INC.
Query Match 2.5%; Score 43.2; DB 2; Length 783;
Best Local Similarity 48.2%; Pred. No. 0.049;
RESULT 1022
ID ACN44248 standard; DNA; 21230 BP.
DE Mouse genomic sequence mCG1647.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 43.2; DB 11; Length 21230;
Best Local Similarity 60.0%; Pred. No. 0.36;
RESULT 1023
ID ADC85340 standard; DNA; 96597 BP.
DE Human Lmo2 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 43.2; DB 10; Length 96597;
Best Local Similarity 85.7%; Pred. No. 0.89;
RESULT 1024
ID ADA02861 standard; DNA; 96598 BP.
DE Mouse Itpr1 carcinoma associated gene, SEQ ID NO:1379.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 43.2; DB 9; Length 96598;
Best Local Similarity 85.7%; Pred. No. 0.89;
RESULT 1025
ID ADB72599 standard; DNA; 96598 BP.
DE Mouse Itpr1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 43.2; DB 10; Length 96598;
Best Local Similarity 85.7%; Pred. No. 0.89;
RESULT 1026
ID ADM74456 standard; DNA; 96598 BP.
DE Murine carcinoma associated (CA) nucleic acid #64.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.5%; Score 43.2; DB 12; Length 96598;
Best Local Similarity 85.7%; Pred. No. 0.89;
RESULT 1027
ID ACN45148 standard; DNA; 188017 BP.
DE Mouse genomic sequence mCG8993.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 43.2; DB 11; Length 188017;
Best Local Similarity 64.5%; Pred. No. 1.3;
RESULT 1028

ID ADO00750 standard; cDNA; 909 BP.
DE Novel human cDNA sequence #1565.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 43; DB 12; Length 909;
Best Local Similarity 58.0%; Pred. No. 0.062;
RESULT 1029
ID ADN99181 standard; cDNA; 909 BP.
DE Novel human cDNA sequence #781.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 43; DB 12; Length 909;
Best Local Similarity 58.0%; Pred. No. 0.062;
RESULT 1030
ID ABA96042 standard; cDNA; 984 BP.
DE Human carbonic anhydrase (CAH) cDNA coding region.
PN WO200190321-A2.
PD 29-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.5%; Score 43; DB 6; Length 984;
Best Local Similarity 44.5%; Pred. No. 0.065;
RESULT 1031
ID ADA09127 standard; cDNA; 984 BP.
DE Novel human carbonic anhydrase CAH coding sequence.
PN US2003059919-A1.
PD 27-MAR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.5%; Score 43; DB 9; Length 984;
Best Local Similarity 44.5%; Pred. No. 0.065;
RESULT 1032
ID ABA96041 standard; cDNA; 1855 BP.
DE Human carbonic anhydrase (CAH) cDNA.
PN WO200190321-A2.
PD 29-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.5%; Score 43; DB 6; Length 1855;
Best Local Similarity 44.5%; Pred. No. 0.095;
RESULT 1033
ID ADA09125 standard; cDNA; 1855 BP.
DE cDNA encoding novel human carbonic anhydrase CAH.
PN US2003059919-A1.
PD 27-MAR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.5%; Score 43; DB 9; Length 1855;
Best Local Similarity 44.5%; Pred. No. 0.095;
RESULT 1034
ID AAS21260 standard; cDNA; 2531 BP.
DE Human cDNA sequence encoding for PRO1076 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 4; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1035
ID ACA03619 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 8; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1036
ID ABX89157 standard; cDNA; 2531 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1076.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 8; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1037
ID ACD41811 standard; cDNA; 2531 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 8; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1038
ID ACA04040 standard; cDNA; 2531 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 33.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 8; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1039
ID ADA45552 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1040
ID ADA75983 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1041
ID ADA18633 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1042
ID ADA61256 standard; cDNA; 2531 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1043
ID ADB19041 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1044
ID ADB27582 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1045
ID ADA86061 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1046
ID ADB15625 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.

PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1047
ID ADA47411 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1048
ID ADA67206 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1049
ID ADB30213 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1050
ID ADA85509 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1051
ID ADA96721 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1052
ID ADA79025 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1053
ID ADA87164 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1054
ID ADB16366 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1055
ID ADA91458 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1056
ID ADB14521 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1057
ID ADB18482 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1058
ID ADA93697 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1059
ID ADB19593 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1060
ID ADB12905 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1061
ID ACD98440 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1062
ID ADA74159 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1063
ID ADB24392 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1064
ID ADA81916 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082701-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1065
ID ADA74879 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1066
ID ADA84957 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1067
ID ADA84405 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1068
ID ADB29661 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1069
ID ADA80189 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1070
ID ADA75431 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1071
ID ADA46656 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1072
ID ADB24952 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1073
ID ADA93128 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1074
ID ADB26478 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1075
ID ADB30765 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1076
ID ADA60693 standard; cDNA; 2531 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1077
ID ADB23840 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1078
ID ADA96169 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1079
ID ADA80741 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1080
ID ADA95617 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1081
ID ADB25926 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1082
ID ADB21411 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;

Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1083
ID ADA77190 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1084
ID ADB17930 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1085
ID ADA86613 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1086
ID ADA87716 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1087
ID ADA46104 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1088
ID ADB28134 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1089
ID ADB28686 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1090
ID ADA76638 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1091
ID ADA88268 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1092
ID ADA97273 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1093
ID ADB27030 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1094
ID ADB21963 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1095
ID ADA66654 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1096
ID ADB22515 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1097
ID ADB23288 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1098
ID ADA92010 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1099
ID ADB15073 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1100
ID ADB38325 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1101
ID ADB37773 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.

PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1102
ID ADB66245 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 9; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1103
ID ADB89325 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1104
ID ADB90057 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1105
ID ADB39158 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1106
ID ADB46781 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1107
ID ADB86388 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1108
ID ADB76993 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1109
ID ADB34150 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1110
ID ADB35254 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1111
ID ADB33598 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1112
ID ADB34702 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1113
ID ADB35806 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide SEQ ID NO 33.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1114
ID ADB46201 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1115
ID ADC50074 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1116
ID ADC71621 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1117
ID ADC59600 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1118
ID ADC52607 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1119
ID ADC56961 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087366-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1120
ID ADC60152 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1121
ID ADC50627 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1122
ID ADC65154 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1123
ID ADC54252 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1124
ID ADC53213 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1125
ID ADC58736 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1126
ID ADC55614 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1127
ID ADC58184 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID33.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1128
ID ADD02858 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1129
ID ADC89850 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1130
ID ADC69269 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1131
ID ADC48158 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1132
ID ADD09687 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1133
ID ADD04262 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1134
ID ADC80218 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1135
ID ADD10725 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1136
ID ADC47606 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1137
ID ADC79666 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;

Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1138
ID ADD09135 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1139
ID ADD40848 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1140
ID ADD51987 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1141
ID ADD52727 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1142
ID ADD53279 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1143
ID ADD51435 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1144
ID ADD02234 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1145
ID ADD01668 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1146
ID ADD53850 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1147
ID ADD92167 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1148
ID ADD91063 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1149
ID ADE03677 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1150
ID ADE31974 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1151
ID ADE21906 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1152
ID ADD79130 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1153
ID ADE41666 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1154
ID ADE17483 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1155
ID ADD91615 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1156

ID ADE33078 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1157
ID ADE33630 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1158
ID ADD79682 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1159
ID ADD92719 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1160
ID ADE19139 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1161
ID ADE18587 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1162
ID ADE42783 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1163
ID ADD95572 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1164
ID ADE22458 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1165
ID ADD78576 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1166
ID ADE32526 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1167
ID ADE42218 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1168
ID ADD80234 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1169
ID ADD89262 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1170
ID ADE40546 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1171
ID ADE04345 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1172
ID ADE92474 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1173
ID ADG21183 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1174
ID ADG22824 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.

PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1175
ID ADF97159 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1176
ID ADG80223 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1177
ID ADG79671 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1178
ID ADH54963 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1179
ID ADH55515 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1180
ID ADI63734 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1181
ID ADI64683 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1182
ID ADH81596 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1183
ID ADH81044 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1184
ID ACD23869 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1185
ID ACA67010 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 10; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1186
ID ADM82213 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1187
ID ADN15612 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1188
ID ADN16241 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1189
ID ADN15060 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1190
ID ADN14508 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1191
ID ADI63182 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 11; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1192
ID ADC80770 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1193
ID ADD76218 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1194
ID ADD87582 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1195
ID ADD85986 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1196
ID ADE75434 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1197
ID ADE23010 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1198
ID ADE23562 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1199
ID ADE24205 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1200
ID ADD87030 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1201
ID ADE88896 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1202
ID ADE18035 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1203
ID ADE88344 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1204
ID ADE94364 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1205
ID ADE90775 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1206
ID ADE94916 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1207
ID ADE93026 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1208
ID ADF34607 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1209
ID ADE91922 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1210
ID ADE90223 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;

Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1211
ID ADE91370 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1212
ID ADG01949 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1213
ID ADG21735 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1214
ID ADG19805 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1215
ID ADF97711 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1216
ID ADG23928 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1217
ID ADF98282 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1218
ID ADG03113 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1219
ID ADF98834 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1220
ID ADG16419 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1221
ID ADG04878 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1222
ID ADG19145 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1223
ID ADG12982 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1224
ID ADG08039 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1225
ID ADG15209 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1226
ID ADF96607 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1227
ID ADG05792 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1228
ID ADG23376 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1229

ID ADG03665 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1230
ID ADG24566 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1231
ID ADG06863 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1232
ID ADG07415 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1233
ID ADG54910 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1234
ID ADG60574 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1235
ID ADG61678 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1236
ID ADG81879 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1237
ID ADG57118 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1238
ID ADG56566 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1239
ID ADG55462 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1240
ID ADG58222 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1241
ID ADG70588 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1242
ID ADG57670 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1243
ID ADG53254 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1244
ID ADG71140 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1245
ID ADG81327 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1246
ID ADH30289 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1247
ID ADH11656 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207419-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1248
ID ADG52078 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1249
ID ADG53806 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1250
ID ADG80775 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1251
ID ADG56014 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1252
ID ADH12280 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1253
ID ADG61126 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1254
ID ADH28213 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1255
ID ADG54358 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1256
ID ADG59398 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1257
ID ADI80822 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1258
ID ADG09565 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1259
ID ADI15036 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1260
ID ADG08913 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1261
ID ADI14368 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1262
ID ADI17963 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1263
ID ADJ63244 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1264
ID ADJ77139 standard; cDNA; 2531 BP.
DE Human PRO polynucleotide #17.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1265
ID ADJ65261 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1266
ID ADM27397 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1267
ID ADM42121 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1268
ID ADM27983 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 12; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1269
ID ADI95465 standard; cDNA; 2531 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 13; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1270
ID ADI96017 standard; cDNA; 2531 BP.
DE Novel human secreted and transmembrane protein PRO1076 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 43; DB 13; Length 2531;
Best Local Similarity 44.5%; Pred. No. 0.11;
RESULT 1271
ID ABA97693 standard; DNA; 2938 BP.
DE Human lyase HLYA-3 encoding cDNA.
PN WO200200840-A2.
PD 03-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.5%; Score 43; DB 6; Length 2938;
Best Local Similarity 44.5%; Pred. No. 0.13;
RESULT 1272
ID AAS44677 standard; DNA; 3177 BP.
DE Human full-length polynucleotide sequence #102.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 43; DB 4; Length 3177;
Best Local Similarity 44.5%; Pred. No. 0.13;
RESULT 1273
ID ACF62736 standard; DNA; 183610 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 43; DB 8; Length 183610;
Best Local Similarity 67.0%; Pred. No. 1.5;
RESULT 1274
ID ADB20851 standard; DNA; 183610 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:664.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 43; DB 8; Length 183610;
Best Local Similarity 67.0%; Pred. No. 1.5;
RESULT 1275
ID ADB87940 standard; DNA; 183610 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:664.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 43; DB 10; Length 183610;
Best Local Similarity 67.0%; Pred. No. 1.5;
RESULT 1276
ID ADB96923 standard; DNA; 183610 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:664.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 43; DB 10; Length 183610;
Best Local Similarity 67.0%; Pred. No. 1.5;
RESULT 1277
ID ADB92114 standard; DNA; 183610 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:664.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 43; DB 10; Length 183610;
Best Local Similarity 67.0%; Pred. No. 1.5;
RESULT 1278
ID ADQ97831 standard; DNA; 199868 BP.
DE Mouse cancer associated sequence MD11-008, SEQ ID 808.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 43; DB 12; Length 199868;
Best Local Similarity 77.6%; Pred. No. 1.6;
RESULT 1279
ID ADO35739 standard; DNA; 2597 BP.
DE Novel mouse gene sequence #412.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 42.8; DB 12; Length 2597;
Best Local Similarity 80.6%; Pred. No. 0.13;
RESULT 1280
ID AAH28355 standard; DNA; 52216 BP.
DE Nucleotide sequence of the human musashi promoter.
PN WO200146384-A2.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 2.5%; Score 42.8; DB 4; Length 52216;
Best Local Similarity 58.7%; Pred. No. 0.81;
RESULT 1281
ID ABL50307 standard; DNA; 52216 BP.
DE Human musashi promoter DNA sequence SEQ ID NO:1.
PN JP2002034580-A.
PD 05-FEB-2002.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 42.8; DB 6; Length 52216;
Best Local Similarity 58.7%; Pred. No. 0.81;
RESULT 1282
Query Match 2.5%; Score 42.8; DB 10; Length 110000;
Best Local Similarity 63.7%; Pred. No. 1.3;
RESULT 1283
ID ACN45060 standard; DNA; 21558 BP.
DE Mouse genomic sequence mCG7522.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.6; DB 11; Length 21558;
Best Local Similarity 62.4%; Pred. No. 0.55;
RESULT 1284
ID ADQ97240 standard; DNA; 28449 BP.
DE Mouse cancer associated sequence MD08-019, SEQ ID 216.

PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.6; DB 12; Length 28449;
Best Local Similarity 62.4%; Pred. No. 0.65;
RESULT 1285
ID ABD32933 standard; DNA; 108566 BP.
DE Mouse cancer-associated genomic DNA MD20-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.6; DB 13; Length 108566;
Best Local Similarity 55.1%; Pred. No. 1.5;
RESULT 1286
ID ADQ97284 standard; DNA; 215248 BP.
DE Mouse cancer associated sequence MD08-026, SEQ ID 261.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.6; DB 12; Length 215248;
Best Local Similarity 59.5%; Pred. No. 2.2;
RESULT 1287
ID ABL78474 standard; cDNA; 490 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1452.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.5%; Score 42.4; DB 6; Length 490;
Best Local Similarity 66.4%; Pred. No. 0.065;
RESULT 1288
ID AAA55967 standard; cDNA; 5566 BP.
DE Human G713 encoding cDNA SEQ ID NO:4.
PN WO200022122-A2.
PD 20-APR-2000.
PA (GEST) GENSET.
Query Match 2.5%; Score 42.4; DB 3; Length 5566;
Best Local Similarity 66.3%; Pred. No. 0.28;
RESULT 1289
ID ABD32794 standard; DNA; 42063 BP.
DE Mouse cancer-associated genomic DNA MD16-042.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.4; DB 13; Length 42063;
Best Local Similarity 55.4%; Pred. No. 0.95;
RESULT 1290
ID ADO47033 standard; DNA; 48480 BP.
DE Human oligonucleotide #2399.
PN US2004049022-A1.
PD 11-MAR-2004.
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
Query Match 2.5%; Score 42.4; DB 12; Length 48480;
Best Local Similarity 71.9%; Pred. No. 1;
RESULT 1291
ID AAD56108 standard; DNA; 63845 BP.
DE Mouse Wnt3 carcinoma associated (CA) gene.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.4; DB 8; Length 63845;
Best Local Similarity 88.5%; Pred. No. 1.2;
RESULT 1292
ID ADA02470 standard; DNA; 63845 BP.
DE Mouse Wnt3 carcinoma associated gene, SEQ ID NO:989.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.4; DB 9; Length 63845;
Best Local Similarity 88.5%; Pred. No. 1.2;
RESULT 1293
ID ADB72209 standard; DNA; 63845 BP.
DE Mouse Wnt3 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.4; DB 10; Length 63845;
Best Local Similarity 88.5%; Pred. No. 1.2;
RESULT 1294
ID ABX16390 standard; DNA; 659158 BP.
DE Mouse high growth region.
PN US2002155564-A1.
PD 24-OCT-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.5%; Score 42.4; DB 8; Length 110000;
Best Local Similarity 58.9%; Pred. No. 1.7;
RESULT 1295
ID ACN45206 standard; DNA; 139214 BP.
DE Human genomic sequence hCG23831.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.4; DB 11; Length 139214;
Best Local Similarity 66.3%; Pred. No. 2;
RESULT 1296
ID ABD32719 standard; DNA; 146793 BP.
DE Mouse cancer-associated genomic DNA MD15-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.4; DB 13; Length 146793;
Best Local Similarity 62.9%; Pred. No. 2;
RESULT 1297
ID ACN45096 standard; DNA; 148815 BP.
DE Mouse genomic sequence mCG7964.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.4; DB 11; Length 148815;
Best Local Similarity 69.2%; Pred. No. 2;
RESULT 1298
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 42.4; DB 11; Length 304905;
Best Local Similarity 57.6%; Pred. No. 3.1;
RESULT 1299
ID AAF66777 standard; cDNA; 412 BP.
DE Novel human polynucleotide, SEQ ID NO: 2533.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 42.2; DB 5; Length 412;
Best Local Similarity 79.4%; Pred. No. 0.068;
RESULT 1300
ID ADJ87509 standard; DNA; 16984 BP.
DE Murine receptor protein OT7T022 SEQ ID NO:27.
PN WO2004014414-A1.
PD 19-FEB-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.5%; Score 42.2; DB 12; Length 16984;
Best Local Similarity 85.5%; Pred. No. 0.64;
RESULT 1301
ID ADJ87513 standard; DNA; 17833 BP.
DE Murine receptor protein OT7T022 SEQ ID NO:32.
PN WO2004014414-A1.
PD 19-FEB-2004.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.5%; Score 42.2; DB 12; Length 17833;
Best Local Similarity 85.5%; Pred. No. 0.65;
RESULT 1302
ID ACN45156 standard; DNA; 53158 BP.
DE Mouse genomic sequence mCG9049.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.2; DB 11; Length 53158;
Best Local Similarity 58.3%; Pred. No. 1.3;
RESULT 1303
ID ABD33379 standard; DNA; 61396 BP.
DE Murine cancer-associated (CA) gene MD07-070.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.2; DB 13; Length 61396;
Best Local Similarity 73.6%; Pred. No. 1.4;
RESULT 1304
ID ADA02981 standard; DNA; 96599 BP.
DE Mouse Map2k5 carcinoma associated gene, SEQ ID NO:1499.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.2; DB 9; Length 96599;
Best Local Similarity 70.9%; Pred. No. 1.8;
RESULT 1305
ID ADB72719 standard; DNA; 96599 BP.
DE Mouse Map2k5 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.2; DB 10; Length 96599;
Best Local Similarity 70.9%; Pred. No. 1.8;
RESULT 1306
ID ADC85461 standard; DNA; 96599 BP.
DE Mouse Map2k5 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42.2; DB 10; Length 96599;
Best Local Similarity 70.9%; Pred. No. 1.8;
RESULT 1307
ID ADM74576 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #124.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.5%; Score 42.2; DB 12; Length 96599;
Best Local Similarity 70.9%; Pred. No. 1.8;
RESULT 1308
ID ADL13678 standard; DNA; 97700 BP.
DE Osteoarthritis-associated polymorphic nucleotide #210.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.5%; Score 42.2; DB 10; Length 97700;
Best Local Similarity 74.6%; Pred. No. 1.8;
RESULT 1309
ID ACF62750 standard; DNA; 186591 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:682.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 186591;
Best Local Similarity 85.5%; Pred. No. 2.7;
RESULT 1310
ID ADB20869 standard; DNA; 186591 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:682.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 186591;
Best Local Similarity 85.5%; Pred. No. 2.7;
RESULT 1311
ID ADB87958 standard; DNA; 186591 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:682.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 186591;
Best Local Similarity 85.5%; Pred. No. 2.7;
RESULT 1312
ID ADB96941 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 186591;
Best Local Similarity 85.5%; Pred. No. 2.7;
RESULT 1313
ID ADB92132 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 186591;
Best Local Similarity 85.5%; Pred. No. 2.7;
RESULT 1314
ID ACF62735 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:663.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1315
ID ACF62740 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:668.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1316
ID ADB20850 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:663.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1317
ID ADB20855 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:668.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 8; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1318
ID ADB87944 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:668.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1319
ID ADB87939 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:663.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1320
ID ADB96922 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:663.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1321
ID ADB96927 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:668.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1322
ID ADB92113 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:663.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1323
ID ADB92118 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:668.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 42.2; DB 10; Length 208648;
Best Local Similarity 85.5%; Pred. No. 2.9;
RESULT 1324
ID ADQ97135 standard; DNA; 254481 BP.
DE Mouse cancer associated sequence MD08-006, SEQ ID 111.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 42.2; DB 12; Length 254481;
Best Local Similarity 66.1%; Pred. No. 3.2;
RESULT 1325
ID ADH05256 standard; DNA; 160 BP.
DE Gene polymorphism detection method-related primer/probe #222.
PN WO2003097877-A1.
PD 27-NOV-2003.
PA (RIKE) RIKEN KK.
PA (NAKA/) NAKAMURA Y.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
Query Match 2.5%; Score 42; DB 12; Length 160;
Best Local Similarity 65.9%; Pred. No. 0.044;
RESULT 1326
ID ADH06008 standard; DNA; 160 BP.
DE Gene polymorphism detection method-related primer/probe #974.
PN WO2003097877-A1.
PD 27-NOV-2003.
PA (RIKE) RIKEN KK.
PA (NAKA/) NAKAMURA Y.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
Query Match 2.5%; Score 42; DB 12; Length 160;
Best Local Similarity 65.9%; Pred. No. 0.044;
RESULT 1327
ID ADA98451 standard; DNA; 677 BP.
DE Human secreted protein-related DNA sequence #44.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 8; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1328
ID ADA98450 standard; DNA; 677 BP.
DE Human secreted protein-related DNA sequence #43.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 8; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1329
ID ADA44236 standard; DNA; 677 BP.
DE Human secreted protein DNA SEQ ID 429.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 8; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1330
ID ADA44237 standard; DNA; 677 BP.
DE Human secreted protein DNA SEQ ID 430.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 8; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1331
ID ADC20618 standard; DNA; 677 BP.
DE Human secreted protein-related DNA sequence #36.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 10; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1332
ID ADC20619 standard; DNA; 677 BP.
DE Human secreted protein-related DNA sequence #37.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 10; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1333
ID ADF10826 standard; DNA; 677 BP.
DE Human secreted protein encoding sequence #148.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 10; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1334
ID ADF10825 standard; DNA; 677 BP.
DE Human secreted protein encoding sequence #147.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 42; DB 10; Length 677;
Best Local Similarity 51.0%; Pred. No. 0.11;
RESULT 1335
ID AAQ05263 standard; DNA; 700 BP.
DE Sequence of neuronal growth related protein (GAP-4) promoter region.
PN WO9006948-A.
PD 28-JUN-1990.
PA (FISH/) FISHMAN M C.
Query Match 2.5%; Score 42; DB 2; Length 700;
Best Local Similarity 69.6%; Pred. No. 0.11;
RESULT 1336
ID AAQ57505 standard; DNA; 700 BP.
DE Rat GAP-43 promoter.
PN AU9062068-A.
PD 03-JAN-1991.
PA (FISH/) FISHMAN M C.
PA (FEDE) FEDEROFF H J.
PA (ZUBE/) ZUBER M X.

PA (STRI/) STRITTMATTER S M.
PA (VALE/) VALENZUELA D.
Query Match 2.5%; Score 42; DB 2; Length 700;
Best Local Similarity 69.6%; Pred. No. 0.11;
RESULT 1337
ID AAQ57506 standard; DNA; 700 BP.
DE Rat GAP-43 promoter.
PN AU9347435-A.
PD 23-DEC-1993.
PA (FISH/) FISHMAN M C.
PA (FEDE/) FEDEROFF H J.
PA (ZUBE/) ZUBER M X.
PA (STRI/) STRITTMATTER S M.
PA (VALE/) VALENZUELA D.
Query Match 2.5%; Score 42; DB 2; Length 700;
Best Local Similarity 69.6%; Pred. No. 0.11;
RESULT 1338
ID ABA93715 standard; cDNA; 2267 BP.
DE Human amygdala derived cDNA clone amy2_16e14.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 2.5%; Score 42; DB 6; Length 2267;
Best Local Similarity 52.2%; Pred. No. 0.22;
RESULT 1339
ID ADA02753 standard; DNA; 54355 BP.
DE Mouse Morf carcinoma associated gene, SEQ ID NO:1271.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42; DB 9; Length 54355;
Best Local Similarity 82.8%; Pred. No. 1.5;
RESULT 1340
ID ADB72491 standard; DNA; 54355 BP.
DE Mouse Morf gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42; DB 10; Length 54355;
Best Local Similarity 82.8%; Pred. No. 1.5;
RESULT 1341
ID ADC85233 standard; DNA; 54355 BP.
DE Mouse Morf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42; DB 10; Length 54355;
Best Local Similarity 82.8%; Pred. No. 1.5;
RESULT 1342
ID ADM74348 standard; DNA; 54355 BP.
DE Murine carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.5%; Score 42; DB 12; Length 54355;
Best Local Similarity 82.8%; Pred. No. 1.5;
RESULT 1343
ID ACN44932 standard; DNA; 374849 BP.
DE Mouse genomic sequence mCG5728.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 42; DB 11; Length 110000;
Best Local Similarity 60.5%; Pred. No. 2.3;
RESULT 1344
Query Match 2.5%; Score 42; DB 13; Length 110000;
Best Local Similarity 69.6%; Pred. No. 2.3;
RESULT 1345
ID AAF64496 standard; cDNA; 427 BP.
DE Novel human polynucleotide, SEQ ID NO: 252.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 41.8; DB 5; Length 427;
Best Local Similarity 63.4%; Pred. No. 0.092;
RESULT 1346
ID ACN41706 standard; cDNA; 1475 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:581.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.5%; Score 41.8; DB 13; Length 1475;
Best Local Similarity 48.9%; Pred. No. 0.19;
RESULT 1347
ID ABZ11737 standard; cDNA; 1825 BP.
DE Human polynucleotide SEQ ID NO 619.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 41.8; DB 6; Length 1825;
Best Local Similarity 48.9%; Pred. No. 0.22;
RESULT 1348
ID ADM44255 standard; cDNA; 1825 BP.
DE Novel human arginine-rich protein cDNA #619.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 2.5%; Score 41.8; DB 12; Length 1825;
Best Local Similarity 48.9%; Pred. No. 0.22;
RESULT 1349
ID ABA19374 standard; DNA; 4407 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11705.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 41.8; DB 5; Length 4407;
Best Local Similarity 56.0%; Pred. No. 0.38;
RESULT 1350
ID AAS45458 standard; DNA; 13606 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #82.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.5%; Score 41.8; DB 4; Length 13606;
Best Local Similarity 63.4%; Pred. No. 0.74;
RESULT 1351
ID AAS46562 standard; DNA; 13606 BP.
DE Tumour suppressor gene derived chemically modified sequence #284.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.5%; Score 41.8; DB 4; Length 13606;
Best Local Similarity 63.4%; Pred. No. 0.74;
RESULT 1352
ID ABL33811 standard; DNA; 13606 BP.
DE Human immune system associated gene SEQ ID NO: 1784.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.5%; Score 41.8; DB 6; Length 13606;
Best Local Similarity 63.4%; Pred. No. 0.74;
RESULT 1353
ID ABK28314 standard; DNA; 13606 BP.
DE DNA transcription associated complementary genomic DNA #94.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.5%; Score 41.8; DB 6; Length 13606;
Best Local Similarity 63.4%; Pred. No. 0.74;
RESULT 1354
ID ABA19375 standard; DNA; 25525 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11706.

PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 41.8; DB 5; Length 25525;
Best Local Similarity 56.0%; Pred. No. 1.1;
RESULT 1355
ID ABK84796 standard; cDNA; 97835 BP.
DE Human cDNA differentially expressed in granulocytic cells #1367.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 41.8; DB 6; Length 97835;
Best Local Similarity 63.4%; Pred. No. 2.4;
RESULT 1356
ID ABD33148 standard; DNA; 104399 BP.
DE Murine cancer-associated (CA) gene MD07-019.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 41.8; DB 13; Length 104399;
Best Local Similarity 29.3%; Pred. No. 2.5;
RESULT 1357
ID ABD32627 standard; DNA; 421609 BP.
DE Mouse cancer-associated genomic DNA MD13-017.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 41.8; DB 13; Length 110000;
Best Local Similarity 64.5%; Pred. No. 2.6;
RESULT 1358
Query Match 2.5%; Score 41.8; DB 13; Length 110000;
Best Local Similarity 86.8%; Pred. No. 2.6;
RESULT 1359
ID ABN81158 standard; DNA; 296 BP.
DE Shrimp polynucleotide TUDGLv1-3.224R.
PN WO200034476-A2.
PD 15-JUN-2000.
PA (TUFT) TUFTS COLLEGE.
Query Match 2.4%; Score 41.6; DB 3; Length 296;
Best Local Similarity 83.9%; Pred. No. 0.086;
RESULT 1360
ID AAZ13219 standard; cDNA; 300 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:688.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 41.6; DB 2; Length 300;
Best Local Similarity 43.6%; Pred. No. 0.086;
RESULT 1361
ID AAF64903 standard; cDNA; 411 BP.
DE Novel human polynucleotide, SEQ ID NO: 659.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 41.6; DB 5; Length 411;
Best Local Similarity 66.4%; Pred. No. 0.1;
RESULT 1362
ID ABL02505 standard; cDNA; 797 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1997.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.4%; Score 41.6; DB 4; Length 797;
Best Local Similarity 46.5%; Pred. No. 0.16;
RESULT 1363
ID AAS86190 standard; cDNA; 3266 BP.
DE DNA encoding novel human diagnostic protein #21994.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 41.6; DB 5; Length 3266;
Best Local Similarity 52.3%; Pred. No. 0.36;
RESULT 1364
ID ADM91303 standard; DNA; 4226 BP.
DE DNA homologue of a human DNA sequence encoding a protein SeqID 628.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 2.4%; Score 41.6; DB 12; Length 4226;
Best Local Similarity 78.1%; Pred. No. 0.42;
RESULT 1365
ID AAF22295 standard; DNA; 80450 BP.
DE BAC containing repeats from centromeres 1-4 #18.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 2.4%; Score 41.6; DB 3; Length 80450;
Best Local Similarity 83.9%; Pred. No. 2.5;
RESULT 1366
Query Match 2.4%; Score 41.6; DB 12; Length 110000;
Best Local Similarity 83.9%; Pred. No. 3;
RESULT 1367
ID ACN44744 standard; DNA; 110218 BP.
DE Mouse genomic sequence mCG3264.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 41.6; DB 11; Length 110218;
Best Local Similarity 67.6%; Pred. No. 3;
RESULT 1368
ID ABD33161 standard; DNA; 120144 BP.
DE Murine cancer-associated (CA) gene MD07-022.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 41.6; DB 13; Length 120144;
Best Local Similarity 70.0%; Pred. No. 3.2;
RESULT 1369
ID ADQ19389 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 41.6; DB 12; Length 155937;
Best Local Similarity 60.7%; Pred. No. 3.7;
RESULT 1370
ID ADL13643 standard; DNA; 170170 BP.
DE Osteoarthritis-associated polymorphic nucleotide #175.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 41.6; DB 10; Length 170170;
Best Local Similarity 78.1%; Pred. No. 3.9;
RESULT 1371
ID AAS68431 standard; cDNA; 462 BP.
DE DNA encoding novel human diagnostic protein #4235.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 41.4; DB 5; Length 462;
Best Local Similarity 58.5%; Pred. No. 0.13;
RESULT 1372
ID ACH26864 standard; cDNA; 496 BP.
DE Human adult ovary cDNA #5244.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 41.4; DB 9; Length 496;

Best Local Similarity 58.5%; Pred. No. 0.13;
RESULT 1373
ID ADO62108 standard; DNA; 2304 BP.
DE Transcription factor G2869 coding sequence, SEQ ID 575.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 2.4%; Score 41.4; DB 12; Length 2304;
Best Local Similarity 55.2%; Pred. No. 0.34;
RESULT 1374
ID ABD33037 standard; DNA; 32829 BP.
DE Mouse cancer-associated genomic DNA MD22-025.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 41.4; DB 13; Length 32829;
Best Local Similarity 66.7%; Pred. No. 1.7;
RESULT 1375
ID ABD33518 standard; DNA; 34261 BP.
DE Murine cancer-associated (CA) gene MD07-102.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 41.4; DB 13; Length 34261;
Best Local Similarity 63.6%; Pred. No. 1.7;
RESULT 1376
ID ACN44228 standard; DNA; 43400 BP.
DE Mouse genomic sequence mCG16239.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 41.4; DB 11; Length 43400;
Best Local Similarity 81.4%; Pred. No. 2;
RESULT 1377
ID ADQ97275 standard; DNA; 45764 BP.
DE Mouse cancer associated sequence MD08-025, SEQ ID 251.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 41.4; DB 12; Length 45764;
Best Local Similarity 52.9%; Pred. No. 2;
RESULT 1378
ID ACN44428 standard; DNA; 164841 BP.
DE Mouse genomic sequence mCG19072.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 41.4; DB 11; Length 164841;
Best Local Similarity 53.4%; Pred. No. 4.4;
RESULT 1379
ID ADQ59413 standard; DNA; 177049 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:49.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 41.4; DB 12; Length 177049;
Best Local Similarity 63.0%; Pred. No. 4.6;
RESULT 1380
ID ABL63688 standard; DNA; 1031 BP.
DE Breast cancer related gene sequence SEQ ID NO:2025.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.4%; Score 41.2; DB 6; Length 1031;
Best Local Similarity 59.3%; Pred. No. 0.24;
RESULT 1381
ID AAD57522 standard; cDNA; 1196 BP.
DE Human enzyme (ENZM) cDNA #34.
PN WO2003052075-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1196;
Best Local Similarity 47.1%; Pred. No. 0.26;
RESULT 1382
ID ADQ83705 standard; cDNA; 1455 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #519.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 41.2; DB 12; Length 1455;
Best Local Similarity 47.1%; Pred. No. 0.3;
RESULT 1383
ID AAZ27633 standard; DNA; 1514 BP.
DE Human carbonic anhydrase VIII coding sequence.
PN US5972684-A.
PD 26-OCT-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.4%; Score 41.2; DB 2; Length 1514;
Best Local Similarity 47.1%; Pred. No. 0.3;
RESULT 1384
ID AAZ34195 standard; cDNA; 1670 BP.
DE Human PRO237 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 2; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1385
ID AAA88440 standard; cDNA; 1670 BP.
DE Antitumour PRO237 cDNA clone DNA34353-1428.
PN WO200053751-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 3; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1386
ID AAC78549 standard; cDNA; 1670 BP.
DE Human PRO237 (UNQ211) nucleotide sequence SEQ ID NO:357.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 3; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1387
ID AAC58225 standard; cDNA; 1670 BP.
DE Human PRO237 nucleotide sequence SEQ ID NO:1.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 3; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1388
ID AAS21406 standard; cDNA; 1670 BP.
DE Human cDNA sequence encoding for PRO237 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 4; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1389
ID ACA63763 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1390
ID ACA03765 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;

Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1391
ID ACA71927 standard; cDNA; 1670 BP.
DE Human secreted and transmembrane PRO polypeptide #1 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1392
ID ABX89303 standard; cDNA; 1670 BP.
DE DNA encoding novel secreted and transmembrane protein PRO237.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1393
ID ABX92567 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO237 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1394
ID ACD41957 standard; cDNA; 1670 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #163.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1395
ID ACA66308 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO237.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1396
ID ACA04186 standard; cDNA; 1670 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 325.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 8; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1397
ID ADA45844 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1398
ID ADA76275 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1399
ID ADA18925 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1400
ID ADA61548 standard; cDNA; 1670 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1401
ID ADB19333 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1402
ID ADB27874 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1403
ID ADA86353 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1404
ID ADB15917 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1405
ID ADA47703 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1406
ID ADA67498 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1407
ID ADB30505 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1408
ID ADA85801 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1409

ID ADA97013 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1410
ID ADA79317 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1411
ID ADA87456 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1412
ID ADB16658 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1413
ID ADA91750 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1414
ID ADB14813 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1415
ID ADA24896 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1416
ID ADB18774 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1417
ID ADA93989 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1418
ID ADB19885 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1419
ID ADB13197 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1420
ID ACD98586 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1421
ID ACD29909 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1422
ID ADA12557 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO237.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1423
ID ADA74451 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1424
ID ADB24684 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1425
ID ADA82208 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1426
ID ADA75171 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1427
ID ADA85249 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.

PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1428
ID ADA84697 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1429
ID ADB29953 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1430
ID ADA80481 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1431
ID ADA75723 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1432
ID ADA46948 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1433
ID ADB25244 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1434
ID ADA93420 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1435
ID ADB26770 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1436
ID ADB31057 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1437
ID ADA60985 standard; cDNA; 1670 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1438
ID ADB24132 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1439
ID ADA96461 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1440
ID ADA81033 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1441
ID ADA95909 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1442
ID ADB26218 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1443
ID ADB21703 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1444
ID ACD29324 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #92.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1445
ID ADA77482 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1446
ID ADB18222 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1447
ID ADA86905 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1448
ID ADA88008 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1449
ID ADA46396 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1450
ID ADB28426 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1451
ID ADB28978 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1452
ID ADA76930 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1453
ID ADA88560 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1454
ID ADA97565 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1455
ID ADB27322 standard; cDNA; 1670 BP.
DE cDNA encoding human PRO polypeptide #163.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1456
ID ADB22255 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1457
ID ADA66946 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1458
ID ADB22807 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1459
ID ADB23580 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1460
ID ADA92302 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1461
ID ADB15365 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1462
ID ADB38617 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1463
ID ADB38065 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 9; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1464
ID ADB66537 standard; cDNA; 1670 BP.

DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1465
ID ADB89617 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1466
ID ADB90349 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1467
ID ADB39450 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1468
ID ADB73863 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide sequence #92.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1469
ID ADB47073 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1470
ID ADB86680 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1471
ID ADB76579 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide sequence #92.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1472
ID ADB77285 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1473
ID ADB34442 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1474
ID ADB35546 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1475
ID ADB33890 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1476
ID ADB34994 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1477
ID ADB36098 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide SEQ ID NO 325.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1478
ID ADB46493 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1479
ID ADC44005 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1480
ID ADC61765 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1481
ID ADC63729 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1482
ID ADC66829 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003060406-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1483
ID ADC68953 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1484
ID ADC63013 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1485
ID ADC68078 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1486
ID ADC41398 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1487
ID ADC67453 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1488
ID ADC62389 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1489
ID ADC42022 standard; cDNA; 1670 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO237.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1490
ID ADC50366 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1491
ID ADC71913 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1492
ID ADC59892 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1493
ID ADC52899 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID325.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1494
ID ADC57253 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID325.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1495
ID ADC60444 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1496
ID ADC50919 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein PRO237 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1497
ID ADC65446 standard; cDNA; 1670 BP.
DE Human PRO polynucleotide #163.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1498
ID ADC54544 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID325.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1499
ID ADC53505 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID325.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;
RESULT 1500
ID ADC59028 standard; cDNA; 1670 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID325.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 2.4%; Score 41.2; DB 10; Length 1670;
Best Local Similarity 47.1%; Pred. No. 0.32;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 15:55:34 ; Search time 5143 Seconds
(without alignments)
12589.407 Million cell updates/sec

Title: US-10-063-583-73
Perfect score: 1701
Sequence: 1 gagactgcagagggagataa.....aaattaaagtttctgacttt 1701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	933.6	54.9	1096	4	BM545283	BM545283 AGENCOURT
	2	828.4	48.7	895	5	BU194155	BU194155 AGENCOURT
	3	808.4	47.5	844	4	BI756209	BI756209 603024235
	4	800	47.0	821	4	BI820831	BI820831 603034045
c	5	729.8	42.9	821	1	AI800075	AI800075 wc15c05.x
	6	728	42.8	1080	5	BQ070550	BQ070550 AGENCOURT
	7	727.8	42.8	844	6	CD652789	CD652789 AGENCOURT
	8	724.4	42.6	735	4	BI819281	BI819281 603037722
	9	691.6	40.7	1096	4	BM544660	BM544660 AGENCOURT
	10	664.8	39.1	668	6	CB154932	CB154932 K-EST0213
	11	638.2	37.5	643	7	CV030245	CV030245 9296 Full
	12	615.4	36.2	755	7	CR455585	CR455585
	13	610.2	35.9	897	5	BU152476	BU152476 AGENCOURT
	14	596	35.0	747	6	CB999941	CB999941 AGENCOURT
	15	591.6	34.8	819	7	CO566350	CO566350 AGENCOURT
	16	586.4	34.5	629	4	BM690902	BM690902 UI-E-CI1-
	17	585.6	34.4	595	7	CN356209	CN356209 170004240
	18	583.4	34.3	1089	4	BM548598	BM548598 AGENCOURT
c	19	564.6	33.2	602	5	BU731403	BU731403 UI-E-CI1-
	20	560.4	32.9	652	4	BM726824	BM726824 UI-E-EJ0-
c	21	540.4	31.8	550	1	AI686505	AI686505 tu34e09.x
	22	539	31.7	724	7	CO746899	CO746899 EST00013
	23	532	31.3	532	4	BM707998	BM707998 UI-E-CI1-
c	24	507	29.8	545	7	H97489	H97489 yw11e06.s1
	25	496.4	29.2	720	4	BG965756	BG965756 602829517
	26	494.6	29.1	713	7	CK359361	CK359361 AGENCOURT
	27	489.4	28.8	492	1	AA418208	AA418208 zv97g09.r
	28	484.8	28.5	637	5	BX669419	BX669419 BX669419
	29	483.4	28.4	623	4	BM699421	BM699421 UI-E-DX1-
	30	482.8	28.4	747	7	CF734915	CF734915 UI-M-HA0-
c	31	482.4	28.4	522	4	BM670068	BM670068 UI-E-DX1-
	32	479.8	28.2	750	1	AV726613	AV726613 AV726613
	33	478.4	28.1	1027	3	AK012316	AK012316 Mus muscu
	34	477	28.0	489	1	AA401879	AA401879 zv65g10.r
	35	476.8	28.0	568	2	BE667122	BE667122 151239 MA
	36	468.4	27.5	500	2	AW023374	AW023374 df54a04.y
	37	467	27.5	583	5	BP361793	BP361793 BP361793
c	38	466.4	27.4	470	1	AA418073	AA418073 zv97g09.s
	39	464	27.3	896	5	BU510846	BU510846 AGENCOURT
	40	462.8	27.2	619	1	AV610369	AV610369 AV610369
c	41	462.4	27.2	465	2	AW027850	AW027850 ws62a01.x
c	42	462.2	27.2	850	7	CK846350	CK846350 968838 MA
	43	461	27.1	488	5	BX092864	BX092864 BX092864
	44	460	27.0	632	5	BM986159	BM986159 LM24HW001
	45	458.6	27.0	751	6	CB599647	CB599647 AGENCOURT
c	46	455.8	26.8	473	7	N67776	N67776 za03c10.s1
	47	450.2	26.5	575	2	BF198911	BF198911 248907 MA
c	48	449.4	26.4	470	1	AA620395	AA620395 ae57c05.s
c	49	446.4	26.2	449	7	N36146	N36146 yy29c02.s1
c	50	442.4	26.0	467	1	AI168759	AI168759 ox66f09.s
c	51	438.4	25.8	454	1	AA700811	AA700811 zi69e08.s
	52	430.4	25.3	462	7	N28007	N28007 yx50a12.r1
	53	425	25.0	755	6	CB600518	CB600518 AGENCOURT
	54	417	24.5	575	2	BF198442	BF198442 248368 MA
	55	414.4	24.4	574	2	BF198229	BF198229 247976 MA
	56	412.8	24.3	518	2	BE666699	BE666699 150309 MA
	57	412	24.2	786	4	BI144669	BI144669 602909964
	58	404	23.8	554	4	BI341092	BI341092 368357 MA
	59	403.6	23.7	600	6	CA529055	CA529055 8093-55 M
c	60	400.4	23.5	584	2	AW952793	AW952793 EST364863
c	61	398	23.4	462	1	AA012999	AA012999 ze27f11.s
c	62	394.2	23.2	676	1	AV610368	AV610368 AV610368
c	63	390.8	23.0	772	7	CK770747	CK770747 958958 MA
c	64	385	22.6	406	2	AW904436	AW904436 RC5-NN105
	65	383.4	22.5	386	7	CN356210	CN356210 170005999
	66	380.4	22.4	407	7	H83666	H83666 ys88g09.r1
	67	376.6	22.1	469	2	AW653845	AW653845 102723 MA
	68	374.4	22.0	376	7	CN356208	CN356208 170005829
	69	374	22.0	375	5	BX952561	BX952561 DKFZp781K
	70	374	22.0	547	6	CD559919	CD559919 B0403H12-
	71	372.2	21.9	824	7	CK602317	CK602317 AGENCOURT
	72	369.4	21.7	678	4	BI824229	BI824229 603040607
	73	368.4	21.7	457	7	H82563	H82563 yv77c05.r1
	74	367.8	21.6	374	7	H60753	H60753 yr54c12.r1
	75	367	21.6	383	7	R87427	R87427 ym88g12.r1
	76	362	21.3	744	7	CF952338	CF952338 UI-M-HL0-
	77	362	21.3	950	5	BU504033	BU504033 AGENCOURT
	78	361.6	21.3	514	7	W03403	W03403 za03c10.r1
c	79	358.2	21.1	482	7	H99095	H99095 yx18e07.s1
	80	356.2	20.9	739	7	CR455622	CR455622 CR455622
c	81	353.2	20.8	359	1	AA688368	AA688368 nv15c06.s
	82	351.2	20.6	589	1	AV601214	AV601214 AV601214
c	83	347.2	20.4	365	2	BE702596	BE702596 RC5-NN106
c	84	342.4	20.1	376	1	AI015805	AI015805 ot83d10.s
	85	338	19.9	677	7	CK358512	CK358512 AGENCOURT
	86	335	19.7	474	7	R85022	R85022 yo42b01.r1
c	87	331.8	19.5	457	7	H59689	H59689 yr35a10.s1
	88	331	19.5	641	7	CK626081	CK626081 mj17g12.y
c	89	329.4	19.4	334	1	AI582759	AI582759 tn17c05.x
	90	328	19.3	801	5	BQ887126	BQ887126 AGENCOURT
c	91	325.4	19.1	349	7	H83667	H83667 ys88g09.s1
	92	323.2	19.0	734	4	BI753712	BI753712 603028224
c	93	321.4	18.9	330	1	AA205528	AA205528 zq66h10.s
	94	315	18.5	625	7	CK626066	CK626066 mj17f08.y
c	95	314.2	18.5	470	2	AW072108	AW072108 wz98b07.x
	96	312.2	18.4	434	7	N35665	N35665 yx62f03.r1
	97	305.4	18.0	320	1	AA322820	AA322820 EST25507

c 98	299.2	17.6	622	9	AG133406	AG133406 Pan trogl
99	298.4	17.5	444	4	BM484333	BM484333 538154 MA
c 100	298.4	17.5	644	7	CO718162	CO718162 DG14-5n21
101	296	17.4	548	1	AA529743	AA529743 vi42f05.r
102	287.2	16.9	669	4	BI734456	BI734456 603350655
103	283.4	16.7	556	6	CB613363	CB613363 AMGNNUC:N
c 104	282	16.6	657	7	CO713231	CO713231 DG14-201a
105	277.8	16.3	606	2	AW106009	AW106009 um20h11.y
c 106	271.4	16.0	417	7	H60754	H60754 yr54c12.s1
c 107	269.4	15.8	626	7	CO712859	CO712859 DG14-197j
c 108	269.2	15.8	291	7	R07653	R07653 ye98h08.s1
109	268.8	15.8	499	1	AJ681779	AJ681779 AJ681779
110	267.8	15.7	458	1	AA075400	AA075400 zm87e04.s
111	266.8	15.7	278	7	H59688	H59688 yr35a10.r1
c 112	265.4	15.6	637	7	CO593354	CO593354 DG2-71f10
c 113	264.8	15.6	269	1	AA339201	AA339201 EST44307
114	264.4	15.5	618	5	BX676409	BX676409 BX676409
c 115	255	15.0	273	7	N26551	N26551 yx62f03.s1
c 116	255	15.0	590	7	CO716837	CO716837 DG14-31f1
117	253.2	14.9	401	7	R07706	R07706 ye98h08.r1
c 118	253.2	14.9	727	2	AW536446	AW536446 G0104F01-
119	245.8	14.5	305	1	AJ670427	AJ670427 AJ670427
120	244.4	14.4	404	2	AW427506	AW427506 63362 MAR
121	242.4	14.3	535	1	AL024448	AL024448 w8408b58
122	240	14.1	725	6	CB596027	CB596027 AGENCOURT
123	239	14.1	506	6	CA534588	CA534588 C0207A10-
124	233.6	13.7	547	4	BI682565	BI682565 463683 MA
125	231.2	13.6	566	7	CO896407	CO896407 BovGen_24
c 126	230.4	13.5	717	7	CK844779	CK844779 UI-R-AE0-
c 127	230.2	13.5	706	6	CD741425	CD741425 UI-M-AO0-
128	227.6	13.4	318	1	AI551910	AI551910 vi42f05.y
c 129	225.8	13.3	531	1	AV601213	AV601213 AV601213
130	224.4	13.2	280	7	H84836	H84836 yv86a02.r1
131	220.8	13.0	499	7	CK625264	CK625264 mi31a08.y
132	216.8	12.7	430	1	AA434634	AA434634 ve04g08.r
133	216.2	12.7	1070	5	BX365601	BX365601 BX365601
134	213.6	12.6	2601	3	CR618639	CR618639 full-leng
135	210.2	12.4	282	1	AA080898	AA080898 zn04a05.r
136	203.6	12.0	474	1	AI047125	AI047125 uh58d07.r
c 137	201.2	11.8	269	1	AA084333	AA084333 zn04a05.s
138	200.6	11.8	1068	9	AY415590	AY415590 Homo sapi
139	199.2	11.7	1472	3	AK052639	AK052639 Mus muscu
140	194.4	11.4	690	4	BJ617304	BJ617304 BJ617304
141	193	11.3	867	4	BI597508	BI597508 603247033
142	189.8	11.2	906	7	CR577474	CR577474 CR577474
143	188.6	11.1	662	4	BG427202	BG427202 602494247
144	187.4	11.0	961	5	BQ951338	BQ951338 AGENCOURT
145	187	11.0	868	5	BX703847	BX703847 BX703847
146	186.6	11.0	294	6	CA534735	CA534735 C0208H08-
147	186.2	10.9	808	1	AU143438	AU143438 AU143438
148	185.6	10.9	1068	9	AY415592	AY415592 Mus muscu
149	185.2	10.9	652	4	BJ038969	BJ038969 BJ038969
150	185.2	10.9	676	4	BJ093488	BJ093488 BJ093488
151	183.6	10.8	453	6	CB785297	CB785297 AMGNNUC:N
152	183.4	10.8	868	7	CR414376	CR414376 CR414376
153	182.4	10.7	978	4	BM564808	BM564808 AGENCOURT
c 154	181.8	10.7	211	7	N69337	N69337 yz43d02.s1
155	181	10.6	665	4	BJ069340	BJ069340 BJ069340
156	180.6	10.6	1178	5	BQ918111	BQ918111 AGENCOURT
157	178.2	10.5	462	5	BY259267	BY259267 BY259267
158	176.4	10.4	587	5	BP337011	BP337011 BP337011
159	175.6	10.3	930	6	CD103327	CD103327 AGENCOURT
160	174.2	10.2	921	7	CF257521	CF257521 pha012_c0
161	173.2	10.2	245	1	AA755095	AA755095 vu02e02.r
162	168	9.9	945	7	CN505864	CN505864 AGENCOURT
c 163	162.2	9.5	397	4	BI297030	BI297030 UI-R-DK0-
164	161.4	9.5	513	1	AA237530	AA237530 mx15d07.r
c 165	160.4	9.4	527	8	AQ001929	AQ001929 CIT-HSP-2
c 166	160.4	9.4	947	4	BG105917	BG105917 602290096
167	160.2	9.4	523	4	BM254339	BM254339 515724 MA
168	158.4	9.3	418	1	AA068884	AA068884 mm63a02.r
169	157.6	9.3	581	5	BP277154	BP277154 BP277154
170	157.6	9.3	1143	4	BM480301	BM480301 AGENCOURT
c 171	155.6	9.1	871	5	BP463348	BP463348 BP463348
c 172	153	9.0	709	2	BE162000	BE162000 MR0-HT044
c 173	151.4	8.9	582	4	BM200196	BM200196 C0207A10-
174	150.2	8.8	871	4	BI550175	BI550175 603193063
c 175	150.2	8.8	896	2	BE744699	BE744699 601577575
176	147.8	8.7	460	2	BE030665	BE030665 128905 MA
177	146.4	8.6	1068	9	AY415591	AY415591 Pan trogl
c 178	145	8.5	591	8	AZ016078	AZ016078 RPCI-23-3
179	143.8	8.5	631	4	BI662217	BI662217 603305448
180	143	8.4	930	6	CD251322	CD251322 AGENCOURT
181	142.8	8.4	591	4	BG476625	BG476625 602524902
182	142.4	8.4	582	5	BP329873	BP329873 BP329873
183	142.4	8.4	1042	4	BM560956	BM560956 AGENCOURT
184	141	8.3	830	4	BG918606	BG918606 602819505
185	140.4	8.3	824	5	BX717231	BX717231 BX717231
186	140.2	8.2	923	4	BG394876	BG394876 602457247
187	140	8.2	507	1	AI893693	AI893693 mp47e04.y
188	139.6	8.2	660	5	BP382862	BP382862 BP382862
189	139	8.2	617	7	CR751993	CR751993 DKFZp469L
190	138	8.1	875	5	BQ424292	BQ424292 AGENCOURT
191	136.4	8.0	370	2	BB870274	BB870274 BB870274
192	136.2	8.0	829	5	BQ954479	BQ954479 AGENCOURT
193	136	8.0	532	5	BX477438	BX477438 DKFZp686J
194	135.4	8.0	368	5	BY232450	BY232450 BY232450
195	135.2	7.9	706	4	BG470669	BG470669 602511596
196	134.8	7.9	484	2	BE756956	BE756956 211274 MA
197	133.6	7.9	541	6	CA397258	CA397258 cs88h10.y
198	133.4	7.8	810	6	C82221	C82221 C82221 Leuk
199	133	7.8	752	4	BI143806	BI143806 602907278
200	133	7.8	978	4	BG386479	BG386479 602455717
201	132.6	7.8	1492	3	CR590646	CR590646 full-leng
202	131.8	7.7	459	2	BE756653	BE756653 210862 MA
203	131.2	7.7	516	4	BJ073771	BJ073771 BJ073771
204	131.2	7.7	721	7	CF523558	CF523558 AGENCOURT
c 205	131	7.7	327	2	AW244508	AW244508 BR_END06A
c 206	131	7.7	612	2	BB626776	BB626776 BB626776
c 207	131	7.7	1496	3	AK034693	AK034693 Mus muscu
208	130.6	7.7	482	5	BQ394075	BQ394075 NISC_ng07
209	129.8	7.6	481	2	AW841190	AW841190 RC1-CN001
210	129.8	7.6	618	7	CN482711	CN482711 hw23g05.y
211	129	7.6	544	1	AA108399	AA108399 mp47e04.r
212	129	7.6	559	2	BB759410	BB759410 BB759410
213	128.4	7.5	635	4	BJ701379	BJ701379 BJ701379
214	127.8	7.5	666	1	AL643334	AL643334 AL643334
215	127.2	7.5	392	5	BY232927	BY232927 BY232927
216	126.4	7.4	572	4	BJ059931	BJ059931 BJ059931
217	126.4	7.4	730	4	BJ713749	BJ713749 BJ713749
218	126.4	7.4	785	4	BI689374	BI689374 603315817
219	126.2	7.4	202	6	CA534815	CA534815 C0210C09-
220	125.6	7.4	835	7	CK469638	CK469638 AGENCOURT
221	124.6	7.3	633	2	BE253216	BE253216 601116830
222	124	7.3	735	1	AU143756	AU143756 AU143756
223	123.6	7.3	855	6	CA492724	CA492724 AGENCOURT
224	123.4	7.3	141	1	AA221012	AA221012 zr03a10.r
225	123.2	7.2	516	7	CR771712	CR771712 DKFZp469J
226	123	7.2	824	7	CO811857	CO811857 AGENCOURT
227	122.4	7.2	789	2	AW044980	AW044980 um16c06.y
228	121.2	7.1	766	7	CR764493	CR764493 DKFZp469I
c 229	121	7.1	549	2	BE949023	BE949023 UI-M-BH3-
230	121	7.1	648	1	AL894052	AL894052 AL894052
231	120.6	7.1	693	6	BY734508	BY734508 BY734508
c 232	120	7.1	545	2	AW490789	AW490789 UI-M-BH3-
233	119.8	7.0	366	7	N88280	N88280 K3006F Huma
234	119	7.0	897	2	BE873049	BE873049 601451070
235	118.8	7.0	648	2	AW106603	AW106603 um31c04.y
236	118.8	7.0	768	5	BX865466	BX865466 BX865466
c 237	118.6	7.0	655	2	BB090249	BB090249 BB090249
238	118.4	7.0	1469	3	CR616345	CR616345 full-leng
239	118.4	7.0	1523	3	CR620502	CR620502 full-leng
240	118.4	7.0	1541	3	CR597234	CR597234 full-leng
241	117.8	6.9	638	1	AL847750	AL847750 AL847750
242	117.4	6.9	669	2	BB660870	BB660870 BB660870
243	117	6.9	659	4	BJ617554	BJ617554 BJ617554

	244	116.6	6.9	1033	2	BE781132	BE781132 601469027
	245	116.2	6.8	614	7	CN482772	CN482772 hw24e09.y
	246	116.2	6.8	645	2	AW107088	AW107088 ul92g10.y
	247	115.6	6.8	582	5	BP205423	BP205423 BP205423
c	248	115.4	6.8	530	4	BM200267	BM200267 C0208H08-
	249	115	6.8	857	7	CF780647	CF780647 AGENCOURT
	250	114.6	6.7	577	5	BP269617	BP269617 BP269617
	251	114.4	6.7	781	6	CD052574	CD052574 LITHZF000
	252	114.2	6.7	581	5	BP276231	BP276231 BP276231
	253	114.2	6.7	635	2	AW318593	AW318593 un02b03.y
	254	113.4	6.7	681	2	AW106897	AW106897 um34h10.y
	255	113	6.6	581	5	BP276773	BP276773 BP276773
	256	112.6	6.6	634	4	BJ694000	BJ694000 BJ694000
	257	112.6	6.6	688	7	CN309488	CN309488 170006001
	258	112.2	6.6	413	4	BJ034649	BJ034649 BJ034649
	259	112.2	6.6	833	5	BU169377	BU169377 AGENCOURT
c	260	112	6.6	149	1	AA640177	AA640177 np28d11.s
	261	111.2	6.5	608	2	AW611263	AW611263 un79f11.y
	262	111	6.5	848	7	CK015734	CK015734 AGENCOURT
	263	110.4	6.5	740	7	CK971835	CK971835 4088027 B
	264	110.2	6.5	971	7	CO579387	CO579387 ILLUMIGEN
	265	110	6.5	649	1	AL862023	AL862023 AL862023
	266	109.4	6.4	794	7	CF345391	CF345391 AGENCOURT
c	267	109.2	6.4	397	2	BE182175	BE182175 PM4-HT064
	268	108.8	6.4	571	5	BP275864	BP275864 BP275864
c	269	108	6.3	408	2	BE944068	BE944068 UI-M-BH3-
	270	107.6	6.3	396	2	BF813655	BF813655 IL5-CI014
	271	107.2	6.3	866	7	CR410549	CR410549 CR410549
	272	107	6.3	1084	1	AL542336	AL542336 AL542336
	273	106.6	6.3	708	6	BY752717	BY752717 BY752717
	274	106.2	6.2	779	7	CN059972	CN059972 Salamande
	275	105.4	6.2	363	5	BY233829	BY233829 BY233829
c	276	105	6.2	562	5	BX887273	BX887273 BX887273
	277	104.2	6.1	717	2	AW701559	AW701559 uq87f09.y
	278	103.6	6.1	362	2	BF813517	BF813517 IL5-CI014
c	279	103.6	6.1	485	8	AZ552182	AZ552182 RPCI-23-1
	280	102.8	6.0	845	6	CA470516	CA470516 AGENCOURT
c	281	102.2	6.0	510	1	AI905394	AI905394 IL-BT091-
	282	102.2	6.0	679	4	BI545956	BI545956 603188367
	283	100.6	5.9	722	7	CK978804	CK978804 4110117 B
	284	100.4	5.9	585	2	BF470607	BF470607 UI-M-BH3-
	285	98.4	5.8	366	7	W97454	W97454 mf97d01.r1
	286	97.8	5.7	984	4	BM460423	BM460423 AGENCOURT
	287	97.6	5.7	481	4	BJ095135	BJ095135 BJ095135
	288	97.4	5.7	565	5	BP277488	BP277488 BP277488
	289	97.2	5.7	577	4	BG608469	BG608469 307067 MA
c	290	97	5.7	562	5	BX886619	BX886619 BX886619
	291	96.6	5.7	615	2	AW078302	AW078302 fe47g07.y
	292	96.4	5.7	558	4	BJ501615	BJ501615 BJ501615
	293	96.2	5.7	576	5	BP253184	BP253184 BP253184
	294	96.2	5.7	581	5	BP206222	BP206222 BP206222
	295	96.2	5.7	581	5	BP207743	BP207743 BP207743
	296	95.6	5.6	629	2	BE902645	BE902645 601677323
	297	94.8	5.6	513	6	CA393595	CA393595 cs40b04.y
	298	94.8	5.6	613	4	BM262289	BM262289 dag39c11.
	299	93.6	5.5	930	5	BQ440047	BQ440047 AGENCOURT
	300	93.2	5.5	582	5	BP216868	BP216868 BP216868
	301	92.8	5.5	762	7	CK479698	CK479698 AGENCOURT
	302	92.8	5.5	824	4	BI550427	BI550427 603192491
	303	92.6	5.4	488	6	CA393587	CA393587 cs40a04.y
	304	92.6	5.4	670	7	CK680539	CK680539 ZF101-P00
	305	92.6	5.4	912	4	BG468280	BG468280 602509877
	306	92.6	5.4	951	4	BG335630	BG335630 602404256
	307	92	5.4	589	4	BM790508	BM790508 K-EST0070
	308	92	5.4	614	5	BU612032	BU612032 UI-M-DJ1-
	309	91.6	5.4	800	6	CB957335	CB957335 AGENCOURT
	310	91.4	5.4	515	1	AL971729	AL971729 AL971729
	311	91.2	5.4	823	5	BU914545	BU914545 AGENCOURT
	312	90	5.3	344	1	AL711206	AL711206 DKFZp686O
	313	90	5.3	665	7	CK639551	CK639551 UI-M-HN0-
	314	89	5.2	733	6	CD803011	CD803011 UI-M-GV0-
	315	89	5.2	914	2	BE778877	BE778877 601465136
	316	88.8	5.2	506	1	AL710754	AL710754 DKFZp686P
	317	88.6	5.2	949	5	BQ957720	BQ957720 AGENCOURT
	318	88.4	5.2	737	6	CB522164	CB522164 UI-M-GH0-
	319	88.4	5.2	769	6	CB522165	CB522165 UI-M-GH0-
c	320	87.8	5.2	350	2	BF814936	BF814936 IL5-CI014
	321	87.8	5.2	1421	4	BM804138	BM804138 AGENCOURT
	322	87.6	5.1	967	2	BF781225	BF781225 602106892
c	323	86.8	5.1	830	7	CK849799	CK849799 972939 BA
	324	86.6	5.1	491	7	CR749069	CR749069 CR749069
	325	86.6	5.1	614	4	BM491751	BM491751 pgp2n.pk0
	326	86.2	5.1	576	6	BY709424	BY709424 BY709424
	327	86.2	5.1	581	5	BQ129711	BQ129711 ii29h06.y
	328	86.2	5.1	602	3	AK009805	AK009805 Mus muscu
	329	86.2	5.1	679	5	BX844471	BX844471 BX844471
	330	86.2	5.1	969	5	BQ949332	BQ949332 AGENCOURT
	331	86	5.1	368	5	BY231458	BY231458 BY231458
	332	85.6	5.0	317	2	BE553410	BE553410 ur45h04.y
	333	85.6	5.0	1123	4	BG336334	BG336334 602405262
	334	85.4	5.0	629	1	AU176858	AU176858 AU176858
	335	85.4	5.0	818	6	CD052607	CD052607 LITHZF000
	336	85	5.0	512	2	BE589550	BE589550 195804 BA
	337	84.8	5.0	820	4	BF966479	BF966479 602286815
	338	84.4	5.0	577	5	BQ129761	BQ129761 ii30e10.y
	339	84	4.9	748	5	BU226527	BU226527 603798287
	340	84	4.9	806	2	BF344769	BF344769 602014025
c	341	84	4.9	961	5	BX423969	BX423969 BX423969
	342	83.2	4.9	781	6	CD648161	CD648161 AUF_102_A
	343	82.8	4.9	829	6	CD758578	CD758578 AGENCOURT
	344	82.6	4.9	377	5	BY235198	BY235198 BY235198
	345	82	4.8	589	4	BI346204	BI346204 375258 MA
	346	82	4.8	916	5	BX423970	BX423970 BX423970
	347	81.8	4.8	789	9	AY409020	AY409020 Homo sapi
	348	81.6	4.8	382	4	BM430439	BM430439 1Duo34D10
c	349	81.6	4.8	507	4	BI289989	BI289989 UI-R-DK0-
	350	81.6	4.8	802	5	BU355036	BU355036 603473271
c	351	81.6	4.8	1017	1	AL580216	AL580216 AL580216
	352	81.6	4.8	1046	5	BQ439603	BQ439603 AGENCOURT
c	353	81	4.8	588	4	BJ635627	BJ635627 BJ635627
	354	80.8	4.8	799	2	BF161094	BF161094 601768034
	355	80.8	4.8	1537	3	AK090390	AK090390 Mus muscu
c	356	80.2	4.7	543	7	CK840259	CK840259 UI-R-C2p-
	357	80.2	4.7	789	9	AY409021	AY409021 Pan trogl
c	358	80	4.7	347	2	BF808931	BF808931 IL5-CI014
	359	80	4.7	1374	5	BU164655	BU164655 AGENCOURT
	360	79.8	4.7	823	5	BU221427	BU221427 603105773
	361	79.4	4.7	489	1	AI791726	AI791726 oq68b07.y
c	362	79.4	4.7	626	4	BJ530193	BJ530193 BJ530193
	363	79.4	4.7	727	5	BX370540	BX370540 BX370540
	364	79.2	4.7	528	1	AI956602	AI956602 ul79c07.y
	365	79.2	4.7	530	1	AI790961	AI790961 uk49b04.y
	366	79.2	4.7	541	1	AI746638	AI746638 ul01f05.y
	367	79.2	4.7	710	2	BB612932	BB612932 BB612932
	368	78.8	4.6	649	6	BY735107	BY735107 BY735107
	369	78.8	4.6	693	7	CV006286	CV006286 CS_gil_15
	370	78.6	4.6	782	6	CB326484	CB326484 UI-R-DZ0-
	371	78.2	4.6	487	1	AI747809	AI747809 ul02f09.y
	372	78.2	4.6	616	5	BU209857	BU209857 604154567
	373	77.6	4.6	736	6	CB985290	CB985290 AGENCOURT
	374	77.4	4.6	553	2	AW519384	AW519384 um97h10.y
	375	77.4	4.6	817	5	BU355260	BU355260 603474641
	376	77.4	4.6	945	7	CF579370	CF579370 AGENCOURT
c	377	77.4	4.6	1071	1	AL554665	AL554665 AL554665
	378	77.2	4.5	485	2	AW318435	AW318435 um97a04.y
	379	77.2	4.5	488	1	AI663279	AI663279 uk27a05.y
	380	77.2	4.5	953	6	CA470415	CA470415 AGENCOURT
	381	77	4.5	634	4	BM487151	BM487151 pgm2n.pk0
	382	77	4.5	686	7	CO432207	CO432207 UI-M-HX0-
	383	76.8	4.5	901	9	CL076826	CL076826 CH216-140
c	384	76.4	4.5	490	4	BI288190	BI288190 UI-R-DK0-
	385	76.4	4.5	809	5	BU356283	BU356283 603473316
	386	76.4	4.5	903	5	BU336949	BU336949 603498420
	387	76	4.5	706	7	CN786579	CN786579 4120595 B
	388	75.8	4.5	560	4	BM530773	BM530773 fx67g03.y
	389	75.8	4.5	934	7	CK867967	CK867967 AGENCOURT

390	75.6	4.4	907	5	BX846071	BX846071	BX846071
391	75.6	4.4	1049	5	BU409636	BU409636	603159478
392	75.6	4.4	1070	1	AL554705	AL554705	AL554705
393	75.4	4.4	309	2	BB848413	BB848413	BB848413
c 394	75.2	4.4	354	1	AI715321	AI715321	UI-R-Y0-a
395	75.2	4.4	572	4	BM191625	BM191625	daj89a02.
396	75	4.4	800	6	CD649975	CD649975	CvGil0068
397	74.8	4.4	386	1	AL792574	AL792574	AL792574
398	74.6	4.4	880	6	CA975638	CA975638	AGENCOURT
399	74.4	4.4	204	2	BB603389	BB603389	BB603389
c 400	74.4	4.4	408	8	BH056546	BH056546	RPCI-24-3
401	74.4	4.4	437	6	CB142226	CB142226	K-EST0195
c 402	74.4	4.4	736	9	AG455967	AG455967	Mus muscu
403	74.2	4.4	691	6	CD348329	CD348329	UI-M-FY0-
404	74.2	4.4	962	9	CNS02M5N	AL203684	Tetraodon
c 405	74	4.4	994	1	AL577748	AL577748	AL577748
c 406	73.6	4.3	483	1	AI145601	AI145601	UI-R-BT0-
407	73.6	4.3	740	4	BI145648	BI145648	602910684
408	73.6	4.3	751	5	BW428117	BW428117	BW428117
409	73.6	4.3	766	5	BU474137	BU474137	603364267
410	73.6	4.3	768	5	BW430500	BW430500	BW430500
411	73.6	4.3	782	5	BU220105	BU220105	603758146
c 412	73.6	4.3	802	5	BW070663	BW070663	BW070663
413	73.6	4.3	812	5	BW448858	BW448858	BW448858
c 414	73.2	4.3	347	1	AI112350	AI112350	UI-R-Y0-m
c 415	73.2	4.3	347	1	AI501574	AI501574	UI-R-C2p-
c 416	73.2	4.3	347	1	AI501649	AI501649	UI-R-C2p-
417	73.2	4.3	381	5	BY234923	BY234923	BY234923
c 418	73.2	4.3	825	9	CNS04RJ8	AL303965	Tetraodon
419	73.2	4.3	862	1	AL669078	AL669078	AL669078
420	73.2	4.3	1063	4	BI854391	BI854391	603381352
421	72.8	4.3	621	4	BG244830	BG244830	602356360
c 422	72.8	4.3	639	2	BE200768	BE200768	fk91a02.x
423	72.6	4.3	555	2	AW319258	AW319258	um88d08.y
c 424	72.6	4.3	744	1	AI132225	AI132225	ue32e02.x
425	72.6	4.3	745	5	BW449321	BW449321	BW449321
426	72.6	4.3	871	1	AL667424	AL667424	AL667424
427	72.2	4.2	333	4	BM796946	BM796946	K-EST0079
428	72.2	4.2	668	4	BG824243	BG824243	602729440
429	72.2	4.2	1193	3	CR640806	CR640806	Tetraodon
c 430	72	4.2	504	7	CK838641	CK838641	UI-R-AG0-
431	72	4.2	740	6	CB950052	CB950052	AGENCOURT
432	71.8	4.2	222	2	BE758240	BE758240	212906 MA
433	71.6	4.2	295	1	AA336800	AA336800	EST41441
434	71.6	4.2	354	4	BI886244	BI886244	ZF637-1-0
435	71.6	4.2	940	7	CK019420	CK019420	AGENCOURT
436	71.4	4.2	361	2	AW359358	AW359358	45902 MAR
437	71.4	4.2	918	1	AL668855	AL668855	AL668855
438	71.2	4.2	711	5	BW437486	BW437486	BW437486
439	71.2	4.2	735	5	BW426799	BW426799	BW426799
440	71.2	4.2	739	5	BW434536	BW434536	BW434536
441	71.2	4.2	743	1	AA921535	AA921535	vz04d10.r
442	71.2	4.2	746	5	BW434653	BW434653	BW434653
443	71.2	4.2	756	6	CB950714	CB950714	AGENCOURT
444	71	4.2	481	4	BM433902	BM433902	1Om11G09
445	71	4.2	783	9	AY400385	AY400385	Mus muscu
446	70.8	4.2	610	7	CF177855	CF177855	806374 MA
447	70.8	4.2	728	5	BP001170	BP001170	BP001170
448	70.6	4.2	867	7	CK797844	CK797844	AGENCOURT
c 449	70.4	4.1	332	4	BI050219	BI050219	CM1-GN036
450	70.4	4.1	656	5	BU207101	BU207101	604155933
451	70.4	4.1	837	1	AL669478	AL669478	AL669478
c 452	70.2	4.1	727	6	CA507543	CA507543	UI-R-FS1-
453	70.2	4.1	767	1	AL668856	AL668856	AL668856
454	69.8	4.1	841	2	BF580135	BF580135	602099144
c 455	69.6	4.1	306	8	BH054489	BH054489	RPCI-24-3
c 456	69.6	4.1	426	2	AW176113	AW176113	CM0-BT015
457	69.6	4.1	514	6	CB224455	CB224455	1OM21D12
458	69.6	4.1	598	2	BF121845	BF121845	601759070
459	69.6	4.1	844	7	CK709031	CK709031	ZF201-P00
460	69.6	4.1	906	2	BF384678	BF384678	602046954
461	69.4	4.1	844	6	CB589141	CB589141	AGENCOURT
462	69.2	4.1	746	6	CB986787	CB986787	AGENCOURT
463	69.2	4.1	951	2	BF385396	BF385396	602047134
464	69	4.1	789	9	AY409022	AY409022	Mus muscu
465	69	4.1	822	7	CN509268	CN509268	AGENCOURT
466	69	4.1	1661	3	AK010166	AK010166	Mus muscu
467	68.8	4.0	1102	4	BM475372	BM475372	AGENCOURT
468	68.6	4.0	222	2	BE758241	BE758241	212907 MA
469	68.6	4.0	627	5	BW524070	BW524070	BW524070
470	68.6	4.0	672	4	BJ617283	BJ617283	BJ617283
471	68.6	4.0	679	1	AI529803	AI529803	ui82f07.y
472	68.6	4.0	719	7	CK807358	CK807358	AGENCOURT
c 473	68.6	4.0	770	7	CV121303	CV121303	AGENCOURT
474	68.6	4.0	772	5	BX873108	BX873108	BX873108
c 475	68.6	4.0	824	7	CV115339	CV115339	AGENCOURT
476	68.6	4.0	1015	3	CR650177	CR650177	Tetraodon
477	68.6	4.0	1019	3	CR695251	CR695251	Tetraodon
478	68.6	4.0	1021	3	CR694361	CR694361	Tetraodon
479	68.6	4.0	1031	3	CR691637	CR691637	Tetraodon
480	68.6	4.0	1044	3	CR694537	CR694537	Tetraodon
481	68.6	4.0	1048	3	CR684177	CR684177	Tetraodon
482	68.6	4.0	1051	3	CR686766	CR686766	Tetraodon
483	68.6	4.0	1054	3	CR696147	CR696147	Tetraodon
484	68.6	4.0	1073	3	CR702495	CR702495	Tetraodon
485	68.6	4.0	1081	3	CR691159	CR691159	Tetraodon
486	68.6	4.0	1089	3	CR682626	CR682626	Tetraodon
487	68.6	4.0	1116	3	CR696183	CR696183	Tetraodon
488	68.6	4.0	1201	3	CR642221	CR642221	Tetraodon
489	68.6	4.0	1201	3	CR698761	CR698761	Tetraodon
490	68.6	4.0	1205	3	CR688759	CR688759	Tetraodon
491	68.6	4.0	1205	3	CR701746	CR701746	Tetraodon
492	68.6	4.0	1207	3	CR647871	CR647871	Tetraodon
493	68.6	4.0	1214	3	CR690142	CR690142	Tetraodon
494	68.6	4.0	1469	3	CR693021	CR693021	Tetraodon
495	68.4	4.0	575	4	BI706475	BI706475	fq06e01.y
496	68.4	4.0	1150	3	AK085670	AK085670	Mus muscu
497	68.2	4.0	559	6	CD561651	CD561651	B0434C05-
498	67.8	4.0	683	1	AU169080	AU169080	AU169080
499	67.6	4.0	430	2	BB864995	BB864995	BB864995
500	67.4	4.0	607	1	AV724699	AV724699	AV724699
501	67.2	4.0	472	2	BE200549	BE200549	ug70d12.y
502	67.2	4.0	604	2	BE137791	BE137791	ug67f05.y
c 503	67.2	4.0	615	2	BF322792	BF322792	maa33f07.
504	67.2	4.0	760	2	BF235195	BF235195	602026471
505	67.2	4.0	874	4	BI410739	BI410739	602964283
c 506	67	3.9	631	7	CV108466	CV108466	AGENCOURT
507	67	3.9	644	7	CV075425	CV075425	AGENCOURT
508	67	3.9	714	7	CK803516	CK803516	AGENCOURT
c 509	67	3.9	714	7	CN320816	CN320816	AGENCOURT
510	67	3.9	747	7	CK803296	CK803296	AGENCOURT
c 511	67	3.9	757	7	CV117624	CV117624	AGENCOURT
512	67	3.9	765	7	CK805608	CK805608	AGENCOURT
c 513	67	3.9	783	7	CN321537	CN321537	AGENCOURT
c 514	67	3.9	787	7	CN320679	CN320679	AGENCOURT
c 515	67	3.9	792	7	CN315503	CN315503	AGENCOURT
516	67	3.9	874	4	BG386425	BG386425	602455652
517	67	3.9	883	3	CR703421	CR703421	Tetraodon
c 518	67	3.9	885	7	CV116465	CV116465	AGENCOURT
519	67	3.9	893	7	CK805019	CK805019	AGENCOURT
520	67	3.9	992	3	CR691675	CR691675	Tetraodon
521	67	3.9	1028	3	CR688961	CR688961	Tetraodon
522	67	3.9	1033	3	CR693411	CR693411	Tetraodon
523	67	3.9	1034	3	CR687422	CR687422	Tetraodon
524	67	3.9	1036	3	CR702554	CR702554	Tetraodon
525	67	3.9	1037	3	CR643786	CR643786	Tetraodon
526	67	3.9	1039	3	CR694225	CR694225	Tetraodon
527	67	3.9	1042	3	CR686666	CR686666	Tetraodon
528	67	3.9	1043	3	CR695881	CR695881	Tetraodon
529	67	3.9	1054	3	CR694512	CR694512	Tetraodon
530	67	3.9	1054	3	CR696061	CR696061	Tetraodon
531	67	3.9	1062	3	CR685899	CR685899	Tetraodon
532	67	3.9	1063	3	CR697618	CR697618	Tetraodon
533	67	3.9	1064	3	CR636276	CR636276	Tetraodon
534	67	3.9	1069	3	CR697942	CR697942	Tetraodon
535	67	3.9	1069	3	CR701723	CR701723	Tetraodon

	536	67	3.9	1071	3	CR689095	CR689095 Tetraodon
	537	67	3.9	1075	3	CR700863	CR700863 Tetraodon
	538	67	3.9	1084	3	CR647785	CR647785 Tetraodon
	539	67	3.9	1090	3	CR651205	CR651205 Tetraodon
	540	67	3.9	1091	3	CR693490	CR693490 Tetraodon
	541	67	3.9	1109	3	CR684786	CR684786 Tetraodon
	542	67	3.9	1116	3	CR656310	CR656310 Tetraodon
	543	67	3.9	1144	3	CR687431	CR687431 Tetraodon
	544	67	3.9	1154	3	CR700329	CR700329 Tetraodon
	545	67	3.9	1187	3	CR695743	CR695743 Tetraodon
	546	67	3.9	1197	3	CR654800	CR654800 Tetraodon
	547	67	3.9	1199	3	CR681675	CR681675 Tetraodon
	548	67	3.9	1199	3	CR692031	CR692031 Tetraodon
	549	67	3.9	1199	3	CR702303	CR702303 Tetraodon
	550	67	3.9	1199	3	CR704584	CR704584 Tetraodon
	551	67	3.9	1200	3	CR637585	CR637585 Tetraodon
	552	67	3.9	1200	3	CR685252	CR685252 Tetraodon
	553	67	3.9	1201	3	CR633921	CR633921 Tetraodon
	554	67	3.9	1201	3	CR682882	CR682882 Tetraodon
	555	67	3.9	1201	3	CR689668	CR689668 Tetraodon
	556	67	3.9	1203	3	CR684277	CR684277 Tetraodon
	557	67	3.9	1203	3	CR687328	CR687328 Tetraodon
	558	67	3.9	1203	3	CR704289	CR704289 Tetraodon
	559	67	3.9	1217	3	CR693139	CR693139 Tetraodon
	560	66.6	3.9	882	9	CNS04RJ9	AL303966 Tetraodon
	561	66.6	3.9	1614	3	AK081698	AK081698 Mus muscu
	562	66.2	3.9	761	5	BW431105	BW431105 BW431105
	563	66	3.9	341	2	BF557172	BF557172 UI-R-E1-f
	564	66	3.9	519	2	BE664981	BE664981 152905 MA
	565	66	3.9	558	2	BE664982	BE664982 152906 MA
	566	66	3.9	558	2	BE664986	BE664986 152912 MA
	567	66	3.9	575	4	BI535862	BI535862 415820 MA
	568	66	3.9	582	4	BI534892	BI534892 398098 MA
	569	66	3.9	593	4	BI535194	BI535194 398563 MA
c	570	66	3.9	697	7	CK968874	CK968874 4084328 B
	571	66	3.9	719	5	BW429288	BW429288 BW429288
	572	66	3.9	723	5	BW203643	BW203643 BW203643
	573	66	3.9	726	5	BW427061	BW427061 BW427061
c	574	65.6	3.9	476	1	AI602520	AI602520 UI-R-AG0-
	575	65.6	3.9	603	5	BQ416438	BQ416438 ii55b04.y
	576	65.6	3.9	653	6	CD216281	CD216281 pgp2n.pk0
c	577	65.6	3.9	715	7	CN326356	CN326356 AGENCOURT
	578	65.4	3.8	485	7	CK681231	CK681231 ZF101-P00
c	579	65.4	3.8	776	7	CN322841	CN322841 AGENCOURT
	580	65.4	3.8	799	7	CK798808	CK798808 AGENCOURT
	581	65.4	3.8	1033	3	CR702338	CR702338 Tetraodon
	582	65.4	3.8	1081	3	CR722887	CR722887 Tetraodon
	583	65.4	3.8	1111	3	CR732474	CR732474 Tetraodon
	584	65.4	3.8	1149	3	CR721250	CR721250 Tetraodon
	585	65.4	3.8	1200	3	CR721805	CR721805 Tetraodon
	586	65.2	3.8	1032	3	CR690077	CR690077 Tetraodon
c	587	65	3.8	629	1	AI411132	AI411132 EST239426
	588	65	3.8	730	7	CV078340	CV078340 AGENCOURT
	589	64.8	3.8	722	6	CA588080	CA588080 STR00610
	590	64.8	3.8	762	7	CF999816	CF999816 AGENCOURT
	591	64.6	3.8	268	7	CK387773	CK387773 L0920F08-
	592	64.6	3.8	898	7	CN164182	CN164182 994306 MA
	593	64.4	3.8	481	6	CB353363	CB353363 ZF001-P00
c	594	64.2	3.8	295	5	BX636674	BX636674 BX636674
c	595	64.2	3.8	588	7	CO681017	CO681017 DG11-124c
	596	64.2	3.8	1078	3	CR673292	CR673292 Tetraodon
	597	64	3.8	441	6	CB225277	CB225277 1OM31B12
	598	64	3.8	553	4	BM490391	BM490391 pgp2n.pk0
c	599	64	3.8	700	6	CD612747	CD612747 56053985H
	600	64	3.8	791	5	BX885846	BX885846 BX885846
	601	64	3.8	1057	3	CR721583	CR721583 Tetraodon
	602	63.8	3.8	701	5	BP140468	BP140468 BP140468
	603	63.8	3.8	769	7	CO558249	CO558249 AGENCOURT
	604	63.8	3.8	1099	3	CR697485	CR697485 Tetraodon
c	605	63.6	3.7	264	4	BG981245	BG981245 RC4-CN008
	606	63.6	3.7	767	7	CO571301	CO571301 AGENCOURT
	607	63.6	3.7	791	6	CB987092	CB987092 AGENCOURT
	608	63.6	3.7	1531	7	CF110983	CF110983 Shultzomi
	609	63.4	3.7	471	6	BY593024	BY593024 BY593024
	610	63.4	3.7	714	7	CN034926	CN034926 Math_p3_P
	611	63.4	3.7	751	7	CO560897	CO560897 AGENCOURT
	612	63.4	3.7	774	7	CO809221	CO809221 AGENCOURT
	613	63.4	3.7	778	7	CO811582	CO811582 AGENCOURT
	614	63.4	3.7	795	7	CO804142	CO804142 AGENCOURT
	615	63.4	3.7	806	7	CO556818	CO556818 AGENCOURT
	616	63.4	3.7	881	6	CD754092	CD754092 AGENCOURT
c	617	63.2	3.7	309	1	AI136659	AI136659 UI-R-C2p-
c	618	63.2	3.7	317	1	AI136244	AI136244 UI-R-C2p-
	619	63	3.7	572	5	BP221699	BP221699 BP221699
	620	63	3.7	701	5	BP450348	BP450348 BP450348
	621	63	3.7	725	5	BW437402	BW437402 BW437402
	622	63	3.7	737	4	BI218121	BI218121 602934234
	623	63	3.7	763	7	CK805724	CK805724 AGENCOURT
c	624	62.8	3.7	691	5	BU620600	BU620600 UI-H-FL1-
	625	62.8	3.7	738	5	BW225343	BW225343 BW225343
	626	62.8	3.7	795	6	CB956732	CB956732 AGENCOURT
	627	62.6	3.7	799	5	BW448622	BW448622 BW448622
	628	62.6	3.7	976	3	CR691249	CR691249 Tetraodon
	629	62.6	3.7	1009	1	AL558378	AL558378 AL558378
	630	62.6	3.7	1036	3	CR690681	CR690681 Tetraodon
	631	62.4	3.7	1024	3	CR683560	CR683560 Tetraodon
c	632	62.2	3.7	483	6	CD318818	CD318818 StrPu538.
	633	62.2	3.7	1133	7	CR755395	CR755395 CR755395
	634	62	3.6	524	1	AA510562	AA510562 vg33a03.r
	635	62	3.6	686	2	BB505929	BB505929 BB505929
c	636	62	3.6	791	1	AI326381	AI326381 mm16a05.x
	637	62	3.6	822	7	CK694719	CK694719 ZF101-P00
	638	62	3.6	1096	7	CR755413	CR755413 CR755413
c	639	61.8	3.6	689	6	CA425935	CA425935 UI-H-FE1-
	640	61.6	3.6	623	4	BG244346	BG244346 602356061
	641	61.6	3.6	709	5	BW227003	BW227003 BW227003
	642	61.6	3.6	713	5	BW226788	BW226788 BW226788
	643	61.4	3.6	672	5	BW427414	BW427414 BW427414
	644	61.4	3.6	748	7	CO877764	CO877764 BovGen_06
	645	61.4	3.6	867	7	CF251062	CF251062 esa020_d0
	646	61.2	3.6	697	5	BW217963	BW217963 BW217963
	647	61.2	3.6	725	5	BW233828	BW233828 BW233828
	648	61.2	3.6	738	7	CK831941	CK831941 4055429 B
	649	61.2	3.6	820	4	BI327822	BI327822 602979578
	650	61.2	3.6	1201	3	CR648007	CR648007 Tetraodon
	651	61	3.6	570	7	CN309491	CN309491 170005325
	652	61	3.6	734	7	CK835508	CK835508 4060181 B
	653	61	3.6	742	7	CK806225	CK806225 AGENCOURT
	654	60.8	3.6	317	6	CD602745	CD602745 RK354A2A0
	655	60.8	3.6	674	7	CK804815	CK804815 AGENCOURT
	656	60.8	3.6	732	7	CK835935	CK835935 4060543 B
	657	60.8	3.6	763	7	CO389506	CO389506 AGENCOURT
	658	60.8	3.6	1027	3	CR703054	CR703054 Tetraodon
	659	60.8	3.6	1046	7	CK028323	CK028323 AGENCOURT
	660	60.6	3.6	642	4	BI533194	BI533194 fq97g07.y
	661	60.6	3.6	754	5	BW440664	BW440664 BW440664
	662	60.4	3.6	240	2	BB582041	BB582041 BB582041
	663	60.4	3.6	797	7	CO556202	CO556202 AGENCOURT
	664	60.2	3.5	708	5	BU424477	BU424477 603232634
	665	60	3.5	409	5	BY227721	BY227721 BY227721
	666	60	3.5	485	4	BM434000	BM434000 1Om15G11
	667	60	3.5	630	7	CV224555	CV224555 CS_hyp_15
	668	60	3.5	688	5	BU661216	BU661216 cl69c09.z
	669	60	3.5	734	7	CK806180	CK806180 AGENCOURT
	670	60	3.5	789	4	BG472323	BG472323 602513970
	671	60	3.5	819	7	CK696351	CK696351 ZF101-P00
	672	59.8	3.5	395	6	CB224932	CB224932 1OM27A03
	673	59.8	3.5	613	6	CB056002	CB056002 NISC_jj11
c	674	59.8	3.5	651	6	CB441881	CB441881 692401 MA
	675	59.8	3.5	764	5	BM948958	BM948958 UI-M-EM0-
	676	59.8	3.5	772	7	CK798033	CK798033 AGENCOURT
	677	59.8	3.5	785	7	CF250979	CF250979 esa019_d0
	678	59.8	3.5	892	7	CF250171	CF250171 esa009_d0
	679	59.6	3.5	417	6	CB766697	CB766697 AMGNNUC:T
	680	59.6	3.5	448	6	CB224669	CB224669 1OM23H09
	681	59.6	3.5	460	6	CB225067	CB225067 1OM28E10

c	682	59.6	3.5	593	2	BE605529	BE605529 fl11h11.x
	683	59.6	3.5	762	7	CK806316	CK806316 AGENCOURT
	684	59.6	3.5	839	7	CO919334	CO919334 AGENCOURT
	685	59.4	3.5	582	2	AW951476	AW951476 EST363546
	686	59.4	3.5	628	5	BP150278	BP150278
	687	59.4	3.5	724	5	BU706083	BU706083 UI-M-FR0-
	688	59.2	3.5	382	1	AA155420	AA155420 mn38b09.r
	689	59.2	3.5	576	1	AA537142	AA537142 vk45d04.r
	690	59.2	3.5	852	7	CF375546	CF375546 AGENCOURT
	691	59.2	3.5	887	7	CO921519	CO921519 AGENCOURT
	692	59	3.5	407	5	BQ385873	BQ385873 NISC_mn14
	693	59	3.5	583	5	BP262112	BP262112 BP262112
	694	59	3.5	663	6	CA334696	CA334696 NISC_ls12
	695	59	3.5	757	6	CD350667	CD350667 UI-M-GI0-
	696	59	3.5	1092	3	CR700777	CR700777 Tetraodon
	697	58.8	3.5	691	5	BW440020	BW440020 BW440020
	698	58.8	3.5	719	5	BW435490	BW435490 BW435490
	699	58.8	3.5	754	5	BW448393	BW448393 BW448393
	700	58.8	3.5	779	5	BX674347	BX674347 BX674347
	701	58.6	3.4	730	7	CN791252	CN791252 4125943 B
	702	58.6	3.4	986	4	BG864854	BG864854 602799286
c	703	58.4	3.4	350	8	BZ231053	BZ231053 CH230-488
	704	58.4	3.4	535	5	BU658552	BU658552 cl37e09.z
	705	58.4	3.4	582	5	BP334093	BP334093 BP334093
	706	58.4	3.4	600	1	AA537271	AA537271 vk46a10.r
	707	58.4	3.4	650	2	BE557859	BE557859 fl11h11.y
	708	58.4	3.4	674	5	BU665261	BU665261 cl128h08.
	709	58.4	3.4	675	2	AW945147	AW945147 EST361340
	710	58.4	3.4	721	6	CD642060	CD642060 AGENCOURT
	711	58.4	3.4	790	7	CN539160	CN539160 UI-M-HU0-
	712	58.4	3.4	900	2	BE911555	BE911555 601663028
	713	58.4	3.4	1080	3	CR687617	CR687617 Tetraodon
	714	58.4	3.4	1183	3	AK033719	AK033719 Mus muscu
	715	58.2	3.4	360	1	AU244616	AU244616 AU244616
c	716	58.2	3.4	682	1	AI831707	AI831707 wj40h01.x
	717	58.2	3.4	719	9	AY404087	AY404087 Mus muscu
	718	58.2	3.4	769	7	CK799756	CK799756 AGENCOURT
	719	58.2	3.4	892	7	CK798830	CK798830 AGENCOURT
c	720	58	3.4	548	2	AW251352	AW251352 UI-R-BJ0-
c	721	58	3.4	563	2	AW252112	AW252112 UI-R-BJ0-
	722	58	3.4	754	7	CK677616	CK677616 ZF101-P00
	723	58	3.4	800	4	BI554383	BI554383 603235886
	724	58	3.4	853	7	CK398888	CK398888 AGENCOURT
	725	58	3.4	885	6	CD760193	CD760193 AGENCOURT
	726	58	3.4	1207	6	CD504465	CD504465 CDA68-B07
	727	58	3.4	1808	3	CR692888	CR692888 Tetraodon
	728	57.8	3.4	270	5	BX400952	BX400952 BX400952
c	729	57.8	3.4	452	7	CK705937	CK705937 ZF101-P00
c	730	57.8	3.4	535	1	AL922875	AL922875 AL922875
	731	57.8	3.4	606	7	CV161952	CV161952 CS_gil_50
	732	57.8	3.4	650	6	CD596501	CD596501 RK102A1A0
	733	57.8	3.4	738	5	BX859329	BX859329 BX859329
	734	57.8	3.4	1811	3	CR731003	CR731003 Tetraodon
	735	57.6	3.4	631	7	CK817331	CK817331 AL00078 K
	736	57.6	3.4	676	4	BI145496	BI145496 602910176
	737	57.6	3.4	756	4	BI145427	BI145427 602910276
	738	57.6	3.4	817	6	CB204975	CB204975 AGENCOURT
	739	57.6	3.4	872	7	CK806070	CK806070 AGENCOURT
	740	57.6	3.4	1020	3	CR688390	CR688390 Tetraodon
	741	57.6	3.4	1045	3	CR696906	CR696906 Tetraodon
	742	57.6	3.4	1201	3	CR690036	CR690036 Tetraodon
	743	57.4	3.4	582	1	AA981934	AA981934 ua37a11.r
	744	57.4	3.4	685	5	BU661390	BU661390 cl71c05.z
	745	57.4	3.4	878	4	BI820671	BI820671 603034455
	746	57.2	3.4	756	7	CV078746	CV078746 AGENCOURT
c	747	57.2	3.4	786	6	CB171281	CB171281 KRE602601
	748	57.2	3.4	1344	3	CR696025	CR696025 Tetraodon
	749	57	3.4	418	6	CB224833	CB224833 1OM25H01
c	750	57	3.4	517	7	CO655574	CO655574 DG18-1a3
	751	57	3.4	717	7	CN793964	CN793964 4129070 B
	752	57	3.4	731	7	CN787614	CN787614 4121783 B
	753	56.8	3.3	428	2	BF043907	BF043907 BP250005B
	754	56.8	3.3	637	5	BP448954	BP448954 BP448954
	755	56.8	3.3	701	5	BU421142	BU421142 603957784
	756	56.8	3.3	779	1	AI791848	AI791848 nl03a05.y
	757	56.8	3.3	821	7	CV078918	CV078918 AGENCOURT
	758	56.8	3.3	942	4	BI221725	BI221725 602937166
	759	56.8	3.3	956	3	CR700938	CR700938 Tetraodon
	760	56.8	3.3	978	3	CR700930	CR700930 Tetraodon
	761	56.8	3.3	1053	3	CR693064	CR693064 Tetraodon
	762	56.8	3.3	1204	3	CR701280	CR701280 Tetraodon
	763	56.6	3.3	487	4	BM434019	BM434019 1Om16H12
	764	56.6	3.3	702	5	BU444968	BU444968 603763860
	765	56.4	3.3	510	5	BX298211	BX298211 BX298211
	766	56.4	3.3	707	5	BX858607	BX858607 BX858607
c	767	56.4	3.3	756	6	CB171283	CB171283 KRE602601
	768	56.4	3.3	846	5	BX076024	BX076024 BX076024
	769	56.4	3.3	901	4	BG866647	BG866647 602785631
	770	56.2	3.3	491	4	BM433819	BM433819 1OM06E02
	771	56.2	3.3	691	5	BP137510	BP137510 BP137510
	772	56.2	3.3	793	7	CV076622	CV076622 AGENCOURT
	773	56.2	3.3	858	7	CK460675	CK460675 930972 MA
	774	56.2	3.3	868	7	CN155215	CN155215 942495 MA
	775	56	3.3	207	4	BJ648545	BJ648545 BJ648545
	776	56	3.3	259	2	BB603427	BB603427 BB603427
	777	56	3.3	480	4	BI976574	BI976574 485550 MA
	778	56	3.3	575	5	BP334519	BP334519 BP334519
	779	56	3.3	697	6	CB951417	CB951417 AGENCOURT
	780	56	3.3	733	2	BF539886	BF539886 602052607
	781	56	3.3	752	6	CB946716	CB946716 AGENCOURT
	782	56	3.3	783	9	AY400383	AY400383 Homo sapi
	783	55.8	3.3	276	1	AA094140	AA094140 cl1919.se
	784	55.8	3.3	402	7	CK690339	CK690339 ZF101-P00
	785	55.8	3.3	927	1	AL555184	AL555184 AL555184
	786	55.6	3.3	478	7	CR741086	CR741086 CR741086
	787	55.6	3.3	696	7	CN792774	CN792774 4127693 B
	788	55.6	3.3	699	5	BW246293	BW246293 BW246293
	789	55.6	3.3	760	4	BG869028	BG869028 602784659
	790	55.6	3.3	1631	3	CR647417	CR647417 Tetraodon
	791	55.6	3.3	1758	3	CR682967	CR682967 Tetraodon
	792	55.6	3.3	1816	3	CR704219	CR704219 Tetraodon
	793	55.4	3.3	833	7	CO422353	CO422353 GGEZHT100
	794	55.4	3.3	836	5	BX383092	BX383092 BX383092
	795	55.2	3.2	633	7	CR752255	CR752255 DKFZp469O
	796	55.2	3.2	655	1	AT006809	AT006809 AT006809
	797	55.2	3.2	661	7	CV071283	CV071283 CS_gil_38
	798	55.2	3.2	684	5	BU663150	BU663150 cl96h03.z
	799	55.2	3.2	721	6	CB592324	CB592324 AGENCOURT
	800	55.2	3.2	770	2	BE469074	BE469074 IpHdk0025
	801	55	3.2	500	4	BM433238	BM433238 1Om09A07
c	802	55	3.2	533	5	BW086707	BW086707 BW086707
	803	55	3.2	559	4	BI540118	BI540118 453091 MA
	804	55	3.2	566	5	BP333541	BP333541 BP333541
	805	55	3.2	692	7	CK835139	CK835139 4059835 B
	806	55	3.2	726	5	BP153759	BP153759 BP153759
	807	54.8	3.2	654	5	BW341712	BW341712 BW341712
	808	54.8	3.2	772	4	BG871011	BG871011 602792056
	809	54.8	3.2	1006	3	BC036270	BC036270 Mus muscu
	810	54.8	3.2	1061	3	BC006726	BC006726 Mus muscu
	811	54.8	3.2	1192	3	AK003066	AK003066 Mus muscu
	812	54.8	3.2	1361	3	BC018582	BC018582 Mus muscu
	813	54.6	3.2	665	7	CF416284	CF416284 Lr_LC1ED_
	814	54.6	3.2	699	5	BW431723	BW431723 BW431723
	815	54.6	3.2	733	4	BG819731	BG819731 602783043
	816	54.4	3.2	722	6	CB986048	CB986048 AGENCOURT
	817	54.4	3.2	743	6	CB958858	CB958858 AGENCOURT
	818	54.4	3.2	876	7	CF551842	CF551842 AGENCOURT
	819	54.4	3.2	1058	3	CR701054	CR701054 Tetraodon
	820	54.4	3.2	1108	5	BM924263	BM924263 AGENCOURT
c	821	54.2	3.2	391	1	AA463885	AA463885 aa08b07.s
	822	54.2	3.2	426	1	AA418122	AA418122 zv94d10.r
c	823	54.2	3.2	429	7	CR463840	CR463840 CR463840
c	824	54.2	3.2	453	1	AI230009	AI230009 EST226704
c	825	54.2	3.2	508	1	AA071341	AA071341 ze88e03.s
	826	54.2	3.2	539	1	AI385507	AI385507 mj85g07.y
	827	54.2	3.2	602	7	CK623999	CK623999 mi16a08.y

	828	54.2	3.2	635	6	CB723387	CB723387 UI-M-GK0-
c	829	54.2	3.2	637	9	CNS02EED	AL193630 Tetraodon
	830	54.2	3.2	767	5	BU245279	BU245279 603783511
	831	54.2	3.2	795	6	CB956681	CB956681 AGENCOURT
	832	54.2	3.2	824	7	CV074038	CV074038 AGENCOURT
	833	54.2	3.2	864	5	BU905238	BU905238 AGENCOURT
	834	54.2	3.2	870	7	CO932513	CO932513 AGENCOURT
	835	54.2	3.2	1389	3	AK013465	AK013465 Mus muscu
	836	54	3.2	486	8	AZ796034	AZ796034 2M0051P11
	837	54	3.2	720	7	CF288079	CF288079 AGENCOURT
	838	54	3.2	795	4	BG873340	BG873340 602794311
	839	54	3.2	829	2	BF540118	BF540118 602050355
	840	54	3.2	866	6	CD303437	CD303437 AGENCOURT
	841	54	3.2	895	4	BI331306	BI331306 602982980
	842	54	3.2	1017	5	BX401186	BX401186 BX401186
	843	53.8	3.2	397	2	BF086360	BF086360 RC6-GN007
	844	53.8	3.2	700	7	CK966680	CK966680 4081605 B
	845	53.8	3.2	725	5	BP449480	BP449480 BP449480
	846	53.8	3.2	725	7	CK980747	CK980747 4112499 B
	847	53.8	3.2	737	7	CK965247	CK965247 4080145 B
	848	53.8	3.2	791	5	BP435958	BP435958 BP435958
	849	53.8	3.2	891	7	CK865297	CK865297 AGENCOURT
	850	53.8	3.2	924	5	BU523425	BU523425 AGENCOURT
	851	53.8	3.2	976	1	AJ815627	AJ815627 AJ815627
	852	53.6	3.2	452	2	BB732825	BB732825 BB732825
c	853	53.6	3.2	489	1	AI081559	AI081559 ox59g06.s
c	854	53.6	3.2	716	6	CB167147	CB167147 GWM602702
	855	53.6	3.2	731	7	CK804168	CK804168 AGENCOURT
	856	53.6	3.2	742	4	BJ712017	BJ712017 BJ712017
	857	53.6	3.2	756	7	CK805679	CK805679 AGENCOURT
	858	53.6	3.2	764	7	CV073500	CV073500 AGENCOURT
	859	53.6	3.2	823	7	CK804427	CK804427 AGENCOURT
	860	53.6	3.2	836	7	CV077818	CV077818 AGENCOURT
	861	53.6	3.2	837	7	CV080531	CV080531 AGENCOURT
	862	53.6	3.2	897	7	CK805026	CK805026 AGENCOURT
	863	53.4	3.1	647	5	BU709585	BU709585 UI-M-FR0-
	864	53.4	3.1	685	1	AL648053	AL648053 AL648053
	865	53.4	3.1	719	9	AY404085	AY404085 Homo sapi
	866	53.4	3.1	807	1	AI047315	AI047315 ud64g07.y
	867	53.4	3.1	844	7	CK682137	CK682137 ZF101-P00
	868	53.2	3.1	382	5	BY011911	BY011911 BY011911
c	869	53.2	3.1	473	2	BE690560	BE690560 uw55f07.x
	870	53.2	3.1	585	6	CA879683	CA879683 K0976A09-
	871	53.2	3.1	741	7	CK807062	CK807062 AGENCOURT
	872	53.2	3.1	770	4	BG869940	BG869940 602789494
	873	53.2	3.1	828	2	BF301040	BF301040 602029053
	874	53.2	3.1	883	2	BF537912	BF537912 602049351
	875	53.2	3.1	1039	9	CNS03N14	AL251473 Tetraodon
	876	53	3.1	521	7	CN261456	CN261456 170004245
	877	53	3.1	539	1	AL910230	AL910230 AL910230
	878	53	3.1	574	5	BP334640	BP334640 BP334640
c	879	52.8	3.1	500	5	BP191098	BP191098 BP191098
	880	52.8	3.1	532	7	CF763444	CF763444 CES006009
	881	52.8	3.1	582	5	BP317333	BP317333 BP317333
	882	52.8	3.1	582	5	BP318070	BP318070 BP318070
	883	52.8	3.1	582	5	BP319458	BP319458 BP319458
	884	52.8	3.1	661	5	BP264988	BP264988 BP264988
	885	52.8	3.1	692	7	CF768871	CF768871 CES000987
	886	52.8	3.1	694	1	AA882342	AA882342 vx43g02.r
	887	52.8	3.1	711	5	BW439749	BW439749 BW439749
	888	52.8	3.1	740	2	BF537124	BF537124 602049036
	889	52.8	3.1	750	2	BF536876	BF536876 602048464
	890	52.8	3.1	794	5	BX093441	BX093441 BX093441
	891	52.8	3.1	887	7	CO925435	CO925435 AGENCOURT
	892	52.8	3.1	1103	7	CR755810	CR755810 CR755810
	893	52.8	3.1	1145	4	BG870620	BG870620 602791596
	894	52.6	3.1	338	7	W78562	W78562 me85a08.r1
c	895	52.6	3.1	475	1	AI598705	AI598705 EST250408
	896	52.6	3.1	533	5	BX527682	BX527682 BX527682
c	897	52.6	3.1	568	1	AA848689	AA848689 EST191449
	898	52.6	3.1	699	6	CB056378	CB056378 NISC_jj16
	899	52.6	3.1	705	6	CB055747	CB055747 NISC_jj08
	900	52.6	3.1	766	6	CA463698	CA463698 AGENCOURT
	901	52.4	3.1	177	4	BJ037063	BJ037063 BJ037063
	902	52.4	3.1	602	2	BE849171	BE849171 uw04d03.y
	903	52.4	3.1	695	7	CK805491	CK805491 AGENCOURT
	904	52.4	3.1	719	9	AY404086	AY404086 Pan trogl
	905	52.4	3.1	759	6	CB951165	CB951165 AGENCOURT
	906	52.4	3.1	808	7	CK804515	CK804515 AGENCOURT
	907	52.4	3.1	812	6	CB950826	CB950826 AGENCOURT
	908	52.2	3.1	328	1	AJ495080	AJ495080 AJ495080
	909	52.2	3.1	716	4	BG867873	BG867873 602787106
	910	52.2	3.1	760	2	BF384908	BF384908 602045214
	911	52.2	3.1	816	2	BF784604	BF784604 602110314
	912	52.2	3.1	1203	3	CR691271	CR691271 Tetraodon
	913	52	3.1	620	2	AV971269	AV971269 AV971269
	914	52	3.1	620	2	AV974126	AV974126 AV974126
	915	52	3.1	631	2	AV999028	AV999028 AV999028
	916	52	3.1	656	2	AV995654	AV995654 AV995654
c	917	52	3.1	753	7	CN319703	CN319703 AGENCOURT
c	918	51.8	3.0	427	5	BY437923	BY437923 BY437923
	919	51.8	3.0	465	6	BY596954	BY596954 BY596954
	920	51.8	3.0	589	4	BM433778	BM433778 1OM04E10
	921	51.8	3.0	620	4	BM767035	BM767035 K-EST0049
	922	51.8	3.0	623	7	CF809745	CF809745 Lr_LC1ED_
	923	51.8	3.0	625	7	CF810293	CF810293 Lr_LC1ED_
	924	51.8	3.0	668	4	BI183942	BI183942 UNL-P-FN-
	925	51.8	3.0	710	9	CR130738	CR130738 Forward s
	926	51.8	3.0	770	9	AG588942	AG588942 Mus muscu
	927	51.8	3.0	772	4	BG867676	BG867676 602787467
	928	51.8	3.0	855	7	CF553370	CF553370 AGENCOURT
	929	51.8	3.0	885	5	BQ222079	BQ222079 AGENCOURT
	930	51.8	3.0	2124	3	CR605437	CR605437 full-leng
c	931	51.6	3.0	271	2	BF820811	BF820811 MR0-RT003
	932	51.6	3.0	272	1	AA675882	AA675882 MBAFCW5H0
	933	51.6	3.0	460	1	AI391118	AI391118 mc29c02.y
c	934	51.6	3.0	774	2	BE798344	BE798344 601581594
	935	51.6	3.0	845	9	CG292993	CG292993 OG0FX60TH
c	936	51.6	3.0	856	9	CG211847	CG211847 OGWFZ74TH
c	937	51.6	3.0	897	9	CG293002	CG293002 OG0FX60TV
c	938	51.6	3.0	900	9	CC707300	CC707300 OGLAH17TH
	939	51.6	3.0	902	4	BG868437	BG868437 602785817
	940	51.6	3.0	932	9	CG211856	CG211856 OGWFZ74TV
c	941	51.6	3.0	938	8	CC431931	CC431931 PUHEG76TD
	942	51.6	3.0	942	8	CC431927	CC431927 PUHEG76TB
c	943	51.6	3.0	984	9	CC707767	CC707767 OGOBR78TV
	944	51.4	3.0	290	6	CB710366	CB710366 AMGNNUC:N
c	945	51.4	3.0	513	2	AW330594	AW330594 707037C06
	946	51.4	3.0	580	5	BP333126	BP333126 BP333126
	947	51.4	3.0	762	7	CV075500	CV075500 AGENCOURT
	948	51.4	3.0	766	6	CB208165	CB208165 AGENCOURT
	949	51.4	3.0	784	7	CK127686	CK127686 AGENCOURT
	950	51.4	3.0	881	6	CB955924	CB955924 AGENCOURT
	951	51.2	3.0	218	1	AI835174	AI835174 UI-M-AQ0-
	952	51.2	3.0	247	1	AI427480	AI427480 mj47a03.x
c	953	51.2	3.0	250	1	AV014385	AV014385 AV014385
c	954	51.2	3.0	297	1	AI510115	AI510115 mj47a03.y
	955	51.2	3.0	328	2	BF319248	BF319248 uy55g03.x
c	956	51.2	3.0	383	6	BY630512	BY630512 BY630512
c	957	51.2	3.0	389	6	BY672103	BY672103 BY672103
c	958	51.2	3.0	394	1	AA259517	AA259517 va48b12.r
c	959	51.2	3.0	414	6	BY653401	BY653401 BY653401
	960	51.2	3.0	420	2	AW413642	AW413642 uo38d10.x
c	961	51.2	3.0	424	6	BY695784	BY695784 BY695784
c	962	51.2	3.0	427	2	BB757672	BB757672 BB757672
	963	51.2	3.0	490	1	AA530530	AA530530 vj39f07.r
	964	51.2	3.0	495	9	CG664708	CG664708 OST452269
c	965	51.2	3.0	499	1	AA049271	AA049271 mj45b01.r
	966	51.2	3.0	516	5	BU755969	BU755969 UI-1-CF0-
c	967	51.2	3.0	534	2	AW787533	AW787533 945010G05
	968	51.2	3.0	553	3	AY105354	AY105354 Zea mays
	969	51.2	3.0	561	2	BF074991	BF074991 223716 MA
c	970	51.2	3.0	608	1	AI042827	AI042827 uc75g05.x
c	971	51.2	3.0	614	5	BW564009	BW564009 BW564009
c	972	51.2	3.0	618	7	CK838939	CK838939 UI-R-AB1-
c	973	51.2	3.0	636	1	AV232350	AV232350 AV232350

974	51.2	3.0	647	1	AI006124	AI006124	ua86h04.r
975	51.2	3.0	651	7	CV527804	CV527804	CS_GIL_04
c 976	51.2	3.0	658	9	CC709694	CC709694	OGWEW56TH
977	51.2	3.0	672	7	CV527111	CV527111	CS_GIL_05
978	51.2	3.0	737	2	AW913714	AW913714	uf56c09.y
979	51.2	3.0	740	4	BG869338	BG869338	602788860
980	51.2	3.0	741	5	BQ176277	BQ176277	UI-M-DJ2-
981	51.2	3.0	759	2	BF301010	BF301010	602029022
982	51.2	3.0	775	2	BF540434	BF540434	602052404
983	51.2	3.0	779	7	CO567488	CO567488	AGENCOURT
984	51.2	3.0	782	7	CK969500	CK969500	4084712 B
985	51.2	3.0	811	7	CV073989	CV073989	AGENCOURT
986	51.2	3.0	845	4	BG868843	BG868843	602787693
987	51.2	3.0	856	4	BG869415	BG869415	602788786
988	51.2	3.0	874	4	BG865888	BG865888	602788121
989	51.2	3.0	903	4	BG872420	BG872420	602792724
990	51.2	3.0	1085	4	BM546098	BM546098	AGENCOURT
991	51	3.0	310	1	AU176827	AU176827	AU176827
992	51	3.0	462	8	AZ636481	AZ636481	1M0495A20
993	51	3.0	568	5	BP332806	BP332806	BP332806
994	51	3.0	608	4	BG799727	BG799727	fp13b04.y
995	51	3.0	658	5	BU658617	BU658617	cl38c06.z
996	50.8	3.0	457	1	AU172479	AU172479	AU172479
c 997	50.8	3.0	473	8	AZ046676	AZ046676	nbeb0095E
c 998	50.8	3.0	488	2	AW787532	AW787532	945010G05
999	50.8	3.0	553	1	AV948330	AV948330	AV948330
1000	50.8	3.0	605	5	BU664908	BU664908	cl124b11.
c1001	50.8	3.0	616	6	CD340974	CD340974	StrPu536.
1002	50.8	3.0	632	2	AW355973	AW355973	707017E07
1003	50.8	3.0	645	6	CD674886	CD674886	fs16e01.y
1004	50.8	3.0	666	5	BU662217	BU662217	cl83a03.z
c1005	50.8	3.0	761	1	AV908090	AV908090	AV908090
1006	50.8	3.0	826	6	CB180296	CB180296	AGENCOURT
1007	50.8	3.0	835	7	CO561993	CO561993	AGENCOURT
1008	50.8	3.0	887	7	CF377034	CF377034	AGENCOURT
1009	50.8	3.0	936	7	CK414250	CK414250	AUF_IpGil
1010	50.6	3.0	243	2	AW156533	AW156533	se28c12.y
c1011	50.6	3.0	412	2	AW424540	AW424540	707017E07
c1012	50.6	3.0	500	5	BP188875	BP188875	BP188875
1013	50.6	3.0	628	6	CA755519	CA755519	BR0300220
c1014	50.6	3.0	652	8	AZ146154	AZ146154	SP_0026_B
1015	50.6	3.0	699	5	BW206211	BW206211	BW206211
1016	50.6	3.0	779	4	BG867912	BG867912	602787148
1017	50.6	3.0	799	4	BI221401	BI221401	602938995
1018	50.6	3.0	860	4	BG873155	BG873155	602794559
1019	50.6	3.0	882	7	CF590784	CF590784	AGENCOURT
1020	50.4	3.0	542	5	BW504003	BW504003	BW504003
1021	50.4	3.0	547	5	BW197576	BW197576	BW197576
1022	50.4	3.0	565	2	AV952548	AV952548	AV952548
1023	50.4	3.0	569	5	BW224583	BW224583	BW224583
1024	50.4	3.0	577	4	BI342814	BI342814	370765 MA
1025	50.4	3.0	578	2	AV968753	AV968753	AV968753
1026	50.4	3.0	580	2	AV988017	AV988017	AV988017
1027	50.4	3.0	584	2	AV963815	AV963815	AV963815
1028	50.4	3.0	586	5	BW220790	BW220790	BW220790
1029	50.4	3.0	594	2	AV957357	AV957357	AV957357
1030	50.4	3.0	595	5	BW240118	BW240118	BW240118
1031	50.4	3.0	599	5	BW228423	BW228423	BW228423
1032	50.4	3.0	608	5	BW343525	BW343525	BW343525
1033	50.4	3.0	609	5	BW339215	BW339215	BW339215
1034	50.4	3.0	611	5	BW291657	BW291657	BW291657
1035	50.4	3.0	612	5	BW340570	BW340570	BW340570
1036	50.4	3.0	618	5	BW339844	BW339844	BW339844
1037	50.4	3.0	620	2	AV984561	AV984561	AV984561
1038	50.4	3.0	620	5	BW341217	BW341217	BW341217
1039	50.4	3.0	621	5	BW346281	BW346281	BW346281
1040	50.4	3.0	621	5	BW349279	BW349279	BW349279
1041	50.4	3.0	621	5	BW350908	BW350908	BW350908
1042	50.4	3.0	622	2	AV969860	AV969860	AV969860
1043	50.4	3.0	623	1	AV672274	AV672274	AV672274
1044	50.4	3.0	624	5	BW338094	BW338094	BW338094
1045	50.4	3.0	629	2	AV993120	AV993120	AV993120
1046	50.4	3.0	629	5	BW342021	BW342021	BW342021
1047	50.4	3.0	630	5	BW351352	BW351352	BW351352
1048	50.4	3.0	631	2	AV979325	AV979325	AV979325
1049	50.4	3.0	636	5	BW343709	BW343709	BW343709
1050	50.4	3.0	637	2	AV979227	AV979227	AV979227
1051	50.4	3.0	638	2	AV970421	AV970421	AV970421
1052	50.4	3.0	639	5	BW336485	BW336485	BW336485
1053	50.4	3.0	645	5	BW348783	BW348783	BW348783
1054	50.4	3.0	648	5	BW448488	BW448488	BW448488
1055	50.4	3.0	649	5	BW342379	BW342379	BW342379
1056	50.4	3.0	653	5	BW340466	BW340466	BW340466
1057	50.4	3.0	662	5	BW225683	BW225683	BW225683
1058	50.4	3.0	665	1	AV672514	AV672514	AV672514
1059	50.4	3.0	665	5	BW226713	BW226713	BW226713
1060	50.4	3.0	665	5	BW231225	BW231225	BW231225
1061	50.4	3.0	674	2	AV972184	AV972184	AV972184
1062	50.4	3.0	684	5	BW231044	BW231044	BW231044
1063	50.4	3.0	700	5	BW244119	BW244119	BW244119
1064	50.4	3.0	704	5	BW249961	BW249961	BW249961
c1065	50.4	3.0	830	8	AZ185211	AZ185211	SP_1004_B
1066	50.4	3.0	853	5	BW448689	BW448689	BW448689
1067	50.4	3.0	937	7	CK404478	CK404478	AUF_IfHdk
1068	50.2	3.0	320	2	AW320090	AW320090	unl4g11.x
1069	50.2	3.0	353	5	BY009613	BY009613	BY009613
c1070	50.2	3.0	379	6	BY670222	BY670222	BY670222
c1071	50.2	3.0	387	1	AA958916	AA958916	ua19g09.r
c1072	50.2	3.0	402	6	BY612000	BY612000	BY612000
c1073	50.2	3.0	403	6	BY632832	BY632832	BY632832
c1074	50.2	3.0	406	6	BY633914	BY633914	BY633914
c1075	50.2	3.0	446	1	AA111100	AA111100	mp65c10.r
1076	50.2	3.0	685	7	CV078375	CV078375	AGENCOURT
1077	50.2	3.0	697	2	AW701950	AW701950	uq93c01.y
1078	50.2	3.0	709	4	BG866240	BG866240	602785223
1079	50.2	3.0	769	1	AI528107	AI528107	ui93e07.y
1080	50.2	3.0	772	1	AI196900	AI196900	ui55b11.y
1081	50.2	3.0	775	4	BG867707	BG867707	602786810
1082	50.2	3.0	798	1	AI048529	AI048529	ud61a05.y
c1083	50	2.9	220	2	BB134375	BB134375	BB134375
c1084	50	2.9	448	2	AW497449	AW497449	660052B03
1085	50	2.9	638	7	CF103237	CF103237	hac32e10.
1086	50	2.9	695	7	CO641713	CO641713	USDA-FP_1
1087	50	2.9	706	6	CB592592	CB592592	AGENCOURT
1088	50	2.9	714	6	CA847019	CA847019	hac04g06.
1089	50	2.9	740	4	BG868178	BG868178	602787283
1090	50	2.9	766	4	BG871949	BG871949	602793048
1091	50	2.9	785	5	BU383110	BU383110	603861706
1092	50	2.9	820	5	BU271010	BU271010	603814703
1093	50	2.9	3712	3	AK004896	AK004896	Mus muscu
c1094	49.8	2.9	311	7	CN281167	CN281167	170004237
c1095	49.8	2.9	501	2	BE074274	BE074274	QV3-BT057
c1096	49.8	2.9	699	8	BH060245	BH060245	RPCI-24-2
1097	49.8	2.9	748	7	CV073089	CV073089	AGENCOURT
1098	49.8	2.9	772	7	CR575043	CR575043	CR575043
1099	49.8	2.9	822	5	BX849524	BX849524	BX849524
1100	49.8	2.9	825	9	AG551363	AG551363	Mus muscu
1101	49.8	2.9	833	7	CF250892	CF250892	esa018_d0
c1102	49.8	2.9	838	9	CNS03D0C	AL238485	Tetraodon
c1103	49.8	2.9	918	9	CNS05BZ5	AL330458	Tetraodon
1104	49.8	2.9	923	4	BI217202	BI217202	602933862
1105	49.8	2.9	929	7	CR425623	CR425623	CR425623
1106	49.8	2.9	930	7	CR436205	CR436205	CR436205
c1107	49.8	2.9	1101	9	CNS00BAU	AL056742	Drosophil
c1108	49.6	2.9	267	7	W97393	W97393	mf94b10.r1
c1109	49.6	2.9	414	6	BY631218	BY631218	BY631218
1110	49.6	2.9	424	6	CB592799	CB592799	AGENCOURT
c1111	49.6	2.9	433	5	BY384196	BY384196	BY384196
1112	49.6	2.9	498	6	CA872941	CA872941	K0921G05-
c1113	49.6	2.9	520	2	BB755148	BB755148	BB755148
1114	49.6	2.9	522	6	CA870557	CA870557	K0903A03-
1115	49.6	2.9	537	2	AW786257	AW786257	119192 MA
1116	49.6	2.9	599	8	AZ299589	AZ299589	RPCI-23-4
1117	49.6	2.9	639	7	CF177079	CF177079	805523 MA
c1118	49.6	2.9	674	8	AZ185331	AZ185331	SP_1005_A
1119	49.6	2.9	683	5	BP139300	BP139300	BP139300

1120	49.6	2.9	694	5	BX673035	BX673035	BX673035
1121	49.6	2.9	703	2	BF538208	BF538208	602053680
1122	49.6	2.9	753	4	BG872786	BG872786	602793905
1123	49.6	2.9	827	4	BG872963	BG872963	602794216
1124	49.6	2.9	835	4	BI158671	BI158671	602921746
1125	49.6	2.9	893	4	BG867971	BG867971	602788317
1126	49.6	2.9	935	4	BG865437	BG865437	602783559
c1127	49.6	2.9	1367	9	AG395723	AG395723	Mus muscu
c1128	49.4	2.9	402	6	BY601939	BY601939	BY601939
1129	49.4	2.9	535	7	CK832800	CK832800	4056558 B
1130	49.4	2.9	668	1	AA597276	AA597276	vo36c10.r
1131	49.4	2.9	715	6	CA346252	CA346252	677103 NC
c1132	49.4	2.9	745	9	CL994471	CL994471	ZMMBHf000
1133	49.4	2.9	776	7	CO880947	CO880947	BovGen_09
c1134	49.4	2.9	782	9	AG492700	AG492700	Mus muscu
1135	49.4	2.9	820	7	CV074848	CV074848	AGENCOURT
1136	49.4	2.9	900	4	BG473897	BG473897	602516351
1137	49.2	2.9	432	2	AW464980	AW464980	BP230017A
1138	49.2	2.9	495	7	CR424562	CR424562	CR424562
c1139	49.2	2.9	532	7	CF763444	CF763444	CES006009
c1140	49.2	2.9	581	8	AZ969100	AZ969100	2M0241C16
c1141	49.2	2.9	668	6	CA440015	CA440015	UI-H-DT1-
1142	49.2	2.9	680	5	BU660624	BU660624	cl62d03.z
1143	49.2	2.9	728	4	BI819658	BI819658	603037810
c1144	49.2	2.9	747	5	BW157462	BW157462	BW157462
c1145	49.2	2.9	786	8	BZ264270	BZ264270	CH230-420
c1146	49.2	2.9	813	2	AW025419	AW025419	wu74a05.x
c1147	49.2	2.9	818	7	CN093439	CN093439	EC2BBA8AG
1148	49.2	2.9	823	4	BI819270	BI819270	603037710
1149	49.2	2.9	845	7	CF592698	CF592698	AGENCOURT
1150	49.2	2.9	909	7	CO803486	CO803486	AGENCOURT
1151	49.2	2.9	949	5	BU523833	BU523833	AGENCOURT
1152	49.2	2.9	1798	7	CN210867	CN210867	RJB092G04
1153	49	2.9	182	8	BH360723	BH360723	CH230-18L
1154	49	2.9	275	6	CD709018	CD709018	EST25545
1155	49	2.9	392	5	BY025641	BY025641	BY025641
1156	49	2.9	395	4	BM482160	BM482160	534941 MA
1157	49	2.9	461	5	BU341138	BU341138	603406748
1158	49	2.9	490	5	BX740526	BX740526	BX740526
1159	49	2.9	553	5	BU375927	BU375927	603811912
1160	49	2.9	639	5	BW029454	BW029454	BW029454
1161	49	2.9	653	7	CN288510	CN288510	170005830
1162	49	2.9	672	5	BM957630	BM957630	fy67d05.y
1163	49	2.9	697	5	BU286976	BU286976	603605374
1164	49	2.9	878	5	BX341631	BX341631	BX341631
1165	49	2.9	928	3	CR688830	CR688830	Tetraodon
1166	49	2.9	1025	3	CR691180	CR691180	Tetraodon
1167	49	2.9	1033	5	BX378056	BX378056	BX378056
1168	49	2.9	1722	3	AK003671	AK003671	Mus muscu
1169	49	2.9	1723	3	AK004923	AK004923	Mus muscu
1170	48.8	2.9	500	5	BP188875	BP188875	BP188875
c1171	48.8	2.9	561	8	AZ024138	AZ024138	RPCI-23-3
1172	48.8	2.9	598	4	BJ008039	BJ008039	BJ008039
1173	48.8	2.9	599	4	BJ012808	BJ012808	BJ012808
1174	48.8	2.9	612	5	BW336456	BW336456	BW336456
1175	48.8	2.9	629	1	AU168557	AU168557	AU168557
1176	48.8	2.9	645	4	BJ012031	BJ012031	BJ012031
1177	48.8	2.9	718	6	CB947664	CB947664	AGENCOURT
1178	48.8	2.9	781	9	AG568486	AG568486	Mus muscu
1179	48.8	2.9	828	7	CR442495	CR442495	CR442495
1180	48.8	2.9	857	9	AG315799	AG315799	Mus muscu
c1181	48.8	2.9	1284	9	AG324289	AG324289	Mus muscu
1182	48.6	2.9	376	5	BY025418	BY025418	BY025418
c1183	48.6	2.9	417	6	BY624303	BY624303	BY624303
c1184	48.6	2.9	420	5	BY434899	BY434899	BY434899
c1185	48.6	2.9	467	7	CF186418	CF186418	j4k10j2.f
c1186	48.6	2.9	593	8	BZ138845	BZ138845	CH230-256
c1187	48.6	2.9	594	5	BQ184356	BQ184356	UI-E-EJ1-
1188	48.6	2.9	650	6	CD594773	CD594773	RK093A4G0
1189	48.6	2.9	664	6	CB592946	CB592946	AGENCOURT
1190	48.6	2.9	677	4	BG871724	BG871724	602791956
1191	48.6	2.9	707	6	CA368454	CA368454	644656 NC
1192	48.6	2.9	716	7	CV076632	CV076632	AGENCOURT
c1193	48.6	2.9	751	8	BZ137949	BZ137949	CH230-256
1194	48.6	2.9	755	5	BU375622	BU375622	603810687
c1195	48.6	2.9	865	9	AG400950	AG400950	Mus muscu
c1196	48.4	2.8	240	1	AJ472486	AJ472486	AJ472486
1197	48.4	2.8	248	1	AJ301337	AJ301337	AJ301337
1198	48.4	2.8	450	6	CA878472	CA878472	CA878472
c1199	48.4	2.8	520	4	BJ734372	BJ734372	BJ734372
1200	48.4	2.8	535	2	AW787121	AW787121	120841 MA
1201	48.4	2.8	626	5	BU657551	BU657551	cl25f04.z
1202	48.4	2.8	651	5	BU284785	BU284785	603601595
1203	48.4	2.8	667	6	CB439814	CB439814	689805 MA
1204	48.4	2.8	718	7	CK781524	CK781524	UI-M-GV0-
c1205	48.4	2.8	720	6	CB439466	CB439466	689114 MA
c1206	48.4	2.8	795	8	BZ204973	BZ204973	CH230-425
1207	48.4	2.8	806	9	AG459839	AG459839	Mus muscu
1208	48.4	2.8	815	5	BU935953	BU935953	AGENCOURT
c1209	48.4	2.8	827	8	BZ192827	BZ192827	CH230-248
1210	48.4	2.8	898	5	BQ733463	BQ733463	AGENCOURT
1211	48.4	2.8	932	4	BG871098	BG871098	602790274
1212	48.4	2.8	997	6	BY705131	BY705131	BY705131
1213	48.4	2.8	1018	5	BU142186	BU142186	603136088
1214	48.4	2.8	1240	3	CR692434	CR692434	Tetraodon
1215	48.4	2.8	1273	3	CR700052	CR700052	Tetraodon
1216	48.2	2.8	417	8	AZ807018	AZ807018	2M0069O22
c1217	48.2	2.8	438	6	CB173813	CB173813	OR_2o26B2
1218	48.2	2.8	577	8	BH521990	BH521990	BOGQR64TF
1219	48.2	2.8	626	4	BJ066122	BJ066122	BJ066122
1220	48.2	2.8	650	6	CD596265	CD596265	RK100A4F0
1221	48.2	2.8	712	9	AG369577	AG369577	Mus muscu
1222	48.2	2.8	721	6	CB171248	CB171248	KRE602601
1223	48.2	2.8	771	6	CD779508	CD779508	EST650869
c1224	48.2	2.8	828	1	AI256540	AI256540	ui87f08.x
1225	48.2	2.8	946	5	BQ922926	BQ922926	AGENCOURT
c1226	48.2	2.8	1068	3	CR679291	CR679291	Tetraodon
c1227	48.2	2.8	1229	9	AG320467	AG320467	Mus muscu
1228	48	2.8	382	2	AW475755	AW475755	un71f11.y
c1229	48	2.8	394	6	CA513563	CA513563	10-3/2-C7
c1230	48	2.8	404	8	AZ894158	AZ894158	RPCI-24-1
c1231	48	2.8	442	5	BY472250	BY472250	BY472250
1232	48	2.8	606	4	BJ007149	BJ007149	BJ007149
c1233	48	2.8	611	1	AI659170	AI659170	tu02b07.x
c1234	48	2.8	633	4	BG333208	BG333208	602430925
1235	48	2.8	688	4	BG873085	BG873085	602794668
1236	48	2.8	716	7	CK836685	CK836685	4061498 B
1237	48	2.8	834	4	BG867131	BG867131	602786745
c1238	48	2.8	1101	9	CNS017RP	AL108415	Drosophil
1239	47.8	2.8	146	9	CR133309	CR133309	Reverse s
1240	47.8	2.8	176	1	AA062173	AA062173	mj85g07.r
1241	47.8	2.8	279	4	BJ312482	BJ312482	BJ312482
c1242	47.8	2.8	451	8	BZ265115	BZ265115	CH230-274
1243	47.8	2.8	485	4	BJ277814	BJ277814	BJ277814
1244	47.8	2.8	548	2	BF193785	BF193785	245480 MA
1245	47.8	2.8	626	2	BE576397	BE576397	dc38g01.y
1246	47.8	2.8	641	6	CD650714	CD650714	CvGil0141
1247	47.8	2.8	660	6	CA324934	CA324934	UI-M-FY0-
1248	47.8	2.8	708	7	CN852954	CN852954	Ha_mx0_07
c1249	47.8	2.8	713	2	BF866105	BF866105	963066E04
1250	47.8	2.8	803	9	AG281151	AG281151	Mus muscu
1251	47.8	2.8	882	4	BM425459	BM425459	IpSpn0201
1252	47.8	2.8	892	4	BG869354	BG869354	602788877
1253	47.8	2.8	905	5	BU115615	BU115615	603140674
1254	47.8	2.8	926	4	BG867281	BG867281	602788620
c1255	47.8	2.8	1071	7	CR754127	CR754127	CR754127
c1256	47.6	2.8	247	2	BE519369	BE519369	945023G05
c1257	47.6	2.8	408	8	BZ127201	BZ127201	CH230-357
1258	47.6	2.8	436	2	BB849036	BB849036	BB849036
1259	47.6	2.8	555	8	AZ651354	AZ651354	1M0522G01
1260	47.6	2.8	701	7	CK836626	CK836626	4061548 B
1261	47.6	2.8	706	7	CK973620	CK973620	4104351 B
c1262	47.6	2.8	715	5	BU425026	BU425026	603235192
1263	47.6	2.8	722	7	CO810116	CO810116	AGENCOURT
1264	47.6	2.8	731	8	AZ327485	AZ327485	1M0050M18
1265	47.6	2.8	754	9	AG493661	AG493661	Mus muscu

1266	47.6	2.8	796	7	CK677389	CK677389 ZF101-P00	1339	46.8	2.8	722	5	BU248671	BU248671 603782880		
1267	47.6	2.8	813	7	CO734371	CO734371 SlLH03c08	c1340	46.8	2.8	731	4	BM618019	BM618019 170006871		
1268	47.6	2.8	853	7	CF553235	CF553235 AGENCOURT	1341	46.8	2.8	763	4	BG867098	BG867098 602786709		
1269	47.6	2.8	935	2	BF540168	BF540168 602050211	1342	46.8	2.8	780	5	BX074391	BX074391 BX074391		
1270	47.6	2.8	977	5	BU472470	BU472470 603364302	1343	46.8	2.8	799	5	BU116682	BU116682 603140734		
c1271	47.6	2.8	1220	9	CG752571	CG752571 P047-2-E0	1344	46.8	2.8	844	5	BU242294	BU242294 603591238		
1272	47.6	2.8	1490	7	CN210868	CN210868 WLB042H01	1345	46.8	2.8	847	2	BF535426	BF535426 602051820		
c1273	47.4	2.8	126	6	CB408479	CB408479 IPG016C03	1346	46.8	2.8	856	5	BX735639	BX735639 BX735639		
c1274	47.4	2.8	179	8	BZ235835	BZ235835 CH230-333	1347	46.8	2.8	884	7	CO928237	CO928237 AGENCOURT		
1275	47.4	2.8	242	1	AI875781	AI875781 uj19g05.x	1348	46.8	2.8	903	5	BU121964	BU121964 603146421		
1276	47.4	2.8	413	5	BW528386	BW528386 BW528386	c1349	46.8	2.8	974	9	AG353696	AG353696 Mus muscu		
1277	47.4	2.8	428	8	BH075267	BH075267 RPCI-24-2	1350	46.8	2.8	1117	9	AG425982	AG425982 Mus muscu		
c1278	47.4	2.8	471	8	AZ102843	AZ102843 RPCI-23-3	c1351	46.8	2.8	1341	6	CD325995	CD325995 AGENCOURT		
c1279	47.4	2.8	485	4	BJ277814	BJ277814 BJ277814	1352	46.8	2.8	2753	3	HSM804316	AL833005 Homo sapi		
1280	47.4	2.8	558	4	BM480738	BM480738 531441 MA	1353	46.6	2.7	268	2	AW476381	AW476381 uq75a05.y		
1281	47.4	2.8	561	7	CK685001	CK685001 ZF101-P00	c1354	46.6	2.7	304	8	BH356293	BH356293 CH230-33N		
1282	47.4	2.8	564	7	CN552834	CN552834 tae41b03.	1355	46.6	2.7	443	2	BB759801	BB759801 BB759801		
1283	47.4	2.8	587	6	CB546168	CB546168 AMGNNUC:N	1356	46.6	2.7	468	1	AU031928	AU031928 AU031928		
1284	47.4	2.8	621	7	CK681373	CK681373 ZF101-P00	c1357	46.6	2.7	532	4	BJ235892	BJ235892 BJ235892		
1285	47.4	2.8	659	7	CO874344	CO874344 BovGen_02	1358	46.6	2.7	542	4	BI847338	BI847338 469150 MA		
c1286	47.4	2.8	659	7	CO877511	CO877511 BovGen_05	c1359	46.6	2.7	565	8	BH344998	BH344998 CH230-183		
c1287	47.4	2.8	661	7	CN552584	CN552584 tae41b03.	1360	46.6	2.7	573	5	BQ551532	BQ551532 H4009H06-		
c1288	47.4	2.8	686	2	BF866641	BF866641 963070G09	1361	46.6	2.7	596	1	AV595266	AV595266 AV595266		
1289	47.4	2.8	738	7	CO879022	CO879022 BovGen_07	c1362	46.6	2.7	600	8	AZ904619	AZ904619 RPCI-24-1		
1290	47.4	2.8	793	1	AL667053	AL667053 AL667053	1363	46.6	2.7	617	4	BF974188	BF974188 602243816		
1291	47.4	2.8	827	4	BG868422	BG868422 602787896	1364	46.6	2.7	643	2	BB292750	BB292750 BB292750		
1292	47.4	2.8	855	4	BI218417	BI218417 602937908	c1365	46.6	2.7	644	8	BH057316	BH057316 RPCI-24-3		
1293	47.4	2.8	902	4	BI327679	BI327679 602979194	1366	46.6	2.7	645	2	AW914807	AW914807 EST346111		
1294	47.4	2.8	926	7	CF552222	CF552222 AGENCOURT	1367	46.6	2.7	688	7	CN288991	CN288991 170005999		
1295	47.2	2.8	327	7	CN950615	CN950615 Ha_mx0_36	1368	46.6	2.7	703	5	BU703176	BU703176 UI-M-FD0-		
1296	47.2	2.8	336	5	BY081704	BY081704 BY081704	1369	46.6	2.7	721	2	AW914808	AW914808 EST346112		
1297	47.2	2.8	416	9	CE117224	CE117224 tigr-gss-	1370	46.6	2.7	733	9	AG560158	AG560158 Mus muscu		
1298	47.2	2.8	464	1	AI037378	AI037378 ub52a02.r	c1371	46.6	2.7	762	8	AZ183505	AZ183505 SP_1001_A		
1299	47.2	2.8	470	7	CN950614	CN950614 Ha_mx0_36	1372	46.6	2.7	770	5	BU357489	BU357489 603407609		
1300	47.2	2.8	556	8	BZ189472	BZ189472 CH230-424	c1373	46.6	2.7	803	9	CR239221	CR239221 Reverse s		
1301	47.2	2.8	558	4	BG472850	BG472850 602514746	1374	46.6	2.7	810	6	CB988910	CB988910 AGENCOURT		
c1302	47.2	2.8	600	8	AZ023198	AZ023198 RPCI-23-3	1375	46.6	2.7	811	6	CB960243	CB960243 AGENCOURT		
1303	47.2	2.8	626	5	BQ260159	BQ260159 faa08d12.	1376	46.6	2.7	836	7	CO568804	CO568804 AGENCOURT		
c1304	47.2	2.8	667	5	BU433191	BU433191 603257821	1377	46.6	2.7	869	5	BU410108	BU410108 603159722		
1305	47.2	2.8	699	9	AG303017	AG303017 Mus muscu	c1378	46.6	2.7	882	9	CNS03J9E	AL246587 Tetraodon		
c1306	47.2	2.8	742	1	AI990988	AI990988 wu35e02.x	1379	46.6	2.7	905	7	CF110502	CF110502 Shultzomi		
1307	47.2	2.8	777	7	CK363311	CK363311 AGENCOURT	1380	46.6	2.7	960	6	CA981367	CA981367 AGENCOURT		
1308	47.2	2.8	783	5	BU257243	BU257243 603746633	1381	46.6	2.7	997	9	CNS005TE	AL060767 Drosophil		
c1309	47.2	2.8	847	6	CB963034	CB963034 AGENCOURT	1382	46.6	2.7	1058	3	AK080775	AK080775 Mus muscu		
c1310	47.2	2.8	868	9	CNS03VB8	AL262205 Tetraodon	c1383	46.4	2.7	279	2	BB421238	BB421238 BB421238		
1311	47.2	2.8	884	5	BU255735	BU255735 603413064	1384	46.4	2.7	433	5	BU656839	BU656839 cl16g06.z		
1312	47.2	2.8	922	9	AG508565	AG508565 Mus muscu	c1385	46.4	2.7	437	5	BY480106	BY480106 BY480106		
1313	47.2	2.8	975	5	BQ924401	BQ924401 AGENCOURT	1386	46.4	2.7	500	5	BP189941	BP189941 BP189941		
1314	47.2	2.8	975	9	AG384673	AG384673 Mus muscu	c1387	46.4	2.7	506	1	AI527458	AI527458 uj51h08.x		
1315	47.2	2.8	1503	9	AG321427	AG321427 Mus muscu	1388	46.4	2.7	537	5	BM967715	BM967715 LM24HW011		
1316	47.2	2.8	1770	3	CR720949	CR720949 Tetraodon	1389	46.4	2.7	554	5	BM968022	BM968022 LM24HW007		
1317	47	2.8	441	1	AI386261	AI386261 mm45g07.y	1390	46.4	2.7	562	6	CB449252	CB449252 703437 MA		
c1318	47	2.8	460	2	BB832437	BB832437 BB832437	1391	46.4	2.7	578	7	CF762512	CF762512 CES007624		
c1319	47	2.8	465	8	AZ985283	AZ985283 2M0267P03	1392	46.4	2.7	586	5	BP161132	BP161132 BP161132		
c1320	47	2.8	528	1	AI098043	AI098043 ue31g12.x	1393	46.4	2.7	596	8	AZ251706	AZ251706 RPCI-23-6		
1321	47	2.8	531	5	BX515185	BX515185 BX515185	c1394	46.4	2.7	617	9	CE811089	CE811089 tigr-gss-		
1322	47	2.8	561	2	BE237415	BE237415 146701 MA	c1395	46.4	2.7	632	8	BZ131938	BZ131938 CH230-299		
1323	47	2.8	657	4	BG872756	BG872756 602793857	c1396	46.4	2.7	669	1	AI925646	AI925646 wo32d07.x		
1324	47	2.8	701	9	AG350456	AG350456 Mus muscu	1397	46.4	2.7	682	7	CN792532	CN792532 4127406 B		
1325	47	2.8	713	7	CO046741	CO046741 Lr_LC1CF_	1398	46.4	2.7	699	1	AV611785	AV611785 AV611785		
1326	47	2.8	752	4	BG870967	BG870967 602792001	c1399	46.4	2.7	710	9	AG318888	AG318888 Mus muscu		
1327	47	2.8	763	9	AG535402	AG535402 Mus muscu	1400	46.4	2.7	730	7	CN786329	CN786329 4120309 B		
1328	47	2.8	784	6	CD648176	CD648176 AUF_102_A	1401	46.4	2.7	747	7	CF596089	CF596089 AGENCOURT		
1329	47	2.8	879	7	CK425034	CK425034 AUF_1pSto	1402	46.4	2.7	766	5	BP458170	BP458170 BP458170		
c1330	47	2.8	940	9	CNS03PNX	AL254886 Tetraodon	1403	46.4	2.7	804	9	CR138930	CR138930 Forward s		
c1331	46.8	2.8	275	8	AZ713959	AZ713959 RPCI-24-1	c1404	46.4	2.7	818	8	BZ183183	BZ183183 CH230-340		
c1332	46.8	2.8	398	4	BM602449	BM602449 170006870	1405	46.4	2.7	872	9	CC914163	CC914163 t081k04ba		
c1333	46.8	2.8	482	8	AQ926340	AQ926340 RPCI-23-3	1406	46.4	2.7	1046	4	BG865151	BG865151 602784118		
c1334	46.8	2.8	568	8	BZ132036	BZ132036 CH230-440	1407	46.4	2.7	1104	8	CC287442	CC287442 CH261-64E		
c1335	46.8	2.8	606	8	AQ997822	AQ997822 RPCI-23-3	c1408	46.2	2.7	128	4	BJ683645	BJ683645 BJ683645		
1336	46.8	2.8	619	6	CA846758	CA846758 hab86e09.	c1409	46.2	2.7	160	5	BW044927	BW044927 BW044927		
1337	46.8	2.8	673	5	BU115364	BU115364 603140150	c1410	46.2	2.7	362	6	C14690	C14690 C14690 Clon		
1338	46.8	2.8	703	5	BU121553	BU121553 603146731	1411	46.2	2.7	500	5	BP189387	BP189387 BP189387		

1412	46.2	2.7	582	5	BP331406	BP331406 BP331406
1413	46.2	2.7	663	2	BB621439	BB621439 BB621439
c1414	46.2	2.7	667	7	CV298568	CV298568 EST887027
1415	46.2	2.7	704	4	BG866426	BG866426 602785363
1416	46.2	2.7	735	9	AG422217	AG422217 Mus muscu
1417	46.2	2.7	746	4	BI223232	BI223232 602941237
1418	46.2	2.7	748	5	BU255472	BU255472 603747240
c1419	46.2	2.7	894	9	AG572129	AG572129 Mus muscu
c1420	46.2	2.7	959	9	AG522977	AG522977 Mus muscu
1421	46.2	2.7	1014	9	CNS03PSF	AL255048 Tetraodon
c1422	46.2	2.7	1021	9	AG516610	AG516610 Mus muscu
c1423	46.2	2.7	1246	9	AG324332	AG324332 Mus muscu
c1424	46.2	2.7	2069	2	BF572280	BF572280 602077721
c1425	46	2.7	142	7	CK884076	CK884076 SGP147934
c1426	46	2.7	174	7	CN280882	CN280882 170004177
c1427	46	2.7	298	9	BX995627	BX995627 Forward s
c1428	46	2.7	512	1	AI526889	AI526889 uj47f05.x
1429	46	2.7	534	9	AB039978	AB039978 Mus muscu
1430	46	2.7	544	8	AZ162198	AZ162198 SP_0071_B
c1431	46	2.7	604	8	AZ710946	AZ710946 RPCI-24-1
1432	46	2.7	663	1	AA638622	AA638622 vo55e01.r
1433	46	2.7	692	2	BF536890	BF536890 602048478
1434	46	2.7	703	4	BM726880	BM726880 UI-E-EJ0-
1435	46	2.7	704	8	BH961475	BH961475 odd50h08.
1436	46	2.7	722	9	AG357477	AG357477 Mus muscu
1437	46	2.7	730	9	CE817789	CE817789 tigr-gss-
1438	46	2.7	894	8	BZ148043	BZ148043 CH230-406
1439	46	2.7	910	9	CC707308	CC707308 OGLAH17TV
1440	46	2.7	911	2	BF538809	BF538809 602050742
1441	46	2.7	923	2	BF299858	BF299858 602030487
1442	46	2.7	934	7	CK425585	CK425585 AUF_IpTes
1443	46	2.7	946	2	BF540329	BF540329 602052385
c1444	46	2.7	1135	7	CR754147	CR754147 CR754147
1445	46	2.7	1218	3	CR699567	CR699567 Tetraodon
c1446	45.8	2.7	145	7	CO910044	CO910044 BJ02056C0
1447	45.8	2.7	320	6	CB267906	CB267906 1006812 H
c1448	45.8	2.7	387	8	AZ161894	AZ161894 SP_0070_B
c1449	45.8	2.7	447	2	BB786270	BB786270 BB786270
c1450	45.8	2.7	459	8	AQ861740	AQ861740 nbeb0017B
1451	45.8	2.7	461	8	AZ118568	AZ118568 RPCI-23-1
c1452	45.8	2.7	511	9	BX218237	BX218237 Danio rer
c1453	45.8	2.7	544	2	BF084742	BF084742 MR1-CT052
c1454	45.8	2.7	557	5	BU287130	BU287130 603608187
1455	45.8	2.7	583	5	BP331299	BP331299 BP331299
c1456	45.8	2.7	629	8	AZ944663	AZ944663 2M0205J14
c1457	45.8	2.7	650	6	CA757151	CA757151 BR0500060
c1458	45.8	2.7	666	5	BW115329	BW115329 BW115329
c1459	45.8	2.7	668	7	CF767403	CF767403 CES000274
1460	45.8	2.7	715	5	BU664182	BU664182 cl112e12.
1461	45.8	2.7	741	9	AG427817	AG427817 Mus muscu
c1462	45.8	2.7	763	9	CL987558	CL987558 ZMMBHe000
1463	45.8	2.7	769	4	BG869043	BG869043 602784676
c1464	45.8	2.7	780	6	CA306266	CA306266 UI-H-FT1-
1465	45.8	2.7	792	9	AG468790	AG468790 Mus muscu
1466	45.8	2.7	816	2	BF300168	BF300168 602032064
1467	45.8	2.7	825	2	BE743808	BE743808 601577704
1468	45.8	2.7	826	9	AG528711	AG528711 Mus muscu
c1469	45.8	2.7	832	9	BX137889	BX137889 Danio rer
1470	45.8	2.7	909	9	CNS02OR3	AL207048 Tetraodon
1471	45.8	2.7	987	9	CNS00418	AL066537 Drosophil
1472	45.8	2.7	1087	7	CK208928	CK208928 FGAS02065
1473	45.8	2.7	1474	3	BC035424	BC035424 Homo sapi
1474	45.6	2.7	327	8	AZ414695	AZ414695 1M0189A13
1475	45.6	2.7	349	9	CG726130	CG726130 1119088E0
c1476	45.6	2.7	359	6	C14374	C14374 C14374 Clon
1477	45.6	2.7	467	6	CD612730	CD612730 56062127H
1478	45.6	2.7	490	5	BY365634	BY365634 BY365634
c1479	45.6	2.7	493	9	CR240971	CR240971 Forward s
c1480	45.6	2.7	503	7	CF763896	CF763896 CES004929
c1481	45.6	2.7	579	5	BU778825	BU778825 SJEEHD05
1482	45.6	2.7	581	5	BU664206	BU664206 cl113a01.
c1483	45.6	2.7	586	4	BM381313	BM381313 MEST533-A
1484	45.6	2.7	601	5	BU661944	BU661944 cl79a02.z
1485	45.6	2.7	636	6	CB504678	CB504678 ssalplnb5
c1486	45.6	2.7	678	8	BH034209	BH034209 RPCI-24-3
1487	45.6	2.7	708	6	CA353636	CA353636 625182 NC
c1488	45.6	2.7	714	8	AZ963041	AZ963041 2M0232N05
1489	45.6	2.7	745	4	BG869548	BG869548 602789568
1490	45.6	2.7	755	5	BU374378	BU374378 603807806
1491	45.6	2.7	780	9	AG418613	AG418613 Mus muscu
1492	45.6	2.7	784	4	BI327697	BI327697 602979818
c1493	45.6	2.7	795	6	CA747833	CA747833 GAP26B03
1494	45.6	2.7	828	7	CR409982	CR409982 CR409982
1495	45.6	2.7	832	9	AG423255	AG423255 Mus muscu
1496	45.6	2.7	834	7	CR566088	CR566088 CR566088
1497	45.6	2.7	853	2	BF533432	BF533432 602074108
1498	45.6	2.7	1098	8	CC277132	CC277132 CH261-134
1499	45.4	2.7	154	7	CV028700	CV028700 7287 Full
c1500	45.4	2.7	282	2	BB007416	BB007416 BB007416

ALIGNMENTS

RESULT 1
BM545283
LOCUS BM545283 1096 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6497317 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726996 5', mRNA sequence.
ACCESSION BM545283
VERSION BM545283.1 GI:18777237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1096)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12720 row: f column: 21
High quality sequence stop: 726.
FEATURES Location/Qualifiers
source 1. .1096
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5726996"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
ORIGIN

Query Match 54.9%; Score 933.6; DB 4; Length 1096;
Best Local Similarity 97.7%; Pred. No. 2.1e-257;
Matches 999; Conservative 0; Mismatches 17; Indels 7; Gaps 5;

Qy 1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60

```
Db        74 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 133

Qy        61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       134 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 193

Qy       121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       194 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 253

Qy       181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       254 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 313

Qy       241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       314 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 373

Qy       301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       374 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 433

Qy       361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       434 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 493

Qy       421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       494 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 553

Qy       481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       554 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 613

Qy       541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       614 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 673

Qy       601 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       674 CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACA 733

Qy       661 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       734 TTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCT 793

Qy       721 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG 780
             |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db       794 GCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAAATGAGGGGGGTGAGACTAAG 853

Qy       781 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       854 AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAG 913

Qy       841 ACCTCAGTG-CCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCT-GGGGCAGTACT 898
             ||||||||| |||||||||| ||  |||||||||||||||||||||| ||||||||||||
Db       914 ACCTCAGTGCCCTCCCTTCANCCCTAGAGAGCTGCTCCCCAAACAGCTGGGGGCAGTACT 973

Qy       899 TCCGC---TACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAG 955
             |||||    |    | ||||||||||||||||||||||||||||||||||||||  ||
Db       974 TCCGCCTACAATGGGNNTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGGAAG 1033

Qy       956 -TTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGG-AAAAGCTTCAGGGGACATT 1013
              |||||||||||||||||||| ||  |||||||||||||| ||||||||||||||||||||
Db      1034 NTTTTTTATAGAAGGTCCCAGAATTTCATGGAACAGCTGGNAAAAGCTTCAGGGGACATT 1093

Qy      1014 GTT 1016
             |||
Db      1094 GTT 1096
```

RESULT 2
BU194155

```
LOCUS       BU194155                 895 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7932682 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157196
            5', mRNA sequence.
ACCESSION   BU194155
VERSION     BU194155.1  GI:22708139
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13502  row: k  column: 21
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6157196"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN
```

```
  Query Match            48.7%;  Score 828.4;  DB 5;  Length 895;
  Best Local Similarity  97.8%;  Pred. No. 4.3e-227;
  Matches  850;  Conservative    0;  Mismatches   17;  Indels    2;  Gaps    1;

Qy         18 TAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGAT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 TAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGAT 71

Qy         78 ACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAG 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 ACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAG 131

Qy        138 AGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 AGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCACTCCTCCC 191

Qy        198 TCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCC 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCC 251

Qy        258 TTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGC 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 TTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGC 311

Qy        318 AGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTC 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTC 371

Qy        378 TTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGAC 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 TTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGAC 431

Qy        438 ATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCC 497
```

```
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCC 491

Qy        498 TTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCT 557
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 TTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCT 551

Qy        558 GGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGG 617
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGG 611

Qy        618 ATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACAT 677
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACAT 671

Qy        678 TGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGG 737
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGG 731

Qy        738 CCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACA 797
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 CCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACA 791

Qy        798 CATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACC--TCAGTGCCTCCC 855
                  ||||||||||||||||||||||||||||||    ||||||  |||||||        ||  |||
Db        792 CATTCTGAGTCACTTGCATGAAGTCAGGGCATAAGATCCGAAGACCCTCAGTGGCTCCCC 851

Qy        856 TTCAACCTAAGAGAGCTGCTCCCCAAACA 884
                  | ||  ||||||||||||||||||  || |
Db        852 TCCACCCTAAGAGAGCTGCTCCCNCAAAA 880
```

RESULT 3
BI756209

```
LOCUS       BI756209                844 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603024235F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194737 5',
            mRNA sequence.
ACCESSION   BI756209
VERSION     BI756209.1  GI:15747787
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 844)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11487  row: e  column: 10
            High quality sequence stop: 823.
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5194737"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
ORIGIN
```

```
  Query Match           47.5%;  Score 808.4;  DB 4;  Length 844;
  Best Local Similarity  99.6%;  Pred. No. 2.5e-221;
  Matches  831;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy         50 TTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCC 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 TTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCC 70

Qy        110 ACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCG 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCG 130

Qy        170 CTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAG 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAG 190

Qy        230 TCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCC 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 TCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCC 250

Qy        290 TGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCC 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCC 310

Qy        350 CACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGC 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGC 370

Qy        410 CCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCC 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 CCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCC 430

Qy        470 ACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGC 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 ACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGC 490

Qy        530 AACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCC 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 AACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCC 550

Qy        590 AGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACA 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 AGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACA 610

Qy        650 GTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCT 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCT 670

Qy        710 TGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGG 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 TGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGG 730

Qy        770 GTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATA 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 GTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATA 790

Qy        830 AAGATCAG-AAGACCTCAG-TGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAA 881
              ||||||||  ||||||||||  ||  ||||||||||||||||||||||||||||||
Db        791 AAGATCAGAAAGACCTCAGTTGTCTCCCTTCAACCTAAGAGAGCTGCTCCCCAA 844
```

RESULT 4
BI820831

```
LOCUS       BI820831                821 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603034045F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175251 5',
            mRNA sequence.
ACCESSION   BI820831
VERSION     BI820831.1  GI:15932381
```

```
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11436  row: i  column: 12
            High quality sequence start: 3
            High quality sequence stop: 815.
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175251"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             47.0%;  Score 800;  DB 4;  Length 821;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-219;
  Matches  800;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACA 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACA 60

Qy         91 CCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACT 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACT 120

Qy        151 CACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCT 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCT 180

Qy        211 GCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACT 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACT 240

Qy        271 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 300

Qy        331 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 360

Qy        391 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 420

Qy        451 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 480

Qy        511 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 540

Qy        571 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 600

Qy        631 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 660

Qy        691 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 720

Qy        751 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 780

Qy        811 TTGCATGAAGTCAGGCATAA 830
              ||||||||||||||||||||
Db        781 TTGCATGAAGTCAGGCATAA 800


RESULT 5
AI800075/c
LOCUS       AI800075                821 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wc15c05.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2315240 3'
            similar to TR:O43331 O43331 CARBONIC ANHYDRASE ;, mRNA sequence.
ACCESSION   AI800075
VERSION     AI800075.1  GI:5365547
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 575   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2315240"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
```

this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 42.9%; Score 729.8; DB 1; Length 821;
Best Local Similarity 96.6%; Pred. No. 1.2e-198;
Matches 764; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

```
Qy        899 TCCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTT 958
              ||||||||||||||||||||||||||||||| |||||||||||||||||||      ||
Db        796 TCCGCTACAATGGCTCGCTCACAACTCCCCCTGGCTACCAGAGTGTGCTCTG--ACAGTT 739

Qy        959 TTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCT 1018
              | ||||| | ||||||||||||||||||        | |||||||||| | ||||||||||
Db        738 TNTATAGGAAGTCCCAGATTTCAATGGA--CAGCTGNAAAGCTTCAGNGNACATTGTTCT 681

Qy       1019 CCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCA 1078
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        680 CCACAGAAGAGGAGCCTTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCA 621

Qy       1079 ATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAA 1138
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        620 ATCAGCGCATGGTCTNTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAA 561

Qy       1139 TGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATT 1198
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 TGCTGAATCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATT 501

Qy       1199 TCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCT 1258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 TCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCT 441

Qy       1259 CAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTT 1318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTT 381

Qy       1319 CCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGT 1378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGT 321

Qy       1379 AGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAG 1438
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        320 AGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCCTAGAGAGGAATGGACCCAG 261

Qy       1439 GCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATG 1498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATG 201

Qy       1499 AGGAAATCGCTGTGTTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTTG 1558
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        200 AGGAAATCGCTGTGTTGTTGTTAATGCAGAGAACAAACTCTGTTTAGTTGCAGGGGAAGTTTG 141

Qy       1559 GGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGC 1618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GGATATACCCCAAAGTCCTCTACCCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGC 81

Qy       1619 GGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATT 1678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          80 GGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATA 21

Qy       1679 TGGAAATTAAA 1689
              |||||||||||
Db          20 AGGAAATTAAA 10
```

RESULT 6
BQ070550
LOCUS BQ070550 1080 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6839259 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922948 5', mRNA sequence.
ACCESSION BQ070550
VERSION BQ070550.1 GI:19899596
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1080)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2090 row: k column: 13
High quality sequence stop: 543.
FEATURES Location/Qualifiers
source 1. .1080
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5922948"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 42.8%; Score 728; DB 5; Length 1080;
Best Local Similarity 96.0%; Pred. No. 4.4e-198;
Matches 790; Conservative 0; Mismatches 26; Indels 7; Gaps 4;

```
Qy        223 CCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCC 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCC 60

Qy        283 GCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTAT 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTAT 120

Qy        343 GAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCC 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCC 180

Qy        403 CAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTG 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTG 240

Qy        463 CAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCAC 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCAC 300

Qy        523 ACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTA 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTA 360

Qy        583 GCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAG 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAG 420
```

```
Qy        643 ATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTAT 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTAT 480

Qy        703 GACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATT 762
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        481 GACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGNGCATCCTAATT 540

Qy        763 GAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTC 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTC 600

Qy        823 AGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAA 882
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 AGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCCAA 660

Qy        883 CAGCTGGGGCAGTACTT-CCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAG 941
              |||||||||||||||| ||||||| ||||||||||||||||||||||||||||||| ||
Db        661 CAGCTGGGGCAGTACTTCCCGCTACCATGGCTCGCTCACAACTCCCCCTTGCTACCAAAG 720

Qy        942 TGTGCTCTGGACAG--TTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGC--TGGAAA 997
              | ||||||||||  |||||     |||||||| ||||  |||||| |||   |||||
Db        721 GGGGCTCTGGACAGGTTTTTTATAGAAAGGTCCCACATTTTCATGGAAAAGCCTGGGAAA 780

Qy        998 AGCTTCAGGGG--ACATTGTTCTCCACAGAAGAGGAGCCCTCT 1038
              | ||| |||||  |  |||||||| ||||||| |   || ||
Db        781 ACCTTTAGGGGGAAATTTGTTCTCCCCAGAAGAAGGAACCCCT 823
```

RESULT 7
CD652789
LOCUS CD652789 844 bp mRNA linear EST 18-JUN-2003
DEFINITION AGENCOURT_14555137 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30426363 5', mRNA sequence.
ACCESSION CD652789
VERSION CD652789.1 GI:31890451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 844)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c lone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM512 row: b column: 04
High quality sequence stop: 567.
FEATURES Location/Qualifiers
source 1. .844
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30426363"
/tissue_type="Embryonic Stem cells"
/cell_line="WA01"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"
/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01 cell line . Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, Wi, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIzol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Query Match 42.8%; Score 727.8; DB 6; Length 844;
Best Local Similarity 96.6%; Pred. No. 4.6e-198;
Matches 760; Conservative 0; Mismatches 25; Indels 2; Gaps 2;

```
Qy         22 GAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCC 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATGATACCC 71

Qy         82 TACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGAT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 TACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGAT 131

Qy        142 AAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 AAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCC 191

Qy        202 TCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCC 251

Qy        262 TGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGAT 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 TGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGAT 311

Qy        322 GGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTAC 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTAC 371

Qy        382 CCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTT 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTT 431

Qy        442 GACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTG 491

Qy        502 GACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGT 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGT 551

Qy        562 GGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        552 GGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCC 611

Qy        622 CCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTA 681
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 CCANGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTA 671

Qy        682 CATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTG 741
              |||||||||||||||||||||||||||||||||||||||||||||    | ||||||| |||
Db        672 CATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGANGAGGCTCAGGGNCTG 731

Qy        742 GCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATT 801
              |    ||| ||   ||| ||||||||| | ||        |||||||||| | |||||||
Db        732 GNCTGTCTGNGCNATCTANNTGAGGTGGG-GTGAGACTAGATATAGCTTA-GGACACATT 789

Qy        802 CTGAGTC 808
              |||||||
Db        790 CTGAGTC 796
```

```
RESULT 8
BI819281
LOCUS       BI819281                735 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603037722F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178773 5',
            mRNA sequence.
ACCESSION   BI819281
VERSION     BI819281.1  GI:15930831
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11445  row: 1  column: 06
            High quality sequence stop: 691.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5178773"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN
```

```
  Query Match             42.6%;  Score 724.4;  DB 4;  Length 735;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-197;
  Matches  728;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         59 GGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACA 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACA 60

Qy        119 GAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTC 120

Qy        179 TCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAAT 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAAT 180

Qy        239 TCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGG 240

Qy        299 TGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTC 358
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 TGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGCGCCCACATGGTC 300

Qy        359 AGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATA 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATA 360

Qy        419 TTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATG 478
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        361 TTCAGACAGACAGTGTGACATTTGACCCTGATTAGCCTGCTCTGCAGCCCCACGGATATG 420

Qy        479 ACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTC 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTC 480

Qy        539 TGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACC 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACC 540

Qy        599 TGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCA 600

Qy        659 CATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGG 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGG 660

Qy        719 CTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTA 778
              ||||||||| ||||||||||||||||||||||||||||||||| || ||||||||||||
Db        661 CTGCTGAGAAGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATAGAAGTGGGTGAGACTA 720

Qy        779 AGAATATAGCTTAT 792
              |||||||| |||||
Db        721 AGAATATAACTTAT 734
```

```
RESULT 9
BM544660
LOCUS       BM544660                1096 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6494521 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727369
            5', mRNA sequence.
ACCESSION   BM544660
VERSION     BM544660.1  GI:18776090
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1096)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12721 row: f column: 10
High quality sequence start: 67
High quality sequence stop: 617.

FEATURES Location/Qualifiers
source 1. .1096
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5727369"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

ORIGIN

Query Match 40.7%; Score 691.6; DB 4; Length 1096;
Best Local Similarity 96.2%; Pred. No. 1.4e-187;
Matches 752; Conservative 0; Mismatches 24; Indels 6; Gaps 4;

```
Qy          1 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGG 147

Qy         61 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 ATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGA 207

Qy        121 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC 267

Qy        181 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 TCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTC 327

Qy        241 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 CCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG 387

Qy        301 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 ATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAG 447

Qy        361 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 GACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATT 507

Qy        421 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 CAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGAC 567

Qy        481 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTG 627

Qy        541 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        628 CCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCCCCTG 687

Qy        601 CACTG-GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACCACAGATCAACAGTGAAGCCAC 659
              ||||| |||||||||| |||||||||||||||||||| ||||||  ||||||||||||||
Db        688 CACTGAGGGTCAGAAAAGATCCCCAGGGGGGTCAGAACCCCAGATTCACAGTGAAGCCAC 747

Qy        660 ATTTGCAGAGCTCCACATTGTACATTATGACT-CTGATTCCTATGACAGC-TTGAGTGAG 717
              |||||||||||||||||||||||||||||| | |||| |||||||||| | |||||||||
Db        748 ATTTGCAGAGCTCCACATTGTACATTATGAATCCTGAATCCTATGACAACTTTGAGTGAG 807

Qy        718 GCTGCTGAGAGGCCTCAGGGCCTGG---CTGTCCTGGGCATCCTAATTGAGGTGGGTGAG 774
              |||||||| ||||||||||||| |       | ||||||||||||   | |||   |
Db        808 GCTGCTGACAGGCCTCAGGGCCCTGGCTGGTCCTGGGGCATCCTAATTTGAGGGGGGTGG 867

Qy        775 AC 776
              ||
Db        868 AC 869
```

RESULT 10
CB154932
LOCUS CB154932 668 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0213019 B2N807043 Homo sapiens cDNA clone B2N807043-30-F03 5', mRNA sequence.
ACCESSION CB154932
VERSION CB154932.1 GI:28140033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 668)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 30 row: F column: 03
High quality sequence stop: 668.

FEATURES Location/Qualifiers
source 1. .668
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B2N807043-30-F03"
/sex="M"
/lab_host="Top10F'"
/clone_lib="B2N807043"
/note="Organ: Brain; Vector: pCNS-D2; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 39.1%; Score 664.8; DB 6; Length 668;
Best Local Similarity 99.7%; Pred. No. 6.4e-180;
Matches 666; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         48 ATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGC 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTTGTCCTGGGGATCCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGC 60
```

```
Qy        108 CCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCT 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCT 120

Qy        168 CGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCT 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGCTCTCTCTCTCTCTCTCTCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCT 180

Qy        228 AGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCT 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCTCAAATTCCCAGTCCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCT 240

Qy        288 CCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGG 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGG 300

Qy        348 CCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTC 407
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        301 CCCACATGGTCAGGACCATTGGCCAGCCTCTCACCCTGAGTGTGGAAACAATGCCCAGTC 360

Qy        408 GCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCC 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCC 420

Qy        468 CCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGT 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGT 480

Qy        528 GCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGC 587
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGC 540

Qy        588 CCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAA 647
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAA 600

Qy        648 CAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAG 707
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAG 660

Qy        708 CTTGAGTG 715
              ||||| ||
Db        661 CTTGATTG 668
```

RESULT 11
CV030245

```
LOCUS       CV030245                643 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  9296 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC034412, mRNA sequence.
ACCESSION   CV030245
VERSION     CV030245.1  GI:51488482
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGTTGTTCTCCGCCCTC
            BACKWARD: TATGCCTCAGTCGTGGCTT
            Insert Length: 643   Std Error: 63.00
            Plate: 11055  row: 10  column: H
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 104
            High quality sequence stop: 642
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .643
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="mixed"
                      /clone_lib="Full Length cDNA from the Mammalian Gene
                      Collection"
                      /note="Vector: mixed; The ORFs were PCR amplified from the
                      MGC (Mammalian Gene Collection) as of April 2004 and
                      cloned by recombinational Gateway cloning into pDONR223
                      Donor vector. Reference : MGC (Mammalian Gene Collection)
                      Program Team, Generation and Initial Analysis of more than
                      15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                      2002, 99(26), 16899-16903"
ORIGIN
```

Query Match 37.5%; Score 638.2; DB 7; Length 643;
Best Local Similarity 99.5%; Pred. No. 3e-172;
Matches 640; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        271 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAA 60

Qy        331 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT 120

Qy        391 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT 180

Qy        451 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCAC 240

Qy        511 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCC 300

Qy        571 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG 360

Qy        631 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGAC 420

Qy        691 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTG 480

Qy        751 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCAC 540

Qy        811 TTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAG 870
              |||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Db        541 TTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCCTTCACCTAAGAGAG 600
```

```
Qy        871 CTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCT 913
              |||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCT 643


RESULT 12
CR455585
LOCUS       CR455585                755 bp    mRNA    linear   EST 02-JUL-2004
DEFINITION  CR455585 Normalized and Subtracted bovine embryonic and
            extraembryonic tissues (bcaz) Bos taurus cDNA clone bcaz0014e.p.10
            5', mRNA sequence.
ACCESSION   CR455585
VERSION     CR455585.1  GI:49623974
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Renard,J.P., Lewin,H.A., Yang,J., Hernandez,A., Degrelle,S.,
            Everts,R.E. and Hue,I.
  TITLE     Embryonic ESTs (bcaz)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Renard JP
            Biologie du Developpement et Reproduction
            INRA
            Domaine de Vilvert 78350 Jouy en Josas, FRANCE
            Email: renard@jouy.inra.fr
            Funding for EST sequencing was provided by a Genanimal contract
            from FNS- Ministere de la Recherche (INRA, Num: A02085). Funding
            for construction and subtraction of the cDNA library was provided
            by USDA ARS contract No. 58-1275- 2-020 to H. A. Lewin
            The cDNA library was constructed, normalized and subtracted by Dr.
            A. Hernandez (W.M. Keck Center, University of Illinois
            Urbana-Champaign) and S. Degrelle (BDR, Inra) as described in
            Bonaldo et al.(1996), Genome Research 6, 791-806. BE04 library is a
            normalized library of embryonic tissues subtracted with 7800 known
            EST sequences. The double- stranded cDNA was size selected (>450
            bp), adaptored with EcoRI adaptors at both ends and digested with
            NotI. The cDNA was then directionally cloned into EcoRI-NotI
            digested pGEM11Zf(+) phagemid vector. Insert size was between 450-
            2200 bp. Sequence cleaned of vector, adaptator and repetitions.
            Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram
            of this sequence.
FEATURES              Location/Qualifiers
     source           1. .755
                      /organism="Bos taurus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /clone="bcaz0014e.p.10"
                      /tissue_type="embryo (day 36 and day 64), extra-embryonic
                      tissue (day 14 to 25)"
                      /lab_host="DH10B"
                      /clone_lib="Normalized and Subtracted bovine embryonic and
                      extraembryonic tissues (bcaz)"
                      /note="Vector: pGEMZf11; Tagged oligo-dT was used to
                      identify the origin of the ESTs where possible. (A18)TGCGT
                      = extraembryonic tissue; (A18)TCGGT = 36-day oldfetus;
                      (A18)TGCGA = 64-day old fetus (organs); (A18)TCGGA =
                      64-day old fetus (body)"
ORIGIN

  Query Match             36.2%;  Score 615.4;  DB 7;  Length 755;
  Best Local Similarity   89.1%;  Pred. No. 1.2e-165;
  Matches  664;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy        273 GTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACA 332
              |||||||| | |||||||||| |||||||||||||||||| ||||  | ||||||||||
Db         11 GTTGTTCTTCACCCTCCTGCTAGAGGTGATTTGGATCCTGACTGCCAACGGGGGTCAACA 70

Qy        333 CTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGG 392
              ||||||||| ||||| |||||||||||| ||||| ||||| ||||||||||||||| |||||

Db         71 CTGGACGTACGAGGGTCCACATGGTCAAGACCACTGGCCCGCCTCTTACCCTGAATGTGG 130

Qy        393 AAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTT 452
              || |||||||||||| |||||| |||| |||||||||||||||| |||||||||| ||
Db        131 AAGCAATGCCCAGTCCCCCATCAATATCCAGACAGACAGTGTGACTTTTGACCCTGACTT 190

Qy        453 GCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAA 512
              ||   |||||||||||| |||||||| |||||||||| ||||||||| ||||||||||
Db        191 GCTACCTCTGCAGCCCCATGGATATGAACAGCCTGGCACTGAGCCTTTGAACCTGCACAA 250

Qy        513 CAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCG 572
              |||||||||||||| |||||||||||||||||||||||||||||||||  ||||||||||
Db        251 TAATGGCCACACAGTACAACTCTCTCTGCCCTCTACCCTGTATCTGGAAGGACTTCCCCG 310

Qy        573 AAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTC 632
              |||||| |||||||||||||||||||||||||||||||||||||||||||| ||||  |||||||
Db        311 AAAATACGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGAACCCCCTGGGGGTC 370

Qy        633 AGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTC 692
              ||| |||| ||||||| |  |||||||  |||||||||||||||||||||||||| || ||
Db        371 AGAGCACCTGATCAACGGCAAAGCCACAGCTGCAGAGCTCCACATTGTACATTACGATTC 430

Qy        693 TGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGG 752
              ||| ||||| || ||| |||||||||||||| |||||||||||||||||||||| ||||
Db        431 TGAGTCCTACGAAAGCCTGAGTGAGGCTGCTCAGAGGCCTCAGGGCCTGGCTGTCTTGGG 490

Qy        753 CATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTT 812
              |||||| |||||||||||||||||||||  |||||||||||||||||||||||||||||
Db        491 CATCCTCATTGAGGTGGGTGAGACTAAGAATCCAGCTTATGAACACATTCTGAGTCACTT 550

Qy        813 GCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCT 872
              ||||||| ||| | |||||||||||||||||| |||||||||||||| | |||| |||
Db        551 GCATGAAATCAAGTATAAAGATCAGAAGACCTCCATGCCTCCCTTCAACGTGAGAGGGCT 610

Qy        873 GCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCTTG 932
              ||||||    | |||||  |||||||||| |||||||||||||||| ||||| || ||
Db        611 GCTCCCGCTGCTGCTGGCACAGTACTTCCGTTACAATGGCTCGCTCACCACTCCGCCCTG 670

Qy        933 CTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT 992
              |||||||||||||||||||| || ||  || ||||| |||||||||| | |||||||||
Db        671 CTACCAGAGTGTGCTCTGGACTGTCTTCCATCGAAGGGCCCAGATTTCCACGGAACAGCT 730

Qy        993 GGAAAAGCTTCAGGGGACATTGTTC 1017
              |||||||||||  || ||||||||||
Db        731 GGAAAAGCTTCGGGAGACATTGTTC 755


RESULT 13
BU152476
LOCUS       BU152476                897 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_8755667 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6335060
            5', mRNA sequence.
ACCESSION   BU152476
VERSION     BU152476.1  GI:22666008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 897)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
```

```
           Plate: LLAM13796  row: n  column: 21
           High quality sequence stop: 592.
FEATURES             Location/Qualifiers
     source          1. .897
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6335060"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_130"
                     /note="Organ: otocysts; Vector: pCMV-SPORT6.1; Site_1:
                     EcoRV; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT.  Average insert size 1.95  kb.  Constructed by
                     ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            35.9%;  Score 610.2;  DB 5;  Length 897;
  Best Local Similarity  81.9%;  Pred. No. 4e-164;
  Matches  727;  Conservative    0;  Mismatches  159;  Indels    2;  Gaps    2;

Qy        286 CTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAG 345
              |||||| |  |||||| ||||||||||||||||||||||||||||||| ||||||||  |||||
Db          2 CTCCTGTTAAAGGTGACTTGGATCCTGGCTGCAGATGGGGGTCACCACTGGACATATGAA 61

Qy        346 GGCCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAG 405
              |||||||| |||||||||||||||||| ||||||| ||||||||||||  | ||||||||
Db         62 GGCCCACACGGTCAGGACCATTGGCCAACCTCTTATCCTGAGTGTGGAGGCGATGCCCAG 121

Qy        406 TCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAG 465
              || |||||| |||| |||||||||||||||| ||||||||| ||| |||||||| | |||
Db        122 TCCCCCATCAATATCCAGACAGACAGTGTGATATTTGACCCCGATCTGCCTGCTGTACAG 181

Qy        466 CCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACA 525
              ||||| |||||||||||||| ||| || |||||||||||| || ||||| |||||||| |||
Db        182 CCCCATGGATATGACCAGCTTGGGACTGAGCCTTTGGATCTACACAATAATGGCCATACA 241

Qy        526 GTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCT 585
              ||||| || || ||||||| | |||||| | |||||||||||| ||||||||||   |||
Db        242 GTGCAGCTTTCCCTGCCCCCAACCCTGCACCTGGGTGGACTGCCCCGAAAATACACAGCA 301

Qy        586 GCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATC 645
              |||||||||||||||||||||||||||||| ||||||||  | ||| ||||| |||||||||
Db        302 GCCCAGCTCCACCTGCACTGGGGTCAGAGAGGATCCCTCGAGGGATCAGAGCACCAGATC 361

Qy        646 AACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGAC 705
              |||||||||||||    ||| |||||||||| | || || ||||||||  | |||||   |
Db        362 AACAGTGAAGCCACGGCTGCGGAGCTCCACGTGGTTCACTATGACTCCCAGTCCTACAGC 421

Qy        706 AGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGG-CCTGGCTGTCCTGGGCATCCTAATTGA 764
              |||||||||||||| ||| ||| ||| ||||| |||||||||||| |||||||| |||||
Db        422 AGCTTGAGTGAGGCAGCTCAGAAGCCACAGGGCCCTGGCTGTCCTAGGCATCCTCATTGA 481

Qy        765 GGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAG 824
              |||||| |||||| |||||  ||||||||| ||||||||||||   | |||||| | ||
Db        482 GGTGGGCGAGACTGAGAATCCAGCTTATGATCACATTCTGAGTCGTCTACATGAAATAAG 541

Qy        825 GCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACA 884
              | |||||||||||||||| |||||||||||||| | | ||||||||| ||||| ||||
Db        542 ATACAAAGATCAGAAGACCTCTGTGCCTCCCTTCAGCGTGAGAGAGCTGTTCCCCCAACA 601

Qy        885 GCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGT 944
              ||||| ||| | |||||||||||| ||||| |||||||||||||| ||||||||||||||
Db        602 GCTGGAGCAATTCTTCCGCTACAACGGCTCACTCACAACTCCCCCCTGCTACCAGAGTGT 661

Qy        945 GCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAAT-GGAACAGCTGGAAAAGCTTC 1003
              |||||||||||| ||  | |||||| |||||||||||||| || |||| | || ||||| |
Db        662 GCTCTGGACAGTCTTCAACAGAAGGGCCCAGATTTCAATGGGGACAGTTAGAGAAGCTCC 721

Qy       1004 AGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAG 1063
              ||| |||||||| ||| |||||||| || |||||| |||  || |||||||||||| |||
Db        722 AGGAGACATTGTCCTCTACAGAAGAAGACCCCTCTGAGCCCCTTGTACAGAACTACNGAG 781

Qy       1064 CCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGT 1123
              ||  ||||||||| | ||| | |   || ||   |  ||    | | ||||| |   ||
Db        782 TCCCCCAGCCTCTCCAACAGAGGACCATCCTTTGCTTCTTTCATCCAACAGGACCACTGT 841

Qy       1124 ATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCT 1171
              ||||||||||  ||| |||  |        |  ||     ||  ||||||
Db        842 ATACCACAGGAAAAAAGCTTGGGTCCTAAGGGGGGGGATTCCTTGGCT 889


RESULT 14
CB999941
LOCUS       CB999941                747 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  AGENCOURT_13648176 NIH_MGC_186 Homo sapiens cDNA clone
            IMAGE:30324763 5', mRNA sequence.
ACCESSION   CB999941
VERSION     CB999941.1  GI:30294461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM129  row: h  column: 20
            High quality sequence stop: 476.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30324763"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_186"
                     /note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site_1: SfiI
                     (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is
                     oligo-dT primed and directionally cloned. cDNA was
                     prepared from a pooled samples of tissues from Skin,
                     meninges, duramatter, pia matter and choroid plexus.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T). Average
                     insert size 1.47 kb (range 0.50-4.0 kb).  15/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library"
ORIGIN

  Query Match            35.0%;  Score 596;  DB 6;  Length 747;
  Best Local Similarity  98.9%;  Pred. No. 4.7e-160;
  Matches  611;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    1;

Qy        383 CTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTG 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTG 62

Qy        443 ACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGG 122

Qy        503 ACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTG 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        123 ACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTG 182

Qy        563 GACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCC 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCC 242

Qy        623 CAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC 302

Qy        683 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGG 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGG 362

Qy        743 CTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTC 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 CTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTC 422

Qy        803 TGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACC 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACC 482

Qy        863 TAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAA 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAA 542

Qy        923 CTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGA--TTTC 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db        543 CTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGAATTTTC 602

Qy        981 AATGGAACAGCTGGAAAA 998
              ||||||||||   |  ||
Db        603 AATGGAACAGGCTGGGAA 620


RESULT 15
CO566350
LOCUS       CO566350               819 bp    mRNA    linear   EST 19-JUL-2004
DEFINITION  AGENCOURT_28451066 NIH_MGC_247 Rattus norvegicus cDNA clone
            IMAGE:7325412 5', mRNA sequence.
ACCESSION   CO566350
VERSION     CO566350.1  GI:50378946
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
            College of Wisconsin
             cDNA Library Preparation: Open Biosystems
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15395  row: k  column: 10
            High quality sequence start: 13
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .819
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7325412"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_247"
                     /note="Organ: liver; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from testis tissue of 8 wk old
                     animal. Tissues were snap-frozen and kept at -80C before
                     RNA extraction and purification (Tri-reagent method). cDNA
                     was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
                     resulted in an average insert size of 1.6 kb. This primary
                     library is normalized (non-normalized primary library is
                     NIH_MGC_246) and was constructed by Open Biosystems. Note:
                     this is a NIH_MGC library"
ORIGIN

  Query Match             34.8%;  Score 591.6;  DB 7;  Length 819;
  Best Local Similarity   84.8%;  Pred. No. 9.1e-159;
  Matches  675;  Conservative    0;  Mismatches  119;  Indels    2;  Gaps    1;

Qy        355 GGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATC 414
              | |||||||||||||||||||| || ||||| ||||||  ||||||||||||| ||||||
Db         22 GATCAGGACCATTGGCCAGCCTCCTATCCTGAATGTGGAGGCAATGCCCAGTCCCCCATC 81

Qy        415 GATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGA 474
              ||||| |||||||||| |||||| |||||||||| ||| ||||| || ||||||||||||||
Db         82 GATATCCAGACAGACGGTGTGATATTTGACCCCGATCTGCCTACTGTGCAGCCCCACGGA 141

Qy        475 TATGACCAGCCTGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTC 534
              |||||||||| ||| |||||||||||||| || ||||| |||||||| |||||||| |||
Db        142 TATGACCAGCTTGGTACCGAGCCTTTGGATCTACACAATAATGGCCATACAGTGCAGCTC 201

Qy        535 TCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTC 594
              || |||||| | |||||| | || |||||||| ||||| |||||   ||| |||||||||
Db        202 TCCCTGCCCCCAACCCTGCACCTTGGTGGACTGCCCCGGAAATACACAGCAGCCCAGCTC 261

Qy        595 CACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAA 654
              |||||||||||||||||||| ||| ||| |  ||| ||||| ||||||||||||||||||||
Db        262 CACCTGCACTGGGGTCAGAAGGGAACCCTAAAGGGATCAGAGCACCAGATCAACAGTGAA 321

Qy        655 GCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGT 714
              ||||||  |||||||||||||| | || |||||||||| || ||||||| ||||||||||
Db        322 GCCACAGCTGCAGAGCTCCACGTGGTCCATTATGACTCGGAGTCCTATGGCAGCTTGAGT 381

Qy        715 GAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAG 774
              ||||| ||| ||| |||||||||| |||||||||| ||||||||||||||||||||||||
Db        382 GAGGCAGCTCAGAAGCCTCAGGGACTGGCTGTCCTAGGCATCCTAATTGAGGTGGGTGAG 441

Qy        775 ACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGAT 834
              ||| |||||  |||||||| |||||||||||||  |||||||||| ||  | ||||||
Db        442 ACTGAGAATCCAGCTTATGATCACATTCTGAGTCATCTGCATGAAGTAAGATACAAAGAT 501

Qy        835 CAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAG 894
              |||||||||| |||||||||||||  | || ||||| |||||| |||||||| ||||
Db        502 CAGAAGACCTCCGTGCCTCCCTTCAATGTGAGGGAGCTCCTCCCCCAACAGCTGGAGCAG 561

Qy        895 TACTTCCGCTACAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACA 954
              | |||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||
Db        562 TTCTTCCGCTACAATGGCTCGCTCACAACCCCCCCCTGCTACCAGAGTGTGCTCTGGACA 621

Qy        955 GTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTG 1014
              || ||  | ||||| |||||||||||||| |||| | |||||||||||| |||| ||
Db        622 GTGTTCAACAGAAGGGCCCAGATTTCAATGGGACAGTTAGAAAAGCTTCAGGAGACACTG 681

Qy       1015 TTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCT 1074
              | ||| |||||||||| || ||| |||  || ||||| |||||| |||  |  ||||||
Db        682 TCCTCTACAGAAGAGGACCCATCTGAGCCCCTTGTACAAAACTACAGAGTGCCCCAGCCT 741

Qy       1075 CTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGT 1134
              ||||| ||| | |      |||||||||||||||||  |||  | |      ||||||
Db        742 CTCAACCAGAGGAACCATCTTGCTTCTTTCATCCAAGTGGGA--CACTGTATACACAGGA 799

Qy       1135 GAAATGCTGAGTCTAG 1150
```

```
                   || |||||| ||||||
Db         800 GAGATGCTGGGTCTAG 815
```

Search completed: April 30, 2005, 01:53:52
Job time : 5316 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 20:18:15 ; Search time 319 Seconds
(without alignments)
8725.099 Million cell updates/sec

Title: US-10-063-583-73
Perfect score: 1701
Sequence: 1 gagactgcagagggagataa.....aaattaaagtttctgacttt 1701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	522.2	30.7	552	4	US-09-621-976-18060	Sequence 18060, A
2	222.2	13.1	297	4	US-09-313-294A-7148	Sequence 7148, Ap
3	213.6	12.6	1104	1	US-08-276-919-1	Sequence 1, Appli
4	213.6	12.6	1104	1	US-08-776-088-1	Sequence 1, Appli
5	213.6	12.6	1104	3	US-09-325-320-1	Sequence 1, Appli
6	213.6	12.6	1104	3	US-09-585-109-1	Sequence 1, Appli
7	213.6	12.6	1104	5	PCT-US95-09145A-1	Sequence 1, Appli
8	213.6	12.6	2134	1	US-08-776-088-5	Sequence 5, Appli
9	213.6	12.6	2134	5	PCT-US95-09145A-5	Sequence 5, Appli
10	213.6	12.6	2774	4	US-09-949-016-4029	Sequence 4029, Ap
11	213.6	12.6	2775	4	US-09-949-016-172	Sequence 172, App
12	211	12.4	2679	1	US-08-479-328-1	Sequence 1, Appli
13	211	12.4	2679	1	US-08-761-119-1	Sequence 1, Appli
14	211	12.4	2679	2	US-08-668-128B-1	Sequence 1, Appli
15	211	12.4	2679	2	US-08-905-445-1	Sequence 1, Appli
16	211	12.4	2679	3	US-08-959-625-1	Sequence 1, Appli
17	211	12.4	2679	3	US-09-008-466-1	Sequence 1, Appli
18	211	12.4	2679	3	US-08-580-980A-1	Sequence 1, Appli
19	211	12.4	2679	3	US-09-053-453-1	Sequence 1, Appli
20	211	12.4	2679	3	US-08-644-116A-1	Sequence 1, Appli
21	211	12.4	2679	4	US-09-437-858-1	Sequence 1, Appli
22	206	12.1	822	1	US-08-776-088-14	Sequence 14, Appl
23	206	12.1	822	5	PCT-US95-09145A-14	Sequence 14, Appl
24	206	12.1	986	1	US-08-276-919-3	Sequence 3, Appli
25	206	12.1	986	1	US-08-276-919-12	Sequence 12, Appl
26	206	12.1	986	1	US-08-776-088-3	Sequence 3, Appli
27	206	12.1	986	1	US-08-776-088-17	Sequence 17, Appl
28	206	12.1	986	5	PCT-US95-09145A-3	Sequence 3, Appli
29	206	12.1	986	5	PCT-US95-09145A-17	Sequence 17, Appl
30	205.2	12.1	813	1	US-08-276-919-9	Sequence 9, Appli
31	205.2	12.1	813	1	US-08-776-088-12	Sequence 12, Appl
32	205.2	12.1	813	5	PCT-US95-09145A-12	Sequence 12, Appl
33	203	11.9	1190	2	US-08-668-128B-4	Sequence 4, Appli
34	203	11.9	1190	2	US-08-905-445-4	Sequence 4, Appli
35	203	11.9	1190	3	US-08-959-625-4	Sequence 4, Appli
36	203	11.9	1190	3	US-09-008-466-4	Sequence 4, Appli
37	203	11.9	1190	3	US-08-580-980A-4	Sequence 4, Appli
38	203	11.9	1190	3	US-09-053-453-4	Sequence 4, Appli
39	203	11.9	1190	3	US-08-644-116A-4	Sequence 4, Appli
40	203	11.9	1190	4	US-09-437-858-4	Sequence 4, Appli
41	118.4	7.0	1399	3	US-08-335-469-1	Sequence 1, Appli
42	118.4	7.0	1399	4	US-08-260-190-1	Sequence 1, Appli
43	118.4	7.0	1522	2	US-08-481-658B-1	Sequence 1, Appli
44	118.4	7.0	1522	2	US-08-477-504A-1	Sequence 1, Appli
45	118.4	7.0	1522	2	US-08-486-756A-1	Sequence 1, Appli
46	118.4	7.0	1522	2	US-08-485-862B-1	Sequence 1, Appli
47	118.4	7.0	1522	3	US-08-787-739-1	Sequence 1, Appli
48	118.4	7.0	1522	3	US-08-487-077A-1	Sequence 1, Appli
49	118.4	7.0	1522	3	US-08-485-863A-1	Sequence 1, Appli
50	118.4	7.0	1522	3	US-08-485-049D-1	Sequence 1, Appli
51	118.4	7.0	1522	3	US-09-178-115-1	Sequence 1, Appli
52	118.4	7.0	1522	3	US-09-177-776-1	Sequence 1, Appli
53	118.4	7.0	1522	4	US-09-772-719B-1	Sequence 1, Appli
54	118.4	7.0	1522	4	US-08-260-190-5	Sequence 5, Appli
55	118.4	7.0	1552	4	US-09-949-016-171	Sequence 171, App
56	118.4	7.0	1552	4	US-09-949-016-4332	Sequence 4332, Ap
57	117.2	6.9	4338	1	US-08-015-986A-1	Sequence 1, Appli
58	117.2	6.9	4338	2	US-08-446-363-1	Sequence 1, Appli
59	90.8	5.3	1397	1	US-07-964-589-1	Sequence 1, Appli
60	90.8	5.3	1397	5	PCT-US93-02024-1	Sequence 1, Appli
61	90.8	5.3	5052	4	US-08-260-190-23	Sequence 23, Appl
62	82.4	4.8	145	4	US-09-513-999C-36510	Sequence 36510, A
63	66.4	3.9	1428	4	US-09-949-016-728	Sequence 728, App
64	62.8	3.7	61124	4	US-09-949-016-11914	Sequence 11914, A
65	62.8	3.7	61140	4	US-09-949-016-15771	Sequence 15771, A
66	56	3.3	1266	4	US-09-938-270B-2	Sequence 2, Appli
67	56	3.3	2355	4	US-09-949-016-2242	Sequence 2242, Ap
68	55	3.2	7218	1	US-08-232-463-14	Sequence 14, Appl
69	53.8	3.2	6924	1	US-08-015-973-2	Sequence 2, Appli
70	53.8	3.2	6924	2	US-08-448-164-2	Sequence 2, Appli
c 71	53.6	3.2	601	4	US-09-949-016-21248	Sequence 21248, A
c 72	53.6	3.2	601	4	US-09-949-016-142449	Sequence 142449,
73	53.4	3.1	868	4	US-09-949-016-2979	Sequence 2979, Ap
74	52.2	3.1	7941	3	US-09-816-703A-1	Sequence 1, Appli
75	51.8	3.0	112507	4	US-09-949-016-12420	Sequence 12420, A
76	51.8	3.0	112507	4	US-09-949-016-12794	Sequence 12794, A
77	51.8	3.0	112508	4	US-09-949-016-16589	Sequence 16589, A
78	51.8	3.0	112508	4	US-09-949-016-16590	Sequence 16590, A
79	51.4	3.0	408	4	US-09-513-999C-296	Sequence 296, App
80	49	2.9	15621	4	US-09-949-016-16563	Sequence 16563, A
81	49	2.9	15621	4	US-09-949-016-16564	Sequence 16564, A
82	49	2.9	16742	4	US-09-949-016-12782	Sequence 12782, A
83	45.8	2.7	1460	4	US-09-949-016-4541	Sequence 4541, Ap
84	45.8	2.7	1755	4	US-09-566-921-124	Sequence 124, App
85	45.6	2.7	605	1	US-08-469-667-17	Sequence 17, Appl
86	45.6	2.7	605	3	US-09-224-110-17	Sequence 17, Appl
87	45.6	2.7	605	4	US-09-988-292A-17	Sequence 17, Appl
88	45.6	2.7	605	5	PCT-US95-07289-17	Sequence 17, Appl
c 89	44.6	2.6	601	4	US-09-949-016-21252	Sequence 21252, A
c 90	44.6	2.6	601	4	US-09-949-016-142453	Sequence 142453,
c 91	44.6	2.6	109159	4	US-09-949-016-14169	Sequence 14169, A
c 92	44.6	2.6	109159	4	US-09-949-016-14170	Sequence 14170, A
93	44.4	2.6	5840	4	US-09-949-016-5692	Sequence 5692, Ap
94	44.4	2.6	312474	4	US-09-949-016-17434	Sequence 17434, A
95	44.2	2.6	1759	4	US-09-976-594-643	Sequence 643, App
96	44.2	2.6	24139	4	US-09-949-016-14675	Sequence 14675, A
97	44.2	2.6	34414	4	US-09-949-016-12330	Sequence 12330, A
98	44.2	2.6	34414	4	US-09-949-016-16157	Sequence 16157, A
99	44.2	2.6	35256	4	US-09-949-016-11991	Sequence 11991, A
100	44.2	2.6	125188	4	US-09-949-016-11980	Sequence 11980, A

	101	44.2	2.6	199471	4	US-09-949-016-14083	Sequence 14083, A
	102	43.8	2.6	5403	3	US-09-442-143A-3	Sequence 3, Appli
	103	43.8	2.6	5403	4	US-09-902-563-3	Sequence 3, Appli
	104	43.6	2.6	601	4	US-09-949-016-135107	Sequence 135107,
	105	43.4	2.6	61198	4	US-09-949-016-17248	Sequence 17248, A
	106	43.2	2.5	65424	4	US-09-949-016-12426	Sequence 12426, A
c	107	42.8	2.5	18474	4	US-09-949-016-17559	Sequence 17559, A
	108	42.6	2.5	68580	4	US-09-949-016-15844	Sequence 15844, A
	109	42.4	2.5	117807	4	US-09-949-016-15525	Sequence 15525, A
c	110	42.2	2.5	1141	4	US-09-806-708B-22	Sequence 22, Appl
	111	42	2.5	536	4	US-09-621-976-1238	Sequence 1238, Ap
c	112	42	2.5	29927	4	US-09-949-016-11814	Sequence 11814, A
c	113	42	2.5	29927	4	US-09-949-016-17474	Sequence 17474, A
c	114	42	2.5	29927	4	US-09-949-016-17475	Sequence 17475, A
c	115	42	2.5	37802	4	US-09-949-016-12639	Sequence 12639, A
	116	41.8	2.5	1825	4	US-09-799-451-619	Sequence 619, App
	117	41.4	2.4	780	3	US-08-927-128-3	Sequence 3, Appli
	118	41.4	2.4	29172	4	US-09-949-016-15520	Sequence 15520, A
c	119	41.4	2.4	95750	4	US-09-949-016-11926	Sequence 11926, A
	120	41.2	2.4	601	4	US-09-949-016-80756	Sequence 80756, A
	121	41.2	2.4	1455	4	US-09-949-016-5342	Sequence 5342, Ap
	122	41.2	2.4	1512	2	US-08-977-767-2	Sequence 2, Appli
	123	41.2	2.4	14817	4	US-09-949-016-13984	Sequence 13984, A
	124	41.2	2.4	28806	4	US-09-949-016-13217	Sequence 13217, A
	125	41.2	2.4	422592	4	US-09-949-016-14182	Sequence 14182, A
c	126	41	2.4	24214	4	US-09-949-016-15551	Sequence 15551, A
c	127	41	2.4	90618	4	US-09-949-016-15964	Sequence 15964, A
	128	40.8	2.4	158	2	US-08-481-658B-34	Sequence 34, Appl
	129	40.8	2.4	158	2	US-08-477-504A-34	Sequence 34, Appl
	130	40.8	2.4	158	2	US-08-486-756A-34	Sequence 34, Appl
	131	40.8	2.4	158	2	US-08-485-862B-34	Sequence 34, Appl
	132	40.8	2.4	158	3	US-08-787-739-34	Sequence 34, Appl
	133	40.8	2.4	158	3	US-08-487-077A-34	Sequence 34, Appl
	134	40.8	2.4	158	3	US-08-485-863A-34	Sequence 34, Appl
	135	40.8	2.4	158	3	US-08-485-049D-34	Sequence 34, Appl
	136	40.8	2.4	158	3	US-09-178-115-34	Sequence 34, Appl
	137	40.8	2.4	158	3	US-09-177-776-34	Sequence 34, Appl
	138	40.8	2.4	158	4	US-09-772-719B-34	Sequence 34, Appl
	139	40.8	2.4	601	4	US-09-949-016-21239	Sequence 21239, A
	140	40.8	2.4	601	4	US-09-949-016-155019	Sequence 155019,
c	141	40.8	2.4	1124	4	US-09-949-016-2485	Sequence 2485, Ap
	142	40.8	2.4	7301	4	US-09-816-094-3	Sequence 3, Appli
	143	40.8	2.4	7301	4	US-10-233-613-3	Sequence 3, Appli
	144	40.8	2.4	7301	4	US-10-639-429-3	Sequence 3, Appli
	145	40.8	2.4	10898	2	US-08-481-658B-5	Sequence 5, Appli
	146	40.8	2.4	10898	2	US-08-477-504A-5	Sequence 5, Appli
	147	40.8	2.4	10898	2	US-08-486-756A-5	Sequence 5, Appli
	148	40.8	2.4	10898	2	US-08-485-862B-5	Sequence 5, Appli
	149	40.8	2.4	10898	3	US-08-787-739-5	Sequence 5, Appli
	150	40.8	2.4	10898	3	US-08-487-077A-5	Sequence 5, Appli
	151	40.8	2.4	10898	3	US-08-485-863A-5	Sequence 5, Appli
	152	40.8	2.4	10898	3	US-08-485-049D-5	Sequence 5, Appli
	153	40.8	2.4	10898	3	US-09-178-115-5	Sequence 5, Appli
	154	40.8	2.4	10898	3	US-09-177-776-5	Sequence 5, Appli
	155	40.8	2.4	10898	4	US-09-772-719B-5	Sequence 5, Appli
	156	40.8	2.4	11237	4	US-09-949-016-11913	Sequence 11913, A
	157	40.8	2.4	11237	4	US-09-949-016-16074	Sequence 16074, A
c	158	40.6	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	159	40.4	2.4	354	3	US-08-905-223-103	Sequence 103, App
c	160	40.4	2.4	601	4	US-09-949-016-56224	Sequence 56224, A
	161	40.4	2.4	173992	4	US-09-949-016-13379	Sequence 13379, A
c	162	40.2	2.4	7832	3	US-09-004-838-94	Sequence 94, Appl
	163	40.2	2.4	8230	4	US-09-949-016-14183	Sequence 14183, A
c	164	40.2	2.4	25333	4	US-09-949-016-14069	Sequence 14069, A
	165	40.2	2.4	63588	4	US-09-873-404-3	Sequence 3, Appli
	166	40.2	2.4	63588	4	US-10-243-735-3	Sequence 3, Appli
	167	40.2	2.4	390890	4	US-09-949-016-14720	Sequence 14720, A
	168	40.2	2.4	421491	4	US-09-949-016-12805	Sequence 12805, A
	169	40.2	2.4	421494	4	US-09-949-016-14060	Sequence 14060, A
c	170	40	2.4	41737	4	US-09-949-016-12204	Sequence 12204, A
c	171	40	2.4	41741	4	US-09-949-016-16983	Sequence 16983, A
	172	39.8	2.3	181	4	US-09-513-999C-9845	Sequence 9845, Ap
c	173	39.8	2.3	601	4	US-09-949-016-204680	Sequence 204680,
c	174	39.8	2.3	15615	4	US-09-949-016-17221	Sequence 17221, A
	175	39.8	2.3	122626	4	US-09-949-016-17524	Sequence 17524, A
c	176	39.8	2.3	304533	4	US-09-949-016-15371	Sequence 15371, A
c	177	39.8	2.3	304533	4	US-09-949-016-15372	Sequence 15372, A
c	178	39.6	2.3	601	4	US-09-949-016-82626	Sequence 82626, A
	179	39.6	2.3	1657	4	US-09-270-767-9840	Sequence 9840, Ap
c	180	39.6	2.3	55387	4	US-09-949-016-12993	Sequence 12993, A
c	181	39.6	2.3	117807	4	US-09-949-016-15525	Sequence 15525, A
	182	39.6	2.3	121068	4	US-09-949-016-14138	Sequence 14138, A
	183	39.4	2.3	2255	4	US-09-949-016-4177	Sequence 4177, Ap
	184	39.4	2.3	87648	4	US-09-949-016-13655	Sequence 13655, A
	185	39.4	2.3	172677	4	US-09-949-016-13444	Sequence 13444, A
	186	39.4	2.3	177251	4	US-09-949-016-15841	Sequence 15841, A
	187	39.2	2.3	601	4	US-09-949-016-90126	Sequence 90126, A
c	188	39.2	2.3	1377	2	US-08-810-572A-1	Sequence 1, Appli
c	189	39.2	2.3	1377	3	US-09-290-333-1	Sequence 1, Appli
c	190	39.2	2.3	1377	4	US-09-782-857A-1	Sequence 1, Appli
c	191	39.2	2.3	1377	4	US-09-879-919-21	Sequence 21, Appl
	192	39.2	2.3	3981	4	US-09-294-298A-5	Sequence 5, Appli
c	193	39.2	2.3	3981	4	US-09-294-298A-24	Sequence 24, Appl
	194	39.2	2.3	4134	4	US-09-294-298A-3	Sequence 3, Appli
c	195	39.2	2.3	4134	4	US-09-294-298A-23	Sequence 23, Appl
	196	39.2	2.3	4272	4	US-09-294-298A-1	Sequence 1, Appli
c	197	39.2	2.3	4272	4	US-09-294-298A-22	Sequence 22, Appl
	198	39.2	2.3	48974	3	US-08-920-422-17	Sequence 17, Appl
	199	39.2	2.3	455726	4	US-09-949-016-14157	Sequence 14157, A
	200	39.2	2.3	481115	4	US-09-949-016-11940	Sequence 11940, A
	201	39	2.3	601	4	US-09-949-016-58730	Sequence 58730, A
	202	39	2.3	325034	4	US-09-949-016-14957	Sequence 14957, A
	203	39	2.3	389504	4	US-09-949-016-11774	Sequence 11774, A
	204	38.8	2.3	294	4	US-09-513-999C-14469	Sequence 14469, A
	205	38.8	2.3	41041	4	US-09-949-016-15032	Sequence 15032, A
	206	38.8	2.3	54601	4	US-09-949-016-14173	Sequence 14173, A
	207	38.8	2.3	56714	4	US-09-949-016-11960	Sequence 11960, A
c	208	38.8	2.3	392000	4	US-10-027-983-11	Sequence 11, Appl
c	209	38.6	2.3	211	4	US-09-702-705-820	Sequence 820, App
c	210	38.6	2.3	211	4	US-09-736-457-820	Sequence 820, App
c	211	38.6	2.3	211	4	US-09-614-124B-820	Sequence 820, App
c	212	38.6	2.3	211	4	US-09-671-325-820	Sequence 820, App
c	213	38.6	2.3	211	4	US-09-589-184-820	Sequence 820, App
c	214	38.6	2.3	211	4	US-09-658-824-820	Sequence 820, App
	215	38.6	2.3	601	4	US-09-949-016-118178	Sequence 118178,
c	216	38.6	2.3	17922	4	US-09-949-016-15018	Sequence 15018, A
c	217	38.6	2.3	18955	4	US-09-949-016-13343	Sequence 13343, A
c	218	38.6	2.3	30678	4	US-09-949-016-12818	Sequence 12818, A
c	219	38.6	2.3	66428	4	US-09-949-016-12917	Sequence 12917, A
c	220	38.6	2.3	199471	4	US-09-949-016-14083	Sequence 14083, A
c	221	38.6	2.3	271134	4	US-09-949-016-12705	Sequence 12705, A
c	222	38.6	2.3	305491	4	US-09-949-016-17550	Sequence 17550, A
c	223	38.4	2.3	601	4	US-09-949-016-20416	Sequence 20416, A
c	224	38.4	2.3	601	4	US-09-949-016-20417	Sequence 20417, A
	225	38.4	2.3	601	4	US-09-949-016-58731	Sequence 58731, A
c	226	38.4	2.3	601	4	US-09-949-016-149702	Sequence 149702,
c	227	38.4	2.3	601	4	US-09-949-016-149703	Sequence 149703,
	228	38.4	2.3	1298	4	US-09-404-641-69	Sequence 69, Appl
	229	38.4	2.3	1298	4	US-10-414-186-69	Sequence 69, Appl
	230	38.4	2.3	1298	4	US-10-243-072-69	Sequence 69, Appl
	231	38.4	2.3	7208	3	US-09-166-186-107	Sequence 107, App
	232	38.4	2.3	7208	3	US-09-313-932-107	Sequence 107, App
c	233	38.4	2.3	10546	4	US-09-949-016-15624	Sequence 15624, A
c	234	38.4	2.3	23222	4	US-09-949-016-15949	Sequence 15949, A
c	235	38.4	2.3	25922	4	US-09-949-016-11874	Sequence 11874, A
	236	38.4	2.3	49389	4	US-09-949-016-12547	Sequence 12547, A
	237	38.4	2.3	49389	4	US-09-949-016-13630	Sequence 13630, A
	238	38.4	2.3	258775	4	US-09-949-016-16435	Sequence 16435, A
	239	38.2	2.2	54463	4	US-09-949-016-14781	Sequence 14781, A
	240	38.2	2.2	84916	4	US-09-949-016-14736	Sequence 14736, A
c	241	38.2	2.2	88950	4	US-09-949-016-17150	Sequence 17150, A
	242	38.2	2.2	112112	4	US-09-949-016-15639	Sequence 15639, A
	243	38.2	2.2	118136	4	US-09-949-016-12439	Sequence 12439, A
	244	38.2	2.2	134987	4	US-09-949-016-15348	Sequence 15348, A
	245	38.2	2.2	134987	4	US-09-949-016-15349	Sequence 15349, A
	246	38.2	2.2	134987	4	US-09-949-016-15350	Sequence 15350, A

247	38.2	2.2	134987	4	US-09-949-016-15507	Sequence 15507, A
248	38.2	2.2	134987	4	US-09-949-016-15508	Sequence 15508, A
249	38.2	2.2	134987	4	US-09-949-016-15509	Sequence 15509, A
c 250	38.2	2.2	236474	4	US-09-949-016-13418	Sequence 13418, A
251	38.2	2.2	256287	4	US-09-949-016-14608	Sequence 14608, A
c 252	38	2.2	601	4	US-09-949-016-20415	Sequence 20415, A
253	38	2.2	601	4	US-09-949-016-45757	Sequence 45757, A
254	38	2.2	601	4	US-09-949-016-45758	Sequence 45758, A
255	38	2.2	601	4	US-09-949-016-45759	Sequence 45759, A
256	38	2.2	601	4	US-09-949-016-90125	Sequence 90125, A
c 257	38	2.2	601	4	US-09-949-016-115328	Sequence 115328,
c 258	38	2.2	601	4	US-09-949-016-149704	Sequence 149704,
c 259	38	2.2	601	4	US-09-949-016-191370	Sequence 191370,
c 260	38	2.2	601	4	US-09-949-016-198040	Sequence 198040,
c 261	38	2.2	1417	4	US-09-949-016-3944	Sequence 3944, Ap
c 262	38	2.2	1420	4	US-09-949-016-289	Sequence 289, App
c 263	38	2.2	1493	1	US-08-340-820-24	Sequence 24, Appl
c 264	38	2.2	1493	1	US-08-593-535-24	Sequence 24, Appl
265	38	2.2	1763	6	5198542-1	Patent No. 5198542
266	38	2.2	1763	6	5198542-1	Patent No. 5198542
267	38	2.2	2990	3	US-09-009-816-19	Sequence 19, Appl
c 268	38	2.2	26438	4	US-09-949-016-17351	Sequence 17351, A
c 269	38	2.2	34314	4	US-09-949-016-12031	Sequence 12031, A
c 270	38	2.2	34314	4	US-09-949-016-15686	Sequence 15686, A
c 271	38	2.2	42276	4	US-09-949-016-17218	Sequence 17218, A
c 272	38	2.2	45299	4	US-09-949-016-12465	Sequence 12465, A
c 273	38	2.2	45300	4	US-09-949-016-13045	Sequence 13045, A
274	38	2.2	55674	4	US-09-949-016-12563	Sequence 12563, A
275	38	2.2	55675	4	US-09-949-016-15706	Sequence 15706, A
c 276	38	2.2	58844	4	US-09-949-016-13769	Sequence 13769, A
277	38	2.2	112219	4	US-09-949-016-12453	Sequence 12453, A
278	38	2.2	112222	4	US-09-949-016-14324	Sequence 14324, A
279	38	2.2	113186	4	US-09-949-016-17572	Sequence 17572, A
280	38	2.2	119032	4	US-09-949-016-12160	Sequence 12160, A
281	38	2.2	119032	4	US-09-949-016-17268	Sequence 17268, A
c 282	38	2.2	135030	4	US-09-949-016-14896	Sequence 14896, A
c 283	37.8	2.2	421	2	US-08-332-766A-25	Sequence 25, Appl
c 284	37.8	2.2	2397	1	US-07-891-942G-11	Sequence 11, Appl
c 285	37.8	2.2	17056	3	US-09-245-041-3	Sequence 3, Appli
c 286	37.8	2.2	17056	4	US-09-358-055B-3	Sequence 3, Appli
c 287	37.8	2.2	17056	4	US-09-893-238-3	Sequence 3, Appli
288	37.8	2.2	29927	4	US-09-949-016-11814	Sequence 11814, A
289	37.8	2.2	29927	4	US-09-949-016-17474	Sequence 17474, A
290	37.8	2.2	29927	4	US-09-949-016-17475	Sequence 17475, A
291	37.8	2.2	37802	4	US-09-949-016-12639	Sequence 12639, A
c 292	37.8	2.2	37950	3	US-09-338-907-183	Sequence 183, App
c 293	37.8	2.2	37950	3	US-09-218-207-183	Sequence 183, App
294	37.8	2.2	39601	4	US-09-949-016-16045	Sequence 16045, A
295	37.8	2.2	202111	4	US-09-949-016-13877	Sequence 13877, A
296	37.6	2.2	410	4	US-09-220-132-90	Sequence 90, Appl
c 297	37.6	2.2	601	4	US-09-949-016-49990	Sequence 49990, A
c 298	37.6	2.2	601	4	US-09-949-016-165376	Sequence 165376,
c 299	37.6	2.2	28494	4	US-09-949-016-13200	Sequence 13200, A
300	37.6	2.2	34725	4	US-09-949-016-15797	Sequence 15797, A
301	37.6	2.2	34765	4	US-09-949-016-12808	Sequence 12808, A
c 302	37.6	2.2	38575	4	US-09-949-016-17304	Sequence 17304, A
303	37.6	2.2	100463	4	US-09-949-016-12511	Sequence 12511, A
304	37.6	2.2	100468	4	US-09-949-016-13725	Sequence 13725, A
c 305	37.6	2.2	119153	4	US-09-949-016-12378	Sequence 12378, A
c 306	37.4	2.2	435	3	US-09-171-209-44	Sequence 44, Appl
c 307	37.4	2.2	435	4	US-09-509-712B-21	Sequence 21, Appl
c 308	37.4	2.2	2917	2	US-08-437-607A-3	Sequence 3, Appli
309	37.4	2.2	44453	3	US-09-146-053-5	Sequence 5, Appli
c 310	37.2	2.2	436	3	US-09-397-787-257	Sequence 257, App
311	37.2	2.2	601	4	US-09-949-016-96411	Sequence 96411, A
312	37.2	2.2	601	4	US-09-949-016-96677	Sequence 96677, A
313	37.2	2.2	601	4	US-09-949-016-96943	Sequence 96943, A
314	37.2	2.2	601	4	US-09-949-016-97209	Sequence 97209, A
315	37.2	2.2	601	4	US-09-949-016-97475	Sequence 97475, A
316	37.2	2.2	601	4	US-09-949-016-97741	Sequence 97741, A
317	37.2	2.2	601	4	US-09-949-016-98007	Sequence 98007, A
318	37.2	2.2	601	4	US-09-949-016-98273	Sequence 98273, A
319	37.2	2.2	601	4	US-09-949-016-98539	Sequence 98539, A
320	37.2	2.2	601	4	US-09-949-016-98805	Sequence 98805, A
321	37.2	2.2	601	4	US-09-949-016-99071	Sequence 99071, A
322	37.2	2.2	601	4	US-09-949-016-99337	Sequence 99337, A
323	37.2	2.2	601	4	US-09-949-016-99603	Sequence 99603, A
324	37.2	2.2	601	4	US-09-949-016-99869	Sequence 99869, A
325	37.2	2.2	601	4	US-09-949-016-100135	Sequence 100135,
326	37.2	2.2	601	4	US-09-949-016-100401	Sequence 100401,
327	37.2	2.2	601	4	US-09-949-016-100667	Sequence 100667,
328	37.2	2.2	601	4	US-09-949-016-100971	Sequence 100971,
329	37.2	2.2	601	4	US-09-949-016-101237	Sequence 101237,
330	37.2	2.2	601	4	US-09-949-016-101503	Sequence 101503,
331	37.2	2.2	601	4	US-09-949-016-101769	Sequence 101769,
c 332	37.2	2.2	601	4	US-09-949-016-107848	Sequence 107848,
c 333	37.2	2.2	601	4	US-09-949-016-107849	Sequence 107849,
334	37.2	2.2	601	4	US-09-949-016-161657	Sequence 161657,
335	37.2	2.2	1374	4	US-09-270-767-2575	Sequence 2575, Ap
336	37.2	2.2	1374	4	US-09-270-767-17857	Sequence 17857, A
337	37.2	2.2	11982	4	US-09-949-016-17084	Sequence 17084, A
338	37.2	2.2	49401	4	US-09-949-016-17080	Sequence 17080, A
339	37.2	2.2	54531	4	US-09-949-016-16267	Sequence 16267, A
340	37.2	2.2	240157	4	US-09-949-016-16264	Sequence 16264, A
c 341	37.2	2.2	818128	4	US-09-949-016-14546	Sequence 14546, A
c 342	37.2	2.2	818128	4	US-09-949-016-14547	Sequence 14547, A
c 343	37.2	2.2	818128	4	US-09-949-016-14548	Sequence 14548, A
c 344	37.2	2.2	818128	4	US-09-949-016-14549	Sequence 14549, A
c 345	37.2	2.2	818128	4	US-09-949-016-14550	Sequence 14550, A
c 346	37.2	2.2	818128	4	US-09-949-016-14551	Sequence 14551, A
c 347	37.2	2.2	818128	4	US-09-949-016-14552	Sequence 14552, A
c 348	37.2	2.2	818128	4	US-09-949-016-14553	Sequence 14553, A
c 349	37.2	2.2	818128	4	US-09-949-016-14554	Sequence 14554, A
c 350	37.2	2.2	818128	4	US-09-949-016-14555	Sequence 14555, A
c 351	37.2	2.2	818128	4	US-09-949-016-14556	Sequence 14556, A
c 352	37.2	2.2	818128	4	US-09-949-016-14557	Sequence 14557, A
c 353	37.2	2.2	818128	4	US-09-949-016-14558	Sequence 14558, A
c 354	37.2	2.2	818128	4	US-09-949-016-14559	Sequence 14559, A
c 355	37.2	2.2	818128	4	US-09-949-016-14560	Sequence 14560, A
c 356	37.2	2.2	818128	4	US-09-949-016-14561	Sequence 14561, A
c 357	37.2	2.2	818128	4	US-09-949-016-14562	Sequence 14562, A
c 358	37.2	2.2	818128	4	US-09-949-016-14564	Sequence 14564, A
c 359	37.2	2.2	818128	4	US-09-949-016-14565	Sequence 14565, A
c 360	37.2	2.2	818128	4	US-09-949-016-14566	Sequence 14566, A
c 361	37.2	2.2	818128	4	US-09-949-016-14567	Sequence 14567, A
362	37	2.2	586	3	US-09-385-982-472	Sequence 472, App
363	37	2.2	601	4	US-09-949-016-58348	Sequence 58348, A
364	37	2.2	601	4	US-09-949-016-58349	Sequence 58349, A
c 365	37	2.2	601	4	US-09-949-016-104951	Sequence 104951,
c 366	37	2.2	601	4	US-09-949-016-104976	Sequence 104976,
c 367	37	2.2	601	4	US-09-949-016-174173	Sequence 174173,
c 368	37	2.2	601	4	US-09-949-016-174174	Sequence 174174,
c 369	37	2.2	601	4	US-09-949-016-174365	Sequence 174365,
c 370	37	2.2	601	4	US-09-949-016-174366	Sequence 174366,
371	37	2.2	601	4	US-09-949-016-196595	Sequence 196595,
372	37	2.2	601	4	US-09-949-016-196596	Sequence 196596,
373	37	2.2	864	2	US-08-595-868C-11	Sequence 11, Appl
374	37	2.2	867	3	US-09-139-819A-11	Sequence 11, Appl
375	37	2.2	867	3	US-09-750-913-11	Sequence 11, Appl
376	37	2.2	895	4	US-09-976-594-137	Sequence 137, App
c 377	37	2.2	3976	4	US-09-244-805-37	Sequence 37, Appl
378	37	2.2	36093	4	US-09-949-016-14664	Sequence 14664, A
379	37	2.2	36093	4	US-09-949-016-14665	Sequence 14665, A
380	37	2.2	36542	4	US-09-949-016-12149	Sequence 12149, A
381	37	2.2	36544	4	US-09-949-016-13434	Sequence 13434, A
c 382	37	2.2	100463	4	US-09-949-016-12511	Sequence 12511, A
c 383	37	2.2	100468	4	US-09-949-016-13725	Sequence 13725, A
384	37	2.2	126237	4	US-09-949-016-16674	Sequence 16674, A
385	37	2.2	126237	4	US-09-949-016-16675	Sequence 16675, A
386	37	2.2	363032	4	US-09-949-016-12415	Sequence 12415, A
387	37	2.2	363033	4	US-09-949-016-15754	Sequence 15754, A
388	37	2.2	451924	4	US-09-949-016-12896	Sequence 12896, A
389	37	2.2	451925	4	US-09-949-016-17305	Sequence 17305, A
390	36.8	2.2	159	4	US-09-513-999C-9377	Sequence 9377, Ap
c 391	36.8	2.2	538	2	US-08-332-766A-24	Sequence 24, Appl
392	36.8	2.2	601	4	US-09-949-016-58024	Sequence 58024, A

	393	36.8	2.2	601	4	US-09-949-016-61384 Sequence 61384, A
	394	36.8	2.2	601	4	US-09-949-016-152800 Sequence 152800,
	395	36.8	2.2	601	4	US-09-949-016-152801 Sequence 152801,
	396	36.8	2.2	601	4	US-09-949-016-166873 Sequence 166873,
	397	36.8	2.2	601	4	US-09-949-016-166874 Sequence 166874,
	398	36.8	2.2	601	4	US-09-949-016-166875 Sequence 166875,
c	399	36.8	2.2	11376	4	US-09-949-016-16035 Sequence 16035, A
c	400	36.8	2.2	29172	4	US-09-949-016-15520 Sequence 15520, A
c	401	36.8	2.2	46823	4	US-09-949-016-12723 Sequence 12723, A
c	402	36.8	2.2	46940	4	US-09-949-016-16252 Sequence 16252, A
c	403	36.8	2.2	47184	4	US-09-949-016-12647 Sequence 12647, A
c	404	36.8	2.2	47184	4	US-09-949-016-15531 Sequence 15531, A
	405	36.8	2.2	85850	4	US-09-949-016-13424 Sequence 13424, A
	406	36.8	2.2	94133	4	US-09-949-016-11901 Sequence 11901, A
	407	36.8	2.2	94133	4	US-09-949-016-12713 Sequence 12713, A
	408	36.8	2.2	94135	4	US-09-949-016-15934 Sequence 15934, A
	409	36.8	2.2	94135	4	US-09-949-016-15935 Sequence 15935, A
	410	36.8	2.2	94135	4	US-09-949-016-15936 Sequence 15936, A
	411	36.8	2.2	94135	4	US-09-949-016-15937 Sequence 15937, A
	412	36.8	2.2	175265	4	US-09-949-016-16089 Sequence 16089, A
	413	36.8	2.2	206433	4	US-09-949-016-13527 Sequence 13527, A
	414	36.8	2.2	254778	4	US-09-949-016-12417 Sequence 12417, A
	415	36.8	2.2	260286	4	US-09-949-016-17037 Sequence 17037, A
	416	36.8	2.2	260293	4	US-09-949-016-12106 Sequence 12106, A
c	417	36.8	2.2	323820	4	US-09-949-016-14139 Sequence 14139, A
	418	36.8	2.2	393753	4	US-09-949-016-14573 Sequence 14573, A
	419	36.8	2.2	393753	4	US-09-949-016-14574 Sequence 14574, A
	420	36.8	2.2	818128	4	US-09-949-016-14546 Sequence 14546, A
	421	36.8	2.2	818128	4	US-09-949-016-14547 Sequence 14547, A
	422	36.8	2.2	818128	4	US-09-949-016-14548 Sequence 14548, A
	423	36.8	2.2	818128	4	US-09-949-016-14549 Sequence 14549, A
	424	36.8	2.2	818128	4	US-09-949-016-14550 Sequence 14550, A
	425	36.8	2.2	818128	4	US-09-949-016-14551 Sequence 14551, A
	426	36.8	2.2	818128	4	US-09-949-016-14552 Sequence 14552, A
	427	36.8	2.2	818128	4	US-09-949-016-14553 Sequence 14553, A
	428	36.8	2.2	818128	4	US-09-949-016-14554 Sequence 14554, A
	429	36.8	2.2	818128	4	US-09-949-016-14555 Sequence 14555, A
	430	36.8	2.2	818128	4	US-09-949-016-14556 Sequence 14556, A
	431	36.8	2.2	818128	4	US-09-949-016-14557 Sequence 14557, A
	432	36.8	2.2	818128	4	US-09-949-016-14558 Sequence 14558, A
	433	36.8	2.2	818128	4	US-09-949-016-14559 Sequence 14559, A
	434	36.8	2.2	818128	4	US-09-949-016-14560 Sequence 14560, A
	435	36.8	2.2	818128	4	US-09-949-016-14561 Sequence 14561, A
	436	36.8	2.2	818128	4	US-09-949-016-14562 Sequence 14562, A
	437	36.8	2.2	818128	4	US-09-949-016-14564 Sequence 14564, A
	438	36.8	2.2	818128	4	US-09-949-016-14565 Sequence 14565, A
	439	36.8	2.2	818128	4	US-09-949-016-14566 Sequence 14566, A
	440	36.8	2.2	818128	4	US-09-949-016-14567 Sequence 14567, A
	441	36.6	2.2	353	4	US-09-949-016-123905 Sequence 123905,
c	442	36.6	2.2	441	4	US-09-854-133-694 Sequence 694, App
	443	36.6	2.2	500	4	US-09-866-108A-15742 Sequence 15742, A
c	444	36.6	2.2	554	4	US-09-489-039A-1758 Sequence 1758, Ap
c	445	36.6	2.2	570	4	US-09-489-039A-1676 Sequence 1676, Ap
c	446	36.6	2.2	601	4	US-09-949-016-56396 Sequence 56396, A
	447	36.6	2.2	601	4	US-09-949-016-92660 Sequence 92660, A
c	448	36.6	2.2	601	4	US-09-949-016-156587 Sequence 156587,
c	449	36.6	2.2	601	4	US-09-949-016-156588 Sequence 156588,
	450	36.6	2.2	10434	4	US-09-949-016-12258 Sequence 12258, A
	451	36.6	2.2	10435	4	US-09-949-016-14654 Sequence 14654, A
c	452	36.6	2.2	21590	4	US-09-949-016-13372 Sequence 13372, A
c	453	36.6	2.2	21590	4	US-09-949-016-13373 Sequence 13373, A
c	454	36.6	2.2	26115	4	US-09-949-016-15959 Sequence 15959, A
c	455	36.6	2.2	27380	4	US-09-949-016-12877 Sequence 12877, A
c	456	36.6	2.2	27383	4	US-09-949-016-14393 Sequence 14393, A
c	457	36.6	2.2	50062	4	US-09-949-016-13809 Sequence 13809, A
c	458	36.6	2.2	113042	4	US-09-949-016-12343 Sequence 12343, A
c	459	36.6	2.2	113042	4	US-09-949-016-15246 Sequence 15246, A
c	460	36.6	2.2	114793	4	US-10-148-806-3 Sequence 3, Appli
c	461	36.6	2.2	144596	4	US-09-949-016-11749 Sequence 11749, A
c	462	36.6	2.2	144596	4	US-09-949-016-13035 Sequence 13035, A
c	463	36.6	2.2	163022	4	US-09-949-016-16515 Sequence 16515, A
	464	36.6	2.2	231129	4	US-09-949-016-16110 Sequence 16110, A
	465	36.6	2.2	234884	4	US-09-949-016-16420 Sequence 16420, A
	466	36.6	2.2	266293	4	US-09-949-016-11934 Sequence 11934, A
	467	36.6	2.2	346112	4	US-09-949-016-13165 Sequence 13165, A
	468	36.6	2.2	390416	4	US-09-949-016-16923 Sequence 16923, A
c	469	36.6	2.2	390416	4	US-09-949-016-16923 Sequence 16923, A
	470	36.6	2.2	536165	4	US-09-214-808-1 Sequence 1, Appli
	471	36.4	2.1	343	4	US-09-232-785-321 Sequence 321, App
	472	36.4	2.1	601	4	US-09-949-016-22185 Sequence 22185, A
c	473	36.4	2.1	601	4	US-09-949-016-127739 Sequence 127739,
c	474	36.4	2.1	601	4	US-09-949-016-128076 Sequence 128076,
c	475	36.4	2.1	601	4	US-09-949-016-165374 Sequence 165374,
c	476	36.4	2.1	601	4	US-09-949-016-165375 Sequence 165375,
c	477	36.4	2.1	601	4	US-09-949-016-165378 Sequence 165378,
	478	36.4	2.1	601	4	US-09-949-016-177926 Sequence 177926,
c	479	36.4	2.1	48940	4	US-09-949-016-16402 Sequence 16402, A
	480	36.4	2.1	107937	4	US-09-949-016-17192 Sequence 17192, A
c	481	36.4	2.1	147321	4	US-09-949-016-15450 Sequence 15450, A
	482	36.4	2.1	304533	4	US-09-949-016-15371 Sequence 15371, A
	483	36.4	2.1	304533	4	US-09-949-016-15372 Sequence 15372, A
c	484	36.2	2.1	601	4	US-09-949-016-57176 Sequence 57176, A
	485	36.2	2.1	601	4	US-09-949-016-76504 Sequence 76504, A
c	486	36.2	2.1	601	4	US-09-949-016-145302 Sequence 145302,
c	487	36.2	2.1	1676	4	US-09-645-593-6 Sequence 6, Appli
	488	36.2	2.1	1797	3	US-09-068-140A-11 Sequence 11, Appl
	489	36.2	2.1	3292	3	US-09-068-140A-12 Sequence 12, Appl
	490	36.2	2.1	8779	2	US-08-750-703-4 Sequence 4, Appli
c	491	36.2	2.1	11174	4	US-09-949-016-14111 Sequence 14111, A
c	492	36.2	2.1	14551	4	US-09-949-016-12313 Sequence 12313, A
c	493	36.2	2.1	14551	4	US-09-949-016-16465 Sequence 16465, A
	494	36.2	2.1	25969	4	US-09-949-016-13397 Sequence 13397, A
	495	36.2	2.1	32327	4	US-09-949-016-14108 Sequence 14108, A
	496	36.2	2.1	37875	4	US-09-949-016-13182 Sequence 13182, A
	497	36.2	2.1	53526	3	US-08-658-136-2 Sequence 2, Appli
	498	36.2	2.1	53577	3	US-08-658-136-1 Sequence 1, Appli
	499	36.2	2.1	69199	4	US-09-949-016-13881 Sequence 13881, A
c	500	36.2	2.1	133559	4	US-09-949-016-15845 Sequence 15845, A
c	501	36.2	2.1	421491	4	US-09-949-016-12805 Sequence 12805, A
c	502	36.2	2.1	421494	4	US-09-949-016-14060 Sequence 14060, A
c	503	36	2.1	162	3	US-09-171-209-17 Sequence 17, Appl
	504	36	2.1	166	3	US-09-171-209-16 Sequence 16, Appl
c	505	36	2.1	601	4	US-09-949-016-82601 Sequence 82601, A
	506	36	2.1	601	4	US-09-949-016-96410 Sequence 96410, A
	507	36	2.1	601	4	US-09-949-016-96676 Sequence 96676, A
	508	36	2.1	601	4	US-09-949-016-96942 Sequence 96942, A
	509	36	2.1	601	4	US-09-949-016-97208 Sequence 97208, A
	510	36	2.1	601	4	US-09-949-016-97474 Sequence 97474, A
	511	36	2.1	601	4	US-09-949-016-97740 Sequence 97740, A
	512	36	2.1	601	4	US-09-949-016-98006 Sequence 98006, A
	513	36	2.1	601	4	US-09-949-016-98272 Sequence 98272, A
	514	36	2.1	601	4	US-09-949-016-98538 Sequence 98538, A
	515	36	2.1	601	4	US-09-949-016-98804 Sequence 98804, A
	516	36	2.1	601	4	US-09-949-016-99070 Sequence 99070, A
	517	36	2.1	601	4	US-09-949-016-99336 Sequence 99336, A
	518	36	2.1	601	4	US-09-949-016-99602 Sequence 99602, A
	519	36	2.1	601	4	US-09-949-016-99868 Sequence 99868, A
	520	36	2.1	601	4	US-09-949-016-100134 Sequence 100134,
	521	36	2.1	601	4	US-09-949-016-100400 Sequence 100400,
	522	36	2.1	601	4	US-09-949-016-100666 Sequence 100666,
	523	36	2.1	601	4	US-09-949-016-100970 Sequence 100970,
	524	36	2.1	601	4	US-09-949-016-101236 Sequence 101236,
	525	36	2.1	601	4	US-09-949-016-101502 Sequence 101502,
	526	36	2.1	601	4	US-09-949-016-101768 Sequence 101768,
c	527	36	2.1	601	4	US-09-949-016-165377 Sequence 165377,
	528	36	2.1	601	4	US-09-949-016-200349 Sequence 200349,
c	529	36	2.1	601	4	US-09-949-016-203127 Sequence 203127,
c	530	36	2.1	601	4	US-09-949-016-203169 Sequence 203169,
c	531	36	2.1	1642	2	US-08-665-037-1 Sequence 1, Appli
c	532	36	2.1	1642	2	US-08-666-067-1 Sequence 1, Appli
c	533	36	2.1	1642	2	US-08-732-870-1 Sequence 1, Appli
c	534	36	2.1	2263	1	US-08-176-126B-1 Sequence 1, Appli
c	535	36	2.1	2263	2	US-08-669-435-1 Sequence 1, Appli
c	536	36	2.1	2263	5	PCT-US94-14431A-1 Sequence 1, Appli
c	537	36	2.1	4122	3	US-09-321-831-1 Sequence 1, Appli
	538	36	2.1	8078	3	US-08-870-126-12 Sequence 12, Appl

539	36	2.1	8078	3	US-09-445-247-12	Sequence 12, Appl
c 540	36	2.1	8523	4	US-09-573-080A-21	Sequence 21, Appl
541	36	2.1	13261	4	US-09-949-016-16870	Sequence 16870, A
c 542	36	2.1	13537	4	US-09-949-016-17382	Sequence 17382, A
543	36	2.1	14985	1	US-08-652-972A-6	Sequence 6, Appli
544	36	2.1	14985	5	PCT-US96-06231A-6	Sequence 6, Appli
545	36	2.1	15271	4	US-09-949-016-17396	Sequence 17396, A
546	36	2.1	18228	4	US-09-949-016-11964	Sequence 11964, A
547	36	2.1	18229	4	US-09-949-016-14056	Sequence 14056, A
c 548	36	2.1	20805	4	US-09-949-016-13772	Sequence 13772, A
549	36	2.1	28720	3	US-09-341-587-7	Sequence 7, Appli
c 550	36	2.1	30402	4	US-09-949-016-12451	Sequence 12451, A
551	36	2.1	33536	4	US-09-949-016-17034	Sequence 17034, A
552	36	2.1	33536	4	US-09-949-016-17035	Sequence 17035, A
553	36	2.1	63319	4	US-09-949-016-16579	Sequence 16579, A
554	36	2.1	183112	4	US-09-949-016-14184	Sequence 14184, A
c 555	36	2.1	194937	4	US-09-949-016-17032	Sequence 17032, A
c 556	36	2.1	194937	4	US-09-949-016-17033	Sequence 17033, A
c 557	35.8	2.1	289	3	US-09-007-005-17	Sequence 17, Appl
c 558	35.8	2.1	289	3	US-09-244-796-17	Sequence 17, Appl
559	35.8	2.1	601	4	US-09-949-016-85089	Sequence 85089, A
560	35.8	2.1	601	4	US-09-949-016-85090	Sequence 85090, A
561	35.8	2.1	601	4	US-09-949-016-85091	Sequence 85091, A
562	35.8	2.1	601	4	US-09-949-016-85092	Sequence 85092, A
563	35.8	2.1	601	4	US-09-949-016-85240	Sequence 85240, A
564	35.8	2.1	601	4	US-09-949-016-85241	Sequence 85241, A
565	35.8	2.1	601	4	US-09-949-016-85242	Sequence 85242, A
566	35.8	2.1	601	4	US-09-949-016-85243	Sequence 85243, A
c 567	35.8	2.1	601	4	US-09-949-016-143592	Sequence 143592,
c 568	35.8	2.1	601	4	US-09-949-016-170282	Sequence 170282,
c 569	35.8	2.1	601	4	US-09-949-016-197001	Sequence 197001,
c 570	35.8	2.1	601	4	US-09-949-016-197002	Sequence 197002,
c 571	35.8	2.1	601	4	US-09-949-016-197003	Sequence 197003,
572	35.8	2.1	4517	3	US-09-140-804-9	Sequence 9, Appli
573	35.8	2.1	4517	4	US-09-686-838B-9	Sequence 9, Appli
574	35.8	2.1	4517	4	US-09-776-976-5	Sequence 5, Appli
575	35.8	2.1	4517	4	US-09-909-547-5	Sequence 5, Appli
c 576	35.8	2.1	8764	4	US-09-949-016-17326	Sequence 17326, A
577	35.8	2.1	12695	4	US-09-949-016-16775	Sequence 16775, A
578	35.8	2.1	15775	4	US-09-949-016-16550	Sequence 16550, A
579	35.8	2.1	23802	4	US-09-949-016-12107	Sequence 12107, A
580	35.8	2.1	23803	4	US-09-949-016-15878	Sequence 15878, A
581	35.8	2.1	34276	4	US-09-949-016-12263	Sequence 12263, A
582	35.8	2.1	34278	4	US-09-949-016-16103	Sequence 16103, A
c 583	35.8	2.1	43255	4	US-09-949-016-11909	Sequence 11909, A
c 584	35.8	2.1	44998	4	US-09-949-016-12824	Sequence 12824, A
c 585	35.8	2.1	44999	4	US-09-949-016-14832	Sequence 14832, A
c 586	35.8	2.1	44999	4	US-09-949-016-14833	Sequence 14833, A
c 587	35.8	2.1	44999	4	US-09-949-016-17108	Sequence 17108, A
c 588	35.8	2.1	44999	4	US-09-949-016-17109	Sequence 17109, A
589	35.8	2.1	70770	4	US-09-949-016-16938	Sequence 16938, A
590	35.8	2.1	76399	4	US-09-949-016-16819	Sequence 16819, A
591	35.8	2.1	86414	4	US-09-949-016-12345	Sequence 12345, A
592	35.8	2.1	86414	4	US-09-949-016-15758	Sequence 15758, A
593	35.8	2.1	109159	4	US-09-949-016-14169	Sequence 14169, A
594	35.8	2.1	109159	4	US-09-949-016-14170	Sequence 14170, A
c 595	35.8	2.1	112114	4	US-09-949-016-17292	Sequence 17292, A
596	35.8	2.1	133559	4	US-09-949-016-15845	Sequence 15845, A
c 597	35.8	2.1	154605	4	US-09-949-016-11894	Sequence 11894, A
598	35.6	2.1	601	4	US-09-949-016-53715	Sequence 53715, A
599	35.6	2.1	601	4	US-09-949-016-53718	Sequence 53718, A
600	35.6	2.1	601	4	US-09-949-016-96409	Sequence 96409, A
601	35.6	2.1	601	4	US-09-949-016-96675	Sequence 96675, A
602	35.6	2.1	601	4	US-09-949-016-96941	Sequence 96941, A
603	35.6	2.1	601	4	US-09-949-016-97207	Sequence 97207, A
604	35.6	2.1	601	4	US-09-949-016-97473	Sequence 97473, A
605	35.6	2.1	601	4	US-09-949-016-97739	Sequence 97739, A
606	35.6	2.1	601	4	US-09-949-016-98005	Sequence 98005, A
607	35.6	2.1	601	4	US-09-949-016-98271	Sequence 98271, A
608	35.6	2.1	601	4	US-09-949-016-98537	Sequence 98537, A
609	35.6	2.1	601	4	US-09-949-016-98803	Sequence 98803, A
610	35.6	2.1	601	4	US-09-949-016-99069	Sequence 99069, A
611	35.6	2.1	601	4	US-09-949-016-99335	Sequence 99335, A
612	35.6	2.1	601	4	US-09-949-016-99601	Sequence 99601, A
613	35.6	2.1	601	4	US-09-949-016-99867	Sequence 99867, A
614	35.6	2.1	601	4	US-09-949-016-100133	Sequence 100133,
615	35.6	2.1	601	4	US-09-949-016-100399	Sequence 100399,
616	35.6	2.1	601	4	US-09-949-016-100665	Sequence 100665,
617	35.6	2.1	601	4	US-09-949-016-100969	Sequence 100969,
618	35.6	2.1	601	4	US-09-949-016-101235	Sequence 101235,
619	35.6	2.1	601	4	US-09-949-016-101501	Sequence 101501,
620	35.6	2.1	601	4	US-09-949-016-101767	Sequence 101767,
c 621	35.6	2.1	601	4	US-09-949-016-150996	Sequence 150996,
622	35.6	2.1	601	4	US-09-949-016-176890	Sequence 176890,
623	35.6	2.1	601	4	US-09-949-016-176891	Sequence 176891,
624	35.6	2.1	601	4	US-09-949-016-176892	Sequence 176892,
625	35.6	2.1	601	4	US-09-949-016-176893	Sequence 176893,
626	35.6	2.1	682	4	US-09-270-767-14807	Sequence 14807, A
627	35.6	2.1	7716	4	US-09-949-016-16614	Sequence 16614, A
628	35.6	2.1	13219	4	US-09-949-016-13522	Sequence 13522, A
629	35.6	2.1	78630	4	US-09-949-016-16790	Sequence 16790, A
630	35.6	2.1	98828	4	US-09-949-016-16630	Sequence 16630, A
631	35.6	2.1	161652	4	US-09-497-855A-40	Sequence 40, Appl
632	35.6	2.1	168394	4	US-09-949-016-13002	Sequence 13002, A
c 633	35.6	2.1	198632	4	US-09-949-016-12781	Sequence 12781, A
c 634	35.6	2.1	198637	4	US-09-949-016-17393	Sequence 17393, A
635	35.6	2.1	235064	4	US-09-949-016-15390	Sequence 15390, A
c 636	35.6	2.1	239527	4	US-09-949-016-15980	Sequence 15980, A
c 637	35.6	2.1	268449	4	US-09-949-016-17244	Sequence 17244, A
638	35.6	2.1	271134	4	US-09-949-016-12705	Sequence 12705, A
639	35.6	2.1	305491	4	US-09-949-016-17550	Sequence 17550, A
c 640	35.6	2.1	524032	4	US-09-949-016-16928	Sequence 16928, A
c 641	35.6	2.1	524032	4	US-09-949-016-16929	Sequence 16929, A
c 642	35.6	2.1	524032	4	US-09-949-016-16930	Sequence 16930, A
c 643	35.6	2.1	524032	4	US-09-949-016-16931	Sequence 16931, A
c 644	35.6	2.1	529885	4	US-09-949-016-14340	Sequence 14340, A
c 645	35.6	2.1	529885	4	US-09-949-016-14341	Sequence 14341, A
c 646	35.6	2.1	529885	4	US-09-949-016-14342	Sequence 14342, A
c 647	35.6	2.1	529885	4	US-09-949-016-14343	Sequence 14343, A
c 648	35.6	2.1	529885	4	US-09-949-016-14344	Sequence 14344, A
c 649	35.6	2.1	529885	4	US-09-949-016-14345	Sequence 14345, A
c 650	35.6	2.1	529885	4	US-09-949-016-14346	Sequence 14346, A
c 651	35.6	2.1	529885	4	US-09-949-016-14347	Sequence 14347, A
652	35.4	2.1	337	4	US-09-949-016-123904	Sequence 123904,
653	35.4	2.1	373	4	US-09-949-016-123907	Sequence 123907,
654	35.4	2.1	374	4	US-09-949-016-123908	Sequence 123908,
655	35.4	2.1	581	3	US-09-385-982-136	Sequence 136, App
656	35.4	2.1	583	4	US-09-949-016-123909	Sequence 123909,
657	35.4	2.1	601	4	US-09-949-016-85094	Sequence 85094, A
658	35.4	2.1	601	4	US-09-949-016-85245	Sequence 85245, A
659	35.4	2.1	1594	2	US-08-955-713-1	Sequence 1, Appli
660	35.4	2.1	2791	3	US-09-570-367C-1	Sequence 1, Appli
661	35.4	2.1	2791	4	US-09-915-524-1	Sequence 1, Appli
662	35.4	2.1	2791	4	US-09-934-634-1	Sequence 1, Appli
663	35.4	2.1	14449	4	US-09-949-016-12108	Sequence 12108, A
c 664	35.4	2.1	51822	4	US-09-949-016-15233	Sequence 15233, A
665	35.4	2.1	56832	4	US-09-949-016-12976	Sequence 12976, A
666	35.4	2.1	58108	4	US-09-949-016-13383	Sequence 13383, A
667	35.4	2.1	63926	4	US-09-949-016-16473	Sequence 16473, A
668	35.4	2.1	64626	4	US-09-949-016-12011	Sequence 12011, A
669	35.4	2.1	67002	4	US-09-949-016-16803	Sequence 16803, A
c 670	35.4	2.1	128175	4	US-09-949-016-16268	Sequence 16268, A
671	35.4	2.1	168174	4	US-10-071-411A-63	Sequence 63, Appl
c 672	35.4	2.1	168174	4	US-10-071-411A-63	Sequence 63, Appl
673	35.4	2.1	168273	4	US-10-071-411A-2	Sequence 2, Appli
c 674	35.4	2.1	168273	4	US-10-071-411A-2	Sequence 2, Appli
675	35.4	2.1	192506	4	US-09-949-016-15830	Sequence 15830, A
676	35.4	2.1	194889	4	US-09-949-016-15654	Sequence 15654, A
c 677	35.4	2.1	256287	4	US-09-949-016-14608	Sequence 14608, A
c 678	35.2	2.1	462	4	US-09-270-767-1672	Sequence 1672, Ap
c 679	35.2	2.1	462	4	US-09-270-767-16954	Sequence 16954, A
680	35.2	2.1	601	4	US-09-949-016-21327	Sequence 21327, A
c 681	35.2	2.1	601	4	US-09-949-016-22874	Sequence 22874, A
c 682	35.2	2.1	601	4	US-09-949-016-22876	Sequence 22876, A
683	35.2	2.1	601	4	US-09-949-016-53717	Sequence 53717, A
684	35.2	2.1	601	4	US-09-949-016-74319	Sequence 74319, A

c 685	35.2	2.1	601	4	US-09-949-016-96415	Sequence 96415, A
c 686	35.2	2.1	601	4	US-09-949-016-96681	Sequence 96681, A
c 687	35.2	2.1	601	4	US-09-949-016-96947	Sequence 96947, A
c 688	35.2	2.1	601	4	US-09-949-016-97213	Sequence 97213, A
c 689	35.2	2.1	601	4	US-09-949-016-97479	Sequence 97479, A
c 690	35.2	2.1	601	4	US-09-949-016-97745	Sequence 97745, A
c 691	35.2	2.1	601	4	US-09-949-016-98011	Sequence 98011, A
c 692	35.2	2.1	601	4	US-09-949-016-98277	Sequence 98277, A
c 693	35.2	2.1	601	4	US-09-949-016-98543	Sequence 98543, A
c 694	35.2	2.1	601	4	US-09-949-016-98809	Sequence 98809, A
c 695	35.2	2.1	601	4	US-09-949-016-99075	Sequence 99075, A
c 696	35.2	2.1	601	4	US-09-949-016-99341	Sequence 99341, A
c 697	35.2	2.1	601	4	US-09-949-016-99607	Sequence 99607, A
c 698	35.2	2.1	601	4	US-09-949-016-99873	Sequence 99873, A
c 699	35.2	2.1	601	4	US-09-949-016-100139	Sequence 100139,
c 700	35.2	2.1	601	4	US-09-949-016-100405	Sequence 100405,
c 701	35.2	2.1	601	4	US-09-949-016-100671	Sequence 100671,
c 702	35.2	2.1	601	4	US-09-949-016-100975	Sequence 100975,
c 703	35.2	2.1	601	4	US-09-949-016-101241	Sequence 101241,
c 704	35.2	2.1	601	4	US-09-949-016-101507	Sequence 101507,
c 705	35.2	2.1	601	4	US-09-949-016-101773	Sequence 101773,
706	35.2	2.1	601	4	US-09-949-016-104175	Sequence 104175,
707	35.2	2.1	601	4	US-09-949-016-148758	Sequence 148758,
708	35.2	2.1	601	4	US-09-949-016-148759	Sequence 148759,
709	35.2	2.1	601	4	US-09-949-016-148786	Sequence 148786,
710	35.2	2.1	601	4	US-09-949-016-148787	Sequence 148787,
c 711	35.2	2.1	601	4	US-09-949-016-186016	Sequence 186016,
712	35.2	2.1	2380	4	US-08-635-130A-3	Sequence 3, Appli
713	35.2	2.1	2993	4	US-09-949-016-5096	Sequence 5096, Ap
714	35.2	2.1	3086	4	US-09-684-708A-20	Sequence 20, Appl
715	35.2	2.1	3394	4	US-09-949-016-205	Sequence 205, App
c 716	35.2	2.1	6913	4	US-09-949-016-17125	Sequence 17125, A
717	35.2	2.1	8610	4	US-09-949-016-14614	Sequence 14614, A
718	35.2	2.1	9948	4	US-09-949-016-16838	Sequence 16838, A
719	35.2	2.1	23535	4	US-09-949-016-14630	Sequence 14630, A
720	35.2	2.1	31214	4	US-09-949-016-17097	Sequence 17097, A
721	35.2	2.1	31214	4	US-09-949-016-17098	Sequence 17098, A
c 722	35.2	2.1	38564	3	US-09-734-673-3	Sequence 3, Appli
c 723	35.2	2.1	39433	4	US-09-949-016-12014	Sequence 12014, A
c 724	35.2	2.1	42053	4	US-09-949-016-15924	Sequence 15924, A
725	35.2	2.1	43102	4	US-09-949-016-16355	Sequence 16355, A
c 726	35.2	2.1	49401	4	US-09-949-016-17080	Sequence 17080, A
c 727	35.2	2.1	54601	4	US-09-949-016-14173	Sequence 14173, A
c 728	35.2	2.1	55130	4	US-09-949-016-11850	Sequence 11850, A
c 729	35.2	2.1	60785	4	US-09-949-016-12774	Sequence 12774, A
c 730	35.2	2.1	60785	4	US-09-949-016-15665	Sequence 15665, A
731	35.2	2.1	84761	4	US-09-949-016-11919	Sequence 11919, A
732	35.2	2.1	84763	4	US-09-949-016-13914	Sequence 13914, A
733	35.2	2.1	89625	4	US-09-949-016-17012	Sequence 17012, A
c 734	35.2	2.1	89716	4	US-09-949-016-11900	Sequence 11900, A
735	35.2	2.1	99498	4	US-09-949-016-12621	Sequence 12621, A
736	35.2	2.1	100836	4	US-09-949-016-12871	Sequence 12871, A
737	35.2	2.1	100837	4	US-09-949-016-17063	Sequence 17063, A
c 738	35.2	2.1	142783	4	US-09-949-016-15127	Sequence 15127, A
739	35.2	2.1	146095	4	US-09-949-016-12872	Sequence 12872, A
740	35.2	2.1	146104	4	US-09-949-016-13239	Sequence 13239, A
741	35.2	2.1	146428	4	US-09-949-016-12620	Sequence 12620, A
742	35.2	2.1	146438	4	US-09-949-016-12081	Sequence 12081, A
743	35.2	2.1	157822	4	US-09-949-016-16723	Sequence 16723, A
744	35.2	2.1	166698	4	US-09-949-016-16038	Sequence 16038, A
745	35.2	2.1	174029	4	US-09-949-016-12610	Sequence 12610, A
746	35.2	2.1	174030	4	US-09-949-016-13880	Sequence 13880, A
747	35.2	2.1	462589	4	US-09-949-016-12900	Sequence 12900, A
748	35.2	2.1	476044	4	US-09-949-016-12412	Sequence 12412, A
c 749	35.2	2.1	636591	4	US-09-949-016-11808	Sequence 11808, A
c 750	35.2	2.1	636591	4	US-09-949-016-13388	Sequence 13388, A
751	35	2.1	361	4	US-09-949-016-123906	Sequence 123906,
c 752	35	2.1	601	4	US-09-949-016-47856	Sequence 47856, A
c 753	35	2.1	601	4	US-09-949-016-47862	Sequence 47862, A
c 754	35	2.1	601	4	US-09-949-016-160832	Sequence 160832,
c 755	35	2.1	601	4	US-09-949-016-160833	Sequence 160833,
c 756	35	2.1	601	4	US-09-949-016-193545	Sequence 193545,
757	35	2.1	680	3	US-09-056-285A-5	Sequence 5, Appli
c 758	35	2.1	2280	1	US-08-415-818-5	Sequence 5, Appli
c 759	35	2.1	2280	2	US-08-894-236-5	Sequence 5, Appli
c 760	35	2.1	2280	5	PCT-US96-01444-5	Sequence 5, Appli
c 761	35	2.1	2281	4	US-09-900-497-1	Sequence 1, Appli
762	35	2.1	3892	2	US-08-555-723B-3	Sequence 3, Appli
763	35	2.1	3892	3	US-09-123-465-3	Sequence 3, Appli
c 764	35	2.1	7409	4	US-09-949-016-12689	Sequence 12689, A
c 765	35	2.1	7409	4	US-09-949-016-15978	Sequence 15978, A
766	35	2.1	10321	4	US-09-949-016-13587	Sequence 13587, A
767	35	2.1	25377	4	US-09-949-016-14260	Sequence 14260, A
768	35	2.1	25377	4	US-09-949-016-14261	Sequence 14261, A
769	35	2.1	45427	4	US-09-949-016-16243	Sequence 16243, A
770	35	2.1	51754	4	US-09-949-016-15009	Sequence 15009, A
771	35	2.1	51754	4	US-09-949-016-15010	Sequence 15010, A
772	35	2.1	51754	4	US-09-949-016-15011	Sequence 15011, A
773	35	2.1	51754	4	US-09-949-016-15012	Sequence 15012, A
774	35	2.1	51754	4	US-09-949-016-15275	Sequence 15275, A
775	35	2.1	51754	4	US-09-949-016-15276	Sequence 15276, A
776	35	2.1	51754	4	US-09-949-016-15277	Sequence 15277, A
777	35	2.1	51754	4	US-09-949-016-15278	Sequence 15278, A
778	35	2.1	52202	4	US-09-949-016-17006	Sequence 17006, A
c 779	35	2.1	75212	4	US-09-949-016-13313	Sequence 13313, A
c 780	35	2.1	75212	4	US-09-949-016-13314	Sequence 13314, A
c 781	35	2.1	75212	4	US-09-949-016-13315	Sequence 13315, A
c 782	35	2.1	87523	4	US-09-949-016-12670	Sequence 12670, A
c 783	35	2.1	87523	4	US-09-949-016-15047	Sequence 15047, A
c 784	35	2.1	87523	4	US-09-949-016-15048	Sequence 15048, A
c 785	35	2.1	87523	4	US-09-949-016-15049	Sequence 15049, A
c 786	35	2.1	87869	4	US-09-949-016-11744	Sequence 11744, A
c 787	35	2.1	87869	4	US-09-949-016-15044	Sequence 15044, A
c 788	35	2.1	87869	4	US-09-949-016-15045	Sequence 15045, A
c 789	35	2.1	87869	4	US-09-949-016-15046	Sequence 15046, A
790	35	2.1	91993	4	US-09-949-016-12757	Sequence 12757, A
c 791	35	2.1	151295	4	US-09-949-016-14568	Sequence 14568, A
c 792	35	2.1	151295	4	US-09-949-016-14569	Sequence 14569, A
c 793	35	2.1	151295	4	US-09-949-016-14570	Sequence 14570, A
c 794	35	2.1	151295	4	US-09-949-016-14571	Sequence 14571, A
c 795	35	2.1	151295	4	US-09-949-016-14572	Sequence 14572, A
796	35	2.1	156651	4	US-09-949-016-17349	Sequence 17349, A
c 797	35	2.1	198942	4	US-09-949-016-13209	Sequence 13209, A
798	35	2.1	268449	4	US-09-949-016-17244	Sequence 17244, A
c 799	35	2.1	393753	4	US-09-949-016-14573	Sequence 14573, A
c 800	35	2.1	393753	4	US-09-949-016-14574	Sequence 14574, A
c 801	34.8	2.0	601	4	US-09-949-016-20880	Sequence 20880, A
c 802	34.8	2.0	601	4	US-09-949-016-62586	Sequence 62586, A
c 803	34.8	2.0	601	4	US-09-949-016-62587	Sequence 62587, A
c 804	34.8	2.0	601	4	US-09-949-016-62588	Sequence 62588, A
c 805	34.8	2.0	601	4	US-09-949-016-126601	Sequence 126601,
c 806	34.8	2.0	601	4	US-09-949-016-131686	Sequence 131686,
c 807	34.8	2.0	601	4	US-09-949-016-131687	Sequence 131687,
808	34.8	2.0	601	4	US-09-949-016-175400	Sequence 175400,
c 809	34.8	2.0	2614	4	US-09-052-753B-8	Sequence 8, Appli
810	34.8	2.0	4064	4	US-09-873-737A-3	Sequence 3, Appli
c 811	34.8	2.0	9052	4	US-09-949-016-13662	Sequence 13662, A
c 812	34.8	2.0	11200	4	US-09-949-016-13580	Sequence 13580, A
c 813	34.8	2.0	25067	4	US-09-949-016-11794	Sequence 11794, A
c 814	34.8	2.0	25441	4	US-09-949-016-14232	Sequence 14232, A
815	34.8	2.0	37155	4	US-09-949-016-16945	Sequence 16945, A
c 816	34.8	2.0	43267	4	US-09-949-016-17117	Sequence 17117, A
817	34.8	2.0	106315	4	US-09-949-016-16613	Sequence 16613, A
818	34.8	2.0	137000	4	US-10-172-911-11	Sequence 11, Appl
c 819	34.8	2.0	145928	4	US-09-949-016-15444	Sequence 15444, A
820	34.8	2.0	163662	4	US-09-949-016-12545	Sequence 12545, A
821	34.8	2.0	163664	4	US-09-949-016-13546	Sequence 13546, A
c 822	34.8	2.0	421118	4	US-09-949-016-16297	Sequence 16297, A
c 823	34.6	2.0	305	1	US-08-253-155A-4	Sequence 4, Appli
c 824	34.6	2.0	349	1	US-08-253-155A-14	Sequence 14, Appl
825	34.6	2.0	372	3	US-09-018-584A-13	Sequence 13, Appl
826	34.6	2.0	372	4	US-09-784-423-13	Sequence 13, Appl
c 827	34.6	2.0	596	2	US-08-676-279-63	Sequence 63, Appl
c 828	34.6	2.0	601	4	US-09-949-016-21250	Sequence 21250, A
829	34.6	2.0	601	4	US-09-949-016-85093	Sequence 85093, A
830	34.6	2.0	601	4	US-09-949-016-85244	Sequence 85244, A

c 831	34.6	2.0	601	4	US-09-949-016-142451	Sequence 142451,
c 832	34.6	2.0	601	4	US-09-949-016-143594	Sequence 143594,
c 833	34.6	2.0	601	4	US-09-949-016-193874	Sequence 193874,
834	34.6	2.0	1541	4	US-09-527-972-4	Sequence 4, Appli
835	34.6	2.0	2191	1	US-08-417-330A-11	Sequence 11, Appl
836	34.6	2.0	4148	3	US-09-399-913-54	Sequence 54, Appl
837	34.6	2.0	4148	4	US-09-350-614-54	Sequence 54, Appl
c 838	34.6	2.0	16924	4	US-09-949-016-13720	Sequence 13720, A
839	34.6	2.0	21000	4	US-09-975-123-11	Sequence 11, Appl
840	34.6	2.0	22908	4	US-09-949-016-17255	Sequence 17255, A
c 841	34.6	2.0	49559	4	US-09-949-016-12892	Sequence 12892, A
c 842	34.6	2.0	49559	4	US-09-949-016-17267	Sequence 17267, A
c 843	34.6	2.0	56448	4	US-09-949-016-16463	Sequence 16463, A
c 844	34.6	2.0	73519	4	US-09-949-016-16344	Sequence 16344, A
845	34.6	2.0	77851	4	US-09-949-016-12508	Sequence 12508, A
846	34.6	2.0	77867	4	US-09-949-016-13211	Sequence 13211, A
847	34.6	2.0	77867	4	US-09-949-016-13212	Sequence 13212, A
848	34.6	2.0	77940	4	US-09-949-016-12509	Sequence 12509, A
c 849	34.6	2.0	105919	4	US-09-949-016-11769	Sequence 11769, A
850	34.6	2.0	107827	4	US-09-949-016-15790	Sequence 15790, A
851	34.6	2.0	151295	4	US-09-949-016-14568	Sequence 14568, A
852	34.6	2.0	151295	4	US-09-949-016-14569	Sequence 14569, A
853	34.6	2.0	151295	4	US-09-949-016-14570	Sequence 14570, A
854	34.6	2.0	151295	4	US-09-949-016-14571	Sequence 14571, A
855	34.6	2.0	151295	4	US-09-949-016-14572	Sequence 14572, A
856	34.6	2.0	236474	4	US-09-949-016-13418	Sequence 13418, A
c 857	34.6	2.0	301828	4	US-09-949-016-13969	Sequence 13969, A
858	34.6	2.0	767677	4	US-09-949-016-12147	Sequence 12147, A
859	34.6	2.0	767677	4	US-09-949-016-17361	Sequence 17361, A
860	34.4	2.0	414	2	US-08-975-316-18	Sequence 18, Appl
861	34.4	2.0	414	3	US-09-615-192A-18	Sequence 18, Appl
862	34.4	2.0	414	3	US-09-615-192A-403	Sequence 403, App
863	34.4	2.0	414	3	US-09-325-932A-203	Sequence 203, App
864	34.4	2.0	414	4	US-09-169-789-18	Sequence 18, Appl
865	34.4	2.0	414	4	US-09-169-789-185	Sequence 185, App
866	34.4	2.0	601	4	US-09-949-016-39411	Sequence 39411, A
867	34.4	2.0	601	4	US-09-949-016-53720	Sequence 53720, A
c 868	34.4	2.0	601	4	US-09-949-016-131688	Sequence 131688,
c 869	34.4	2.0	601	4	US-09-949-016-193794	Sequence 193794,
c 870	34.4	2.0	601	4	US-09-949-016-202254	Sequence 202254,
871	34.4	2.0	601	4	US-09-949-016-202976	Sequence 202976,
872	34.4	2.0	1066	4	US-09-949-016-348	Sequence 348, App
873	34.4	2.0	1081	4	US-09-949-016-1053	Sequence 1053, Ap
874	34.4	2.0	3048	4	US-09-949-016-52	Sequence 52, Appl
875	34.4	2.0	3275	4	US-09-949-016-2490	Sequence 2490, Ap
c 876	34.4	2.0	6167	4	US-09-949-016-12743	Sequence 12743, A
c 877	34.4	2.0	43414	4	US-09-949-016-12839	Sequence 12839, A
c 878	34.4	2.0	43415	4	US-09-949-016-16491	Sequence 16491, A
879	34.4	2.0	57178	4	US-09-949-016-12838	Sequence 12838, A
880	34.4	2.0	57178	4	US-09-949-016-17458	Sequence 17458, A
881	34.4	2.0	67745	4	US-09-949-016-17251	Sequence 17251, A
882	34.4	2.0	77772	4	US-09-949-016-17417	Sequence 17417, A
883	34.4	2.0	77997	4	US-09-949-016-12249	Sequence 12249, A
c 884	34.4	2.0	96922	4	US-09-949-016-17061	Sequence 17061, A
885	34.4	2.0	130724	4	US-09-949-016-13753	Sequence 13753, A
886	34.4	2.0	131332	4	US-09-949-016-15535	Sequence 15535, A
887	34.4	2.0	145320	4	US-09-949-016-15858	Sequence 15858, A
c 888	34.4	2.0	250715	4	US-09-949-016-13294	Sequence 13294, A
889	34.4	2.0	670689	4	US-09-949-016-12505	Sequence 12505, A
890	34.4	2.0	670690	4	US-09-949-016-14207	Sequence 14207, A
891	34.2	2.0	66	4	US-09-270-767-31051	Sequence 31051, A
c 892	34.2	2.0	320	4	US-09-509-712B-35	Sequence 35, Appl
c 893	34.2	2.0	395	4	US-09-894-844-45	Sequence 45, Appl
894	34.2	2.0	601	4	US-09-949-016-57779	Sequence 57779, A
c 895	34.2	2.0	601	4	US-09-949-016-71628	Sequence 71628, A
c 896	34.2	2.0	601	4	US-09-949-016-71701	Sequence 71701, A
c 897	34.2	2.0	601	4	US-09-949-016-71774	Sequence 71774, A
c 898	34.2	2.0	601	4	US-09-949-016-71847	Sequence 71847, A
c 899	34.2	2.0	601	4	US-09-949-016-71920	Sequence 71920, A
c 900	34.2	2.0	601	4	US-09-949-016-71993	Sequence 71993, A
c 901	34.2	2.0	601	4	US-09-949-016-72066	Sequence 72066, A
c 902	34.2	2.0	601	4	US-09-949-016-72139	Sequence 72139, A
c 903	34.2	2.0	601	4	US-09-949-016-72212	Sequence 72212, A
c 904	34.2	2.0	601	4	US-09-949-016-72285	Sequence 72285, A
c 905	34.2	2.0	601	4	US-09-949-016-113841	Sequence 113841,
c 906	34.2	2.0	601	4	US-09-949-016-114009	Sequence 114009,
c 907	34.2	2.0	601	4	US-09-949-016-114177	Sequence 114177,
c 908	34.2	2.0	601	4	US-09-949-016-114345	Sequence 114345,
c 909	34.2	2.0	601	4	US-09-949-016-114513	Sequence 114513,
c 910	34.2	2.0	601	4	US-09-949-016-114681	Sequence 114681,
c 911	34.2	2.0	601	4	US-09-949-016-114849	Sequence 114849,
c 912	34.2	2.0	601	4	US-09-949-016-115017	Sequence 115017,
c 913	34.2	2.0	601	4	US-09-949-016-143593	Sequence 143593,
c 914	34.2	2.0	601	4	US-09-949-016-158649	Sequence 158649,
c 915	34.2	2.0	601	4	US-09-949-016-170281	Sequence 170281,
916	34.2	2.0	612	3	US-09-615-192A-101	Sequence 101, App
917	34.2	2.0	612	4	US-09-169-789-101	Sequence 101, App
918	34.2	2.0	1860	4	US-09-051-994-1	Sequence 1, Appli
c 919	34.2	2.0	9740	4	US-09-949-016-15833	Sequence 15833, A
c 920	34.2	2.0	10718	4	US-09-949-016-11918	Sequence 11918, A
c 921	34.2	2.0	10718	4	US-09-949-016-13816	Sequence 13816, A
c 922	34.2	2.0	11982	4	US-09-949-016-17084	Sequence 17084, A
c 923	34.2	2.0	18228	4	US-09-949-016-11964	Sequence 11964, A
c 924	34.2	2.0	18229	4	US-09-949-016-14056	Sequence 14056, A
c 925	34.2	2.0	19728	4	US-09-949-016-12506	Sequence 12506, A
c 926	34.2	2.0	19728	4	US-09-949-016-15767	Sequence 15767, A
c 927	34.2	2.0	24817	4	US-09-949-016-16177	Sequence 16177, A
c 928	34.2	2.0	37004	4	US-09-949-016-15317	Sequence 15317, A
929	34.2	2.0	38920	4	US-09-949-016-17546	Sequence 17546, A
c 930	34.2	2.0	53562	4	US-09-949-016-16286	Sequence 16286, A
c 931	34.2	2.0	80355	4	US-09-949-016-12735	Sequence 12735, A
c 932	34.2	2.0	80357	4	US-09-949-016-13572	Sequence 13572, A
c 933	34.2	2.0	86945	4	US-09-949-016-13849	Sequence 13849, A
c 934	34.2	2.0	86945	4	US-09-949-016-13850	Sequence 13850, A
c 935	34.2	2.0	86945	4	US-09-949-016-13851	Sequence 13851, A
c 936	34.2	2.0	86945	4	US-09-949-016-13852	Sequence 13852, A
c 937	34.2	2.0	86945	4	US-09-949-016-13853	Sequence 13853, A
c 938	34.2	2.0	86945	4	US-09-949-016-13854	Sequence 13854, A
c 939	34.2	2.0	86945	4	US-09-949-016-13855	Sequence 13855, A
c 940	34.2	2.0	86945	4	US-09-949-016-13856	Sequence 13856, A
c 941	34.2	2.0	86945	4	US-09-949-016-13857	Sequence 13857, A
c 942	34.2	2.0	86945	4	US-09-949-016-13858	Sequence 13858, A
c 943	34.2	2.0	91559	4	US-09-949-016-12581	Sequence 12581, A
c 944	34.2	2.0	91559	4	US-09-949-016-13701	Sequence 13701, A
c 945	34.2	2.0	106199	4	US-09-949-016-12393	Sequence 12393, A
946	34.2	2.0	148567	4	US-09-801-876B-3	Sequence 3, Appli
947	34.2	2.0	148567	4	US-10-254-869-3	Sequence 3, Appli
948	34.2	2.0	148567	4	US-10-667-442-3	Sequence 3, Appli
c 949	34.2	2.0	193303	4	US-09-497-855A-37	Sequence 37, Appl
c 950	34.2	2.0	193303	4	US-09-497-855A-44	Sequence 44, Appl
951	34.2	2.0	312957	4	US-09-949-001-31	Sequence 31, Appl
952	34.2	2.0	312972	4	US-09-949-001-34	Sequence 34, Appl
c 953	34	2.0	350	2	US-08-332-766A-20	Sequence 20, Appl
c 954	34	2.0	601	4	US-09-949-016-20386	Sequence 20386, A
955	34	2.0	601	4	US-09-949-016-53716	Sequence 53716, A
956	34	2.0	601	4	US-09-949-016-53719	Sequence 53719, A
957	34	2.0	601	4	US-09-949-016-145345	Sequence 145345,
c 958	34	2.0	601	4	US-09-949-016-166473	Sequence 166473,
c 959	34	2.0	2440	3	US-08-724-984A-1	Sequence 1, Appli
960	34	2.0	2590	4	US-09-908-988B-3	Sequence 3, Appli
961	34	2.0	2830	1	US-07-882-292-1	Sequence 1, Appli
962	34	2.0	2830	2	US-08-331-644-1	Sequence 1, Appli
963	34	2.0	2830	5	PCT-US93-04102-1	Sequence 1, Appli
c 964	34	2.0	4835	4	US-09-937-521-16	Sequence 16, Appl
965	34	2.0	8831	4	US-09-949-016-17608	Sequence 17608, A
966	34	2.0	9301	3	US-09-449-218D-18	Sequence 18, Appl
967	34	2.0	9301	4	US-09-668-529A-18	Sequence 18, Appl
968	34	2.0	9301	4	US-09-668-037A-18	Sequence 18, Appl
969	34	2.0	9301	4	US-09-668-021-18	Sequence 18, Appl
970	34	2.0	18989	4	US-09-949-016-13435	Sequence 13435, A
971	34	2.0	21885	4	US-09-949-016-12600	Sequence 12600, A
c 972	34	2.0	29326	4	US-09-949-016-15356	Sequence 15356, A
973	34	2.0	29434	4	US-09-949-016-17585	Sequence 17585, A
c 974	34	2.0	30310	4	US-09-657-346A-96	Sequence 96, Appl
c 975	34	2.0	36580	4	US-09-949-016-14136	Sequence 14136, A
c 976	34	2.0	38805	4	US-09-949-016-14932	Sequence 14932, A

c 977	34	2.0	43992	4	US-09-949-016-12172	Sequence 12172, A
c 978	34	2.0	43993	4	US-09-949-016-13406	Sequence 13406, A
979	34	2.0	44180	4	US-09-949-016-12088	Sequence 12088, A
980	34	2.0	90876	4	US-09-949-016-13271	Sequence 13271, A
c 981	34	2.0	92139	4	US-09-918-686-1	Sequence 1, Appli
c 982	34	2.0	99830	4	US-09-949-016-16859	Sequence 16859, A
983	34	2.0	130298	4	US-09-949-016-16664	Sequence 16664, A
984	34	2.0	199945	4	US-09-949-016-15436	Sequence 15436, A
985	34	2.0	248968	4	US-09-949-016-12614	Sequence 12614, A
986	34	2.0	250958	4	US-09-949-016-16061	Sequence 16061, A
987	34	2.0	294836	4	US-09-949-016-15974	Sequence 15974, A
988	33.8	2.0	601	4	US-09-949-016-18586	Sequence 18586, A
989	33.8	2.0	601	4	US-09-949-016-39555	Sequence 39555, A
990	33.8	2.0	601	4	US-09-949-016-39588	Sequence 39588, A
991	33.8	2.0	601	4	US-09-949-016-39650	Sequence 39650, A
c 992	33.8	2.0	601	4	US-09-949-016-40844	Sequence 40844, A
c 993	33.8	2.0	601	4	US-09-949-016-40845	Sequence 40845, A
c 994	33.8	2.0	601	4	US-09-949-016-47855	Sequence 47855, A
c 995	33.8	2.0	601	4	US-09-949-016-47861	Sequence 47861, A
996	33.8	2.0	601	4	US-09-949-016-62244	Sequence 62244, A
997	33.8	2.0	601	4	US-09-949-016-62315	Sequence 62315, A
998	33.8	2.0	601	4	US-09-949-016-62386	Sequence 62386, A
999	33.8	2.0	601	4	US-09-949-016-62457	Sequence 62457, A
1000	33.8	2.0	601	4	US-09-949-016-86262	Sequence 86262, A
c1001	33.8	2.0	601	4	US-09-949-016-86372	Sequence 86372, A
1002	33.8	2.0	601	4	US-09-949-016-104239	Sequence 104239,
1003	33.8	2.0	601	4	US-09-949-016-104310	Sequence 104310,
1004	33.8	2.0	601	4	US-09-949-016-104381	Sequence 104381,
1005	33.8	2.0	601	4	US-09-949-016-104452	Sequence 104452,
1006	33.8	2.0	601	4	US-09-949-016-104523	Sequence 104523,
1007	33.8	2.0	601	4	US-09-949-016-104594	Sequence 104594,
1008	33.8	2.0	601	4	US-09-949-016-104665	Sequence 104665,
1009	33.8	2.0	601	4	US-09-949-016-104736	Sequence 104736,
1010	33.8	2.0	601	4	US-09-949-016-127054	Sequence 127054,
1011	33.8	2.0	601	4	US-09-949-016-127055	Sequence 127055,
1012	33.8	2.0	601	4	US-09-949-016-127056	Sequence 127056,
1013	33.8	2.0	601	4	US-09-949-016-127058	Sequence 127058,
1014	33.8	2.0	601	4	US-09-949-016-127059	Sequence 127059,
1015	33.8	2.0	601	4	US-09-949-016-127060	Sequence 127060,
1016	33.8	2.0	601	4	US-09-949-016-127061	Sequence 127061,
1017	33.8	2.0	601	4	US-09-949-016-176143	Sequence 176143,
c1018	33.8	2.0	601	4	US-09-949-016-180738	Sequence 180738,
1019	33.8	2.0	3088	1	US-08-418-444A-1	Sequence 1, Appli
c1020	33.8	2.0	5789	3	US-09-242-948-3	Sequence 3, Appli
c1021	33.8	2.0	7242	4	US-09-949-016-14729	Sequence 14729, A
c1022	33.8	2.0	12180	4	US-09-949-016-12527	Sequence 12527, A
c1023	33.8	2.0	12180	4	US-09-949-016-14323	Sequence 14323, A
1024	33.8	2.0	17723	4	US-09-949-016-15832	Sequence 15832, A
1025	33.8	2.0	20316	4	US-09-949-016-14360	Sequence 14360, A
1026	33.8	2.0	27630	4	US-09-949-016-16362	Sequence 16362, A
c1027	33.8	2.0	31573	4	US-09-949-016-16327	Sequence 16327, A
1028	33.8	2.0	40586	4	US-09-949-016-16965	Sequence 16965, A
1029	33.8	2.0	52398	4	US-09-949-016-13154	Sequence 13154, A
1030	33.8	2.0	52398	4	US-09-949-016-13155	Sequence 13155, A
c1031	33.8	2.0	57280	4	US-09-949-016-11796	Sequence 11796, A
c1032	33.8	2.0	57280	4	US-09-949-016-12843	Sequence 12843, A
c1033	33.8	2.0	57280	4	US-09-949-016-12844	Sequence 12844, A
c1034	33.8	2.0	57280	4	US-09-949-016-12846	Sequence 12846, A
c1035	33.8	2.0	57280	4	US-09-949-016-13542	Sequence 13542, A
c1036	33.8	2.0	57280	4	US-09-949-016-13543	Sequence 13543, A
c1037	33.8	2.0	57280	4	US-09-949-016-13544	Sequence 13544, A
c1038	33.8	2.0	57280	4	US-09-949-016-13545	Sequence 13545, A
c1039	33.8	2.0	57280	4	US-09-949-016-14633	Sequence 14633, A
c1040	33.8	2.0	57280	4	US-09-949-016-14634	Sequence 14634, A
c1041	33.8	2.0	57280	4	US-09-949-016-14635	Sequence 14635, A
c1042	33.8	2.0	57280	4	US-09-949-016-14636	Sequence 14636, A
c1043	33.8	2.0	57280	4	US-09-949-016-14637	Sequence 14637, A
c1044	33.8	2.0	57280	4	US-09-949-016-14638	Sequence 14638, A
c1045	33.8	2.0	57280	4	US-09-949-016-14639	Sequence 14639, A
c1046	33.8	2.0	57280	4	US-09-949-016-14640	Sequence 14640, A
c1047	33.8	2.0	58768	4	US-09-949-016-13175	Sequence 13175, A
c1048	33.8	2.0	67479	4	US-09-949-016-11804	Sequence 11804, A
c1049	33.8	2.0	71119	4	US-09-949-016-15358	Sequence 15358, A
1050	33.8	2.0	71387	4	US-09-949-016-16754	Sequence 16754, A
1051	33.8	2.0	82494	4	US-09-949-016-16937	Sequence 16937, A
c1052	33.8	2.0	83617	4	US-09-949-016-12254	Sequence 12254, A
c1053	33.8	2.0	87870	4	US-09-949-016-14461	Sequence 14461, A
c1054	33.8	2.0	124700	4	US-09-949-016-11817	Sequence 11817, A
c1055	33.8	2.0	124701	4	US-09-949-016-15439	Sequence 15439, A
c1056	33.8	2.0	129778	4	US-09-949-016-12191	Sequence 12191, A
c1057	33.8	2.0	129778	4	US-09-949-016-17075	Sequence 17075, A
1058	33.8	2.0	139936	4	US-09-949-016-11782	Sequence 11782, A
1059	33.8	2.0	139952	4	US-09-949-016-13280	Sequence 13280, A
1060	33.8	2.0	148794	4	US-09-949-016-12751	Sequence 12751, A
c1061	33.8	2.0	162450	3	US-09-345-882-1	Sequence 1, Appli
1062	33.8	2.0	228896	4	US-09-949-016-17127	Sequence 17127, A
c1063	33.8	2.0	246444	4	US-09-949-016-13113	Sequence 13113, A
c1064	33.8	2.0	254405	4	US-09-949-016-14381	Sequence 14381, A
1065	33.8	2.0	276687	4	US-09-949-016-13840	Sequence 13840, A
c1066	33.8	2.0	288031	4	US-09-949-016-14864	Sequence 14864, A
1067	33.8	2.0	340380	4	US-09-949-016-14179	Sequence 14179, A
c1068	33.8	2.0	422592	4	US-09-949-016-14182	Sequence 14182, A
c1069	33.6	2.0	150	3	US-08-888-077A-38	Sequence 38, Appl
c1070	33.6	2.0	338	2	US-08-454-557C-97	Sequence 97, Appl
c1071	33.6	2.0	338	2	US-08-340-426D-97	Sequence 97, Appl
c1072	33.6	2.0	338	2	US-08-450-673C-97	Sequence 97, Appl
c1073	33.6	2.0	338	5	PCT-US95-17111A-97	Sequence 97, Appl
c1074	33.6	2.0	369	4	US-09-513-999C-28872	Sequence 28872, A
1075	33.6	2.0	432	4	US-09-513-999C-9213	Sequence 9213, Ap
c1076	33.6	2.0	601	4	US-09-949-016-22873	Sequence 22873, A
c1077	33.6	2.0	601	4	US-09-949-016-22875	Sequence 22875, A
1078	33.6	2.0	601	4	US-09-949-016-87565	Sequence 87565, A
1079	33.6	2.0	601	4	US-09-949-016-87566	Sequence 87566, A
1080	33.6	2.0	601	4	US-09-949-016-87567	Sequence 87567, A
c1081	33.6	2.0	601	4	US-09-949-016-95236	Sequence 95236, A
c1082	33.6	2.0	601	4	US-09-949-016-95414	Sequence 95414, A
c1083	33.6	2.0	601	4	US-09-949-016-95592	Sequence 95592, A
c1084	33.6	2.0	601	4	US-09-949-016-95770	Sequence 95770, A
c1085	33.6	2.0	601	4	US-09-949-016-126600	Sequence 126600,
c1086	33.6	2.0	601	4	US-09-949-016-126602	Sequence 126602,
c1087	33.6	2.0	601	4	US-09-949-016-126603	Sequence 126603,
c1088	33.6	2.0	601	4	US-09-949-016-161553	Sequence 161553,
c1089	33.6	2.0	601	4	US-09-949-016-191529	Sequence 191529,
c1090	33.6	2.0	601	4	US-09-949-016-191707	Sequence 191707,
c1091	33.6	2.0	601	4	US-09-949-016-191885	Sequence 191885,
c1092	33.6	2.0	601	4	US-09-949-016-192063	Sequence 192063,
1093	33.6	2.0	981	4	US-09-552-619-5	Sequence 5, Appli
1094	33.6	2.0	1019	3	US-09-177-650-128	Sequence 128, App
1095	33.6	2.0	1166	3	US-09-072-596-323	Sequence 323, App
1096	33.6	2.0	1166	4	US-09-072-967-328	Sequence 328, App
1097	33.6	2.0	1570	3	US-08-617-860B-20	Sequence 20, Appl
c1098	33.6	2.0	2202	3	US-09-388-743-1	Sequence 1, Appli
c1099	33.6	2.0	2202	4	US-10-044-543-1	Sequence 1, Appli
c1100	33.6	2.0	3016	4	US-09-270-767-9898	Sequence 9898, Ap
c1101	33.6	2.0	3303	1	US-08-081-610-3	Sequence 3, Appli
1102	33.6	2.0	7404	4	US-09-902-540-3115	Sequence 3115, Ap
c1103	33.6	2.0	18809	4	US-09-902-540-1141	Sequence 1141, Ap
c1104	33.6	2.0	27056	4	US-09-949-016-12200	Sequence 12200, A
c1105	33.6	2.0	27057	4	US-09-949-016-13115	Sequence 13115, A
1106	33.6	2.0	38326	4	US-09-949-016-15843	Sequence 15843, A
c1107	33.6	2.0	44947	4	US-09-949-016-12018	Sequence 12018, A
c1108	33.6	2.0	44947	4	US-09-949-016-13101	Sequence 13101, A
c1109	33.6	2.0	49144	4	US-09-949-016-15343	Sequence 15343, A
1110	33.6	2.0	49559	4	US-09-949-016-12892	Sequence 12892, A
1111	33.6	2.0	49559	4	US-09-949-016-17267	Sequence 17267, A
1112	33.6	2.0	71119	4	US-09-949-016-15358	Sequence 15358, A
1113	33.6	2.0	95109	4	US-09-949-016-16027	Sequence 16027, A
c1114	33.6	2.0	98962	4	US-09-949-016-14133	Sequence 14133, A
c1115	33.6	2.0	102884	4	US-09-949-016-17100	Sequence 17100, A
1116	33.6	2.0	112874	4	US-09-949-016-13180	Sequence 13180, A
1117	33.6	2.0	116652	4	US-09-949-016-13413	Sequence 13413, A
c1118	33.6	2.0	136264	4	US-09-949-016-12756	Sequence 12756, A
c1119	33.6	2.0	136265	4	US-09-949-016-13001	Sequence 13001, A
1120	33.6	2.0	151088	4	US-09-949-016-16240	Sequence 16240, A
1121	33.6	2.0	152331	3	US-09-128-155-16	Sequence 16, Appl
1122	33.6	2.0	176373	3	US-09-128-155-17	Sequence 17, Appl

1123	33.6	2.0	192956	4	US-09-949-016-14382	Sequence 14382, A
c1124	33.6	2.0	203475	4	US-09-949-016-14516	Sequence 14516, A
c1125	33.6	2.0	203475	4	US-09-949-016-14517	Sequence 14517, A
c1126	33.6	2.0	203475	4	US-09-949-016-14518	Sequence 14518, A
c1127	33.6	2.0	203475	4	US-09-949-016-14519	Sequence 14519, A
c1128	33.6	2.0	203475	4	US-09-949-016-17226	Sequence 17226, A
c1129	33.6	2.0	203475	4	US-09-949-016-17227	Sequence 17227, A
c1130	33.6	2.0	203475	4	US-09-949-016-17228	Sequence 17228, A
c1131	33.6	2.0	203475	4	US-09-949-016-17229	Sequence 17229, A
1132	33.6	2.0	276237	4	US-09-949-016-17504	Sequence 17504, A
1133	33.6	2.0	450395	4	US-09-949-016-15473	Sequence 15473, A
c1134	33.6	2.0	784019	4	US-09-949-016-14033	Sequence 14033, A
c1135	33.6	2.0	828152	4	US-09-949-016-12777	Sequence 12777, A
c1136	33.4	2.0	78	2	US-08-588-983-24	Sequence 24, Appl
c1137	33.4	2.0	78	2	US-08-588-976-24	Sequence 24, Appl
c1138	33.4	2.0	475	3	US-09-328-111-263	Sequence 263, App
c1139	33.4	2.0	601	4	US-09-949-016-35318	Sequence 35318, A
c1140	33.4	2.0	601	4	US-09-949-016-44527	Sequence 44527, A
1141	33.4	2.0	601	4	US-09-949-016-76326	Sequence 76326, A
c1142	33.4	2.0	601	4	US-09-949-016-89942	Sequence 89942, A
1143	33.4	2.0	601	4	US-09-949-016-127053	Sequence 127053,
1144	33.4	2.0	601	4	US-09-949-016-127057	Sequence 127057,
c1145	33.4	2.0	601	4	US-09-949-016-127200	Sequence 127200,
c1146	33.4	2.0	601	4	US-09-949-016-131419	Sequence 131419,
1147	33.4	2.0	601	4	US-09-949-016-138885	Sequence 138885,
1148	33.4	2.0	601	4	US-09-949-016-138886	Sequence 138886,
1149	33.4	2.0	601	4	US-09-949-016-138887	Sequence 138887,
c1150	33.4	2.0	601	4	US-09-949-016-168155	Sequence 168155,
c1151	33.4	2.0	601	4	US-09-949-016-188218	Sequence 188218,
1152	33.4	2.0	699	1	US-08-463-115-65	Sequence 65, Appl
1153	33.4	2.0	699	1	US-08-465-388-65	Sequence 65, Appl
c1154	33.4	2.0	1910	3	US-09-310-463-13	Sequence 13, Appl
c1155	33.4	2.0	1910	3	US-08-842-248A-13	Sequence 13, Appl
c1156	33.4	2.0	1910	4	US-09-949-016-894	Sequence 894, App
c1157	33.4	2.0	2446	3	US-09-310-463-11	Sequence 11, Appl
c1158	33.4	2.0	2446	3	US-08-842-248A-11	Sequence 11, Appl
1159	33.4	2.0	4315	4	US-09-444-905-1	Sequence 1, Appli
c1160	33.4	2.0	5482	4	US-09-949-016-14318	Sequence 14318, A
c1161	33.4	2.0	7605	3	US-09-417-455-8	Sequence 8, Appli
c1162	33.4	2.0	7605	3	US-09-348-942-8	Sequence 8, Appli
c1163	33.4	2.0	7605	3	US-09-457-626-8	Sequence 8, Appli
c1164	33.4	2.0	7605	4	US-09-576-008-8	Sequence 8, Appli
1165	33.4	2.0	9578	4	US-09-949-016-17106	Sequence 17106, A
c1166	33.4	2.0	11428	4	US-09-949-016-12636	Sequence 12636, A
1167	33.4	2.0	12141	3	US-09-488-671-10	Sequence 10, Appl
1168	33.4	2.0	13823	4	US-09-949-016-15942	Sequence 15942, A
1169	33.4	2.0	14516	4	US-09-949-016-17047	Sequence 17047, A
c1170	33.4	2.0	14554	4	US-09-949-016-15908	Sequence 15908, A
1171	33.4	2.0	15907	4	US-09-949-016-16818	Sequence 16818, A
1172	33.4	2.0	23381	4	US-09-949-016-13962	Sequence 13962, A
1173	33.4	2.0	24984	4	US-09-949-016-14950	Sequence 14950, A
c1174	33.4	2.0	27794	4	US-09-949-016-15133	Sequence 15133, A
c1175	33.4	2.0	36791	4	US-09-949-016-16390	Sequence 16390, A
c1176	33.4	2.0	36791	4	US-09-949-016-16391	Sequence 16391, A
1177	33.4	2.0	41243	4	US-09-949-016-13006	Sequence 13006, A
c1178	33.4	2.0	42479	4	US-09-949-016-16631	Sequence 16631, A
c1179	33.4	2.0	42479	4	US-09-949-016-16632	Sequence 16632, A
c1180	33.4	2.0	43576	4	US-09-949-016-15364	Sequence 15364, A
c1181	33.4	2.0	43577	4	US-09-949-016-12183	Sequence 12183, A
1182	33.4	2.0	44120	4	US-09-949-016-12632	Sequence 12632, A
1183	33.4	2.0	44353	4	US-09-949-016-15302	Sequence 15302, A
1184	33.4	2.0	60785	4	US-09-949-016-12774	Sequence 12774, A
1185	33.4	2.0	60785	4	US-09-949-016-15665	Sequence 15665, A
1186	33.4	2.0	62072	4	US-09-949-016-16076	Sequence 16076, A
1187	33.4	2.0	72549	4	US-09-949-016-16477	Sequence 16477, A
1188	33.4	2.0	91559	4	US-09-949-016-12581	Sequence 12581, A
1189	33.4	2.0	91559	4	US-09-949-016-13701	Sequence 13701, A
1190	33.4	2.0	108341	4	US-09-949-016-16621	Sequence 16621, A
1191	33.4	2.0	113379	4	US-09-949-016-17561	Sequence 17561, A
1192	33.4	2.0	113379	4	US-09-949-016-17562	Sequence 17562, A
1193	33.4	2.0	150394	4	US-09-949-016-13042	Sequence 13042, A
c1194	33.4	2.0	212449	4	US-09-949-016-15419	Sequence 15419, A
1195	33.4	2.0	232547	4	US-09-949-016-16603	Sequence 16603, A
c1196	33.4	2.0	283538	4	US-09-949-016-13506	Sequence 13506, A
1197	33.2	2.0	165	4	US-09-636-215-736	Sequence 736, App
1198	33.2	2.0	165	4	US-09-685-166A-736	Sequence 736, App
1199	33.2	2.0	165	4	US-09-679-426-736	Sequence 736, App
1200	33.2	2.0	165	4	US-09-759-143-736	Sequence 736, App
1201	33.2	2.0	165	4	US-09-651-236-736	Sequence 736, App
c1202	33.2	2.0	446	2	US-08-332-766A-26	Sequence 26, Appl
c1203	33.2	2.0	462	4	US-09-107-532A-1349	Sequence 1349, Ap
c1204	33.2	2.0	601	4	US-09-949-016-45416	Sequence 45416, A
c1205	33.2	2.0	601	4	US-09-949-016-45417	Sequence 45417, A
1206	33.2	2.0	601	4	US-09-949-016-87564	Sequence 87564, A
c1207	33.2	2.0	601	4	US-09-949-016-116679	Sequence 116679,
c1208	33.2	2.0	601	4	US-09-949-016-184837	Sequence 184837,
c1209	33.2	2.0	601	4	US-09-949-016-184992	Sequence 184992,
c1210	33.2	2.0	601	4	US-09-949-016-202119	Sequence 202119,
c1211	33.2	2.0	601	4	US-09-949-016-203128	Sequence 203128,
c1212	33.2	2.0	601	4	US-09-949-016-203170	Sequence 203170,
c1213	33.2	2.0	955	3	US-09-641-638-2	Sequence 2, Appli
c1214	33.2	2.0	955	3	US-09-641-638-3	Sequence 3, Appli
c1215	33.2	2.0	955	3	US-09-641-638-4	Sequence 4, Appli
c1216	33.2	2.0	955	3	US-09-641-638-5	Sequence 5, Appli
c1217	33.2	2.0	955	3	US-09-641-638-6	Sequence 6, Appli
c1218	33.2	2.0	955	3	US-09-641-638-7	Sequence 7, Appli
c1219	33.2	2.0	955	4	US-10-170-097-2	Sequence 2, Appli
c1220	33.2	2.0	955	4	US-10-170-097-3	Sequence 3, Appli
c1221	33.2	2.0	955	4	US-10-170-097-4	Sequence 4, Appli
c1222	33.2	2.0	955	4	US-10-170-097-5	Sequence 5, Appli
c1223	33.2	2.0	955	4	US-10-170-097-6	Sequence 6, Appli
c1224	33.2	2.0	955	4	US-10-170-097-7	Sequence 7, Appli
c1225	33.2	2.0	1816	4	US-09-762-258-1	Sequence 1, Appli
1226	33.2	2.0	4545	4	US-09-569-852B-5	Sequence 5, Appli
c1227	33.2	2.0	8100	4	US-09-949-016-13460	Sequence 13460, A
c1228	33.2	2.0	8100	4	US-09-949-016-13461	Sequence 13461, A
c1229	33.2	2.0	8552	4	US-09-949-016-14227	Sequence 14227, A
1230	33.2	2.0	8815	4	US-09-687-731-12	Sequence 12, Appl
c1231	33.2	2.0	10952	1	US-08-602-036A-1	Sequence 1, Appli
c1232	33.2	2.0	10952	2	US-08-502-374A-1	Sequence 1, Appli
c1233	33.2	2.0	10952	2	US-08-642-407A-1	Sequence 1, Appli
c1234	33.2	2.0	11378	4	US-09-949-016-13815	Sequence 13815, A
1235	33.2	2.0	14097	4	US-09-949-016-13661	Sequence 13661, A
1236	33.2	2.0	15252	4	US-09-949-016-13584	Sequence 13584, A
1237	33.2	2.0	16802	4	US-09-949-016-12622	Sequence 12622, A
1238	33.2	2.0	20966	4	US-09-776-976-7	Sequence 7, Appli
1239	33.2	2.0	20966	4	US-09-909-547-7	Sequence 7, Appli
1240	33.2	2.0	20966	4	US-09-569-852B-1	Sequence 1, Appli
c1241	33.2	2.0	26845	4	US-09-949-016-11815	Sequence 11815, A
c1242	33.2	2.0	27132	4	US-09-949-016-15424	Sequence 15424, A
c1243	33.2	2.0	43069	4	US-09-292-542A-1	Sequence 1, Appli
c1244	33.2	2.0	50850	4	US-09-949-016-15083	Sequence 15083, A
c1245	33.2	2.0	50850	4	US-09-949-016-15084	Sequence 15084, A
c1246	33.2	2.0	50850	4	US-09-949-016-15085	Sequence 15085, A
c1247	33.2	2.0	76247	4	US-09-949-016-16136	Sequence 16136, A
c1248	33.2	2.0	87648	4	US-09-949-016-13655	Sequence 13655, A
c1249	33.2	2.0	87752	4	US-09-949-016-16807	Sequence 16807, A
1250	33.2	2.0	99580	4	US-09-949-016-17411	Sequence 17411, A
1251	33.2	2.0	113966	4	US-09-949-016-12277	Sequence 12277, A
1252	33.2	2.0	113967	4	US-09-949-016-17051	Sequence 17051, A
1253	33.2	2.0	167708	4	US-09-949-016-16423	Sequence 16423, A
1254	33.2	2.0	178883	4	US-09-949-016-12733	Sequence 12733, A
1255	33.2	2.0	178884	4	US-09-949-016-13039	Sequence 13039, A
1256	33.2	2.0	237863	4	US-09-949-016-13404	Sequence 13404, A
1257	33.2	2.0	253345	4	US-09-949-016-12656	Sequence 12656, A
1258	33.2	2.0	253364	4	US-09-949-016-13639	Sequence 13639, A
c1259	33.2	2.0	363032	4	US-09-949-016-12415	Sequence 12415, A
c1260	33.2	2.0	363033	4	US-09-949-016-15754	Sequence 15754, A
c1261	33	1.9	145	4	US-09-513-999C-23977	Sequence 23977, A
c1262	33	1.9	261	4	US-09-134-000C-468	Sequence 468, App
c1263	33	1.9	263	4	US-09-513-999C-14228	Sequence 14228, A
c1264	33	1.9	329	1	US-08-253-155A-23	Sequence 23, Appl
1265	33	1.9	505	4	US-09-621-976-15639	Sequence 15639, A
1266	33	1.9	507	4	US-09-401-064-162	Sequence 162, App
1267	33	1.9	601	4	US-09-949-016-26670	Sequence 26670, A
1268	33	1.9	601	4	US-09-949-016-44248	Sequence 44248, A

1269	33	1.9	601	4	US-09-949-016-45927	Sequence 45927, A
c1270	33	1.9	601	4	US-09-949-016-55741	Sequence 55741, A
c1271	33	1.9	601	4	US-09-949-016-113840	Sequence 113840,
c1272	33	1.9	601	4	US-09-949-016-114008	Sequence 114008,
c1273	33	1.9	601	4	US-09-949-016-114176	Sequence 114176,
c1274	33	1.9	601	4	US-09-949-016-114344	Sequence 114344,
c1275	33	1.9	601	4	US-09-949-016-114512	Sequence 114512,
c1276	33	1.9	601	4	US-09-949-016-114680	Sequence 114680,
c1277	33	1.9	601	4	US-09-949-016-114848	Sequence 114848,
c1278	33	1.9	601	4	US-09-949-016-115016	Sequence 115016,
1279	33	1.9	601	4	US-09-949-016-138888	Sequence 138888,
1280	33	1.9	601	4	US-09-949-016-138889	Sequence 138889,
1281	33	1.9	601	4	US-09-949-016-149723	Sequence 149723,
1282	33	1.9	1107	3	US-09-173-300-50	Sequence 50, Appl
1283	33	1.9	1107	4	US-10-027-450-50	Sequence 50, Appl
c1284	33	1.9	1211	4	US-09-023-655-793	Sequence 793, App
c1285	33	1.9	1906	3	US-09-031-962D-5	Sequence 5, Appli
1286	33	1.9	1923	4	US-09-134-000C-466	Sequence 466, App
c1287	33	1.9	1970	4	US-09-621-781B-1	Sequence 1, Appli
1288	33	1.9	2133	3	US-09-187-124-1	Sequence 1, Appli
1289	33	1.9	2133	4	US-09-850-936-1	Sequence 1, Appli
1290	33	1.9	3936	4	US-09-919-172-49	Sequence 49, Appl
1291	33	1.9	6727	3	US-08-629-643A-5	Sequence 5, Appli
1292	33	1.9	6727	3	US-09-280-799-1	Sequence 1, Appli
1293	33	1.9	6727	3	US-09-155-884-5	Sequence 5, Appli
c1294	33	1.9	8625	4	US-09-949-016-16566	Sequence 16566, A
1295	33	1.9	13158	2	US-08-687-080-105	Sequence 105, App
c1296	33	1.9	15632	4	US-09-949-016-15119	Sequence 15119, A
c1297	33	1.9	23902	4	US-09-949-016-14220	Sequence 14220, A
1298	33	1.9	39686	4	US-09-949-016-13633	Sequence 13633, A
1299	33	1.9	41182	4	US-09-949-016-17457	Sequence 17457, A
1300	33	1.9	49487	4	US-09-949-016-11770	Sequence 11770, A
1301	33	1.9	50383	4	US-09-949-016-17600	Sequence 17600, A
1302	33	1.9	51508	4	US-09-949-016-16681	Sequence 16681, A
c1303	33	1.9	51671	4	US-09-949-016-12068	Sequence 12068, A
c1304	33	1.9	51671	4	US-09-949-016-15962	Sequence 15962, A
c1305	33	1.9	57218	4	US-09-949-016-16512	Sequence 16512, A
1306	33	1.9	61158	4	US-09-949-016-15041	Sequence 15041, A
c1307	33	1.9	65966	4	US-09-949-016-17152	Sequence 17152, A
1308	33	1.9	75431	4	US-09-949-016-15122	Sequence 15122, A
1309	33	1.9	90541	4	US-09-759-359A-3	Sequence 3, Appli
1310	33	1.9	90541	4	US-10-207-973-3	Sequence 3, Appli
1311	33	1.9	92387	4	US-09-949-016-14563	Sequence 14563, A
c1312	33	1.9	93778	4	US-09-949-016-15096	Sequence 15096, A
1313	33	1.9	146307	4	US-09-949-016-14881	Sequence 14881, A
1314	33	1.9	146307	4	US-09-949-016-14882	Sequence 14882, A
1315	33	1.9	146307	4	US-09-949-016-14883	Sequence 14883, A
1316	33	1.9	146307	4	US-09-949-016-14884	Sequence 14884, A
1317	33	1.9	146307	4	US-09-949-016-14885	Sequence 14885, A
1318	33	1.9	146307	4	US-09-949-016-14886	Sequence 14886, A
1319	33	1.9	146307	4	US-09-949-016-14887	Sequence 14887, A
1320	33	1.9	146307	4	US-09-949-016-14888	Sequence 14888, A
1321	33	1.9	148405	4	US-09-949-016-11747	Sequence 11747, A
1322	33	1.9	148405	4	US-09-949-016-12835	Sequence 12835, A
1323	33	1.9	148405	4	US-09-949-016-12836	Sequence 12836, A
1324	33	1.9	148405	4	US-09-949-016-12837	Sequence 12837, A
1325	33	1.9	177669	4	US-09-949-016-13713	Sequence 13713, A
1326	33	1.9	187136	4	US-09-949-016-17231	Sequence 17231, A
c1327	33	1.9	194915	4	US-09-949-016-15584	Sequence 15584, A
1328	33	1.9	227390	4	US-09-949-016-12201	Sequence 12201, A
1329	33	1.9	227391	4	US-09-949-016-13365	Sequence 13365, A
c1330	33	1.9	236341	4	US-09-949-016-13978	Sequence 13978, A
c1331	33	1.9	263693	4	US-09-949-016-12386	Sequence 12386, A
c1332	33	1.9	263694	4	US-09-949-016-16915	Sequence 16915, A
c1333	33	1.9	278866	4	US-09-949-016-13922	Sequence 13922, A
c1334	33	1.9	278866	4	US-09-949-016-13923	Sequence 13923, A
c1335	33	1.9	278866	4	US-09-949-016-13924	Sequence 13924, A
c1336	33	1.9	278866	4	US-09-949-016-13925	Sequence 13925, A
c1337	33	1.9	278866	4	US-09-949-016-13926	Sequence 13926, A
c1338	33	1.9	278866	4	US-09-949-016-14699	Sequence 14699, A
c1339	33	1.9	278866	4	US-09-949-016-14700	Sequence 14700, A
c1340	33	1.9	278866	4	US-09-949-016-14701	Sequence 14701, A
c1341	33	1.9	278866	4	US-09-949-016-14702	Sequence 14702, A
c1342	33	1.9	278866	4	US-09-949-016-14703	Sequence 14703, A
1343	32.8	1.9	244	4	US-09-513-999C-8694	Sequence 8694, Ap
c1344	32.8	1.9	418	4	US-09-452-937A-5	Sequence 5, Appli
c1345	32.8	1.9	601	4	US-09-949-016-134111	Sequence 134111,
1346	32.8	1.9	601	4	US-09-949-016-168063	Sequence 168063,
1347	32.8	1.9	601	4	US-09-949-016-168064	Sequence 168064,
1348	32.8	1.9	601	4	US-09-949-016-195979	Sequence 195979,
c1349	32.8	1.9	842	4	US-09-452-937A-17	Sequence 17, Appl
c1350	32.8	1.9	2318	4	US-09-949-016-4687	Sequence 4687, Ap
c1351	32.8	1.9	2561	3	US-09-146-221-7	Sequence 7, Appli
1352	32.8	1.9	6426	4	US-09-976-594-136	Sequence 136, App
1353	32.8	1.9	6822	3	US-09-426-998-3	Sequence 3, Appli
1354	32.8	1.9	7405	4	US-09-949-016-3859	Sequence 3859, Ap
1355	32.8	1.9	7741	3	US-09-426-998-4	Sequence 4, Appli
c1356	32.8	1.9	12880	4	US-09-949-016-16733	Sequence 16733, A
1357	32.8	1.9	13118	4	US-09-949-016-14721	Sequence 14721, A
1358	32.8	1.9	13648	4	US-09-949-016-12470	Sequence 12470, A
1359	32.8	1.9	15141	4	US-09-949-016-14869	Sequence 14869, A
c1360	32.8	1.9	15652	3	US-09-422-936-60	Sequence 60, Appl
1361	32.8	1.9	15766	3	US-09-338-907-73	Sequence 73, Appl
1362	32.8	1.9	15766	3	US-09-218-207-73	Sequence 73, Appl
1363	32.8	1.9	17514	4	US-09-949-016-13121	Sequence 13121, A
1364	32.8	1.9	17740	4	US-09-949-016-13086	Sequence 13086, A
1365	32.8	1.9	18722	4	US-09-949-016-15892	Sequence 15892, A
1366	32.8	1.9	24656	4	US-09-949-016-15575	Sequence 15575, A
c1367	32.8	1.9	30054	4	US-09-949-016-16429	Sequence 16429, A
c1368	32.8	1.9	35122	4	US-09-949-016-11873	Sequence 11873, A
1369	32.8	1.9	37950	3	US-09-338-907-183	Sequence 183, App
1370	32.8	1.9	37950	3	US-09-218-207-183	Sequence 183, App
1371	32.8	1.9	45862	4	US-09-949-016-13928	Sequence 13928, A
c1372	32.8	1.9	57859	4	US-09-949-016-12334	Sequence 12334, A
c1373	32.8	1.9	57859	4	US-09-949-016-14657	Sequence 14657, A
c1374	32.8	1.9	57859	4	US-09-949-016-14658	Sequence 14658, A
1375	32.8	1.9	80717	4	US-09-949-016-14968	Sequence 14968, A
1376	32.8	1.9	133719	4	US-09-949-016-15092	Sequence 15092, A
c1377	32.8	1.9	141560	4	US-09-949-016-16476	Sequence 16476, A
1378	32.8	1.9	162465	4	US-09-949-016-14264	Sequence 14264, A
c1379	32.8	1.9	221958	4	US-09-949-016-12173	Sequence 12173, A
c1380	32.8	1.9	221966	4	US-09-949-016-15498	Sequence 15498, A
c1381	32.8	1.9	251769	4	US-09-949-016-13185	Sequence 13185, A
c1382	32.8	1.9	251769	4	US-09-949-016-13186	Sequence 13186, A
c1383	32.8	1.9	266748	4	US-09-949-016-13187	Sequence 13187, A
c1384	32.8	1.9	266748	4	US-09-949-016-13188	Sequence 13188, A
c1385	32.6	1.9	248	3	US-09-007-005-32	Sequence 32, Appl
c1386	32.6	1.9	248	3	US-09-244-796-32	Sequence 32, Appl
c1387	32.6	1.9	277	3	US-09-007-005-3	Sequence 3, Appli
c1388	32.6	1.9	277	3	US-09-244-796-3	Sequence 3, Appli
1389	32.6	1.9	430	4	US-09-621-976-16656	Sequence 16656, A
1390	32.6	1.9	438	4	US-09-252-991A-8422	Sequence 8422, Ap
1391	32.6	1.9	474	4	US-09-252-991A-8385	Sequence 8385, Ap
c1392	32.6	1.9	533	3	US-09-171-209-80	Sequence 80, Appl
1393	32.6	1.9	601	4	US-09-949-016-51960	Sequence 51960, A
1394	32.6	1.9	601	4	US-09-949-016-61193	Sequence 61193, A
c1395	32.6	1.9	601	4	US-09-949-016-88251	Sequence 88251, A
1396	32.6	1.9	601	4	US-09-949-016-122626	Sequence 122626,
1397	32.6	1.9	601	4	US-09-949-016-122627	Sequence 122627,
c1398	32.6	1.9	601	4	US-09-949-016-169069	Sequence 169069,
1399	32.6	1.9	601	4	US-09-949-016-169255	Sequence 169255,
c1400	32.6	1.9	601	4	US-09-949-016-206932	Sequence 206932,
c1401	32.6	1.9	713	4	US-09-328-475C-260	Sequence 260, App
1402	32.6	1.9	957	4	US-09-328-475C-6	Sequence 6, Appli
c1403	32.6	1.9	1406	4	US-10-101-464A-964	Sequence 964, App
1404	32.6	1.9	1425	3	US-09-134-001C-2116	Sequence 2116, Ap
c1405	32.6	1.9	1533	4	US-09-759-143-908	Sequence 908, App
c1406	32.6	1.9	1536	4	US-09-759-143-907	Sequence 907, App
c1407	32.6	1.9	1623	3	US-09-621-451-1	Sequence 1, Appli
c1408	32.6	1.9	1623	4	US-10-223-355-1	Sequence 1, Appli
c1409	32.6	1.9	1623	4	US-09-621-448-1	Sequence 1, Appli
c1410	32.6	1.9	1761	4	US-09-252-991A-8423	Sequence 8423, Ap
c1411	32.6	1.9	2218	4	US-09-350-457A-1	Sequence 1, Appli
c1412	32.6	1.9	5581	3	US-08-973-544-1	Sequence 1, Appli
c1413	32.6	1.9	10713	4	US-09-949-016-15928	Sequence 15928, A
1414	32.6	1.9	12073	4	US-09-949-016-14924	Sequence 14924, A

1415	32.6	1.9	12176	4	US-09-949-016-3651	Sequence 3651, Ap
1416	32.6	1.9	12368	4	US-09-949-016-13243	Sequence 13243, A
1417	32.6	1.9	19296	4	US-09-949-016-16393	Sequence 16393, A
1418	32.6	1.9	34741	4	US-09-949-016-12475	Sequence 12475, A
1419	32.6	1.9	34745	4	US-09-949-016-16024	Sequence 16024, A
1420	32.6	1.9	41522	4	US-09-949-016-11932	Sequence 11932, A
1421	32.6	1.9	41523	4	US-09-949-016-15764	Sequence 15764, A
1422	32.6	1.9	60465	4	US-09-949-016-15995	Sequence 15995, A
c1423	32.6	1.9	61124	4	US-09-949-016-11914	Sequence 11914, A
c1424	32.6	1.9	61140	4	US-09-949-016-15771	Sequence 15771, A
c1425	32.6	1.9	63804	4	US-09-949-016-15200	Sequence 15200, A
c1426	32.6	1.9	76124	4	US-09-949-016-15976	Sequence 15976, A
c1427	32.6	1.9	96327	4	US-09-949-016-16541	Sequence 16541, A
1428	32.6	1.9	101300	4	US-09-949-016-16108	Sequence 16108, A
1429	32.6	1.9	109690	4	US-09-949-016-13525	Sequence 13525, A
1430	32.6	1.9	115814	4	US-09-949-016-16205	Sequence 16205, A
c1431	32.6	1.9	124480	4	US-09-949-016-15921	Sequence 15921, A
c1432	32.6	1.9	141248	4	US-09-949-016-12241	Sequence 12241, A
c1433	32.6	1.9	143248	4	US-09-949-016-16652	Sequence 16652, A
1434	32.6	1.9	145928	4	US-09-949-016-15444	Sequence 15444, A
c1435	32.6	1.9	161900	4	US-09-949-016-12685	Sequence 12685, A
c1436	32.6	1.9	161914	4	US-09-949-016-12906	Sequence 12906, A
c1437	32.6	1.9	174639	4	US-09-949-016-16509	Sequence 16509, A
1438	32.6	1.9	176006	4	US-09-949-016-16804	Sequence 16804, A
1439	32.6	1.9	194790	4	US-09-949-016-15393	Sequence 15393, A
1440	32.6	1.9	253375	4	US-09-949-016-12849	Sequence 12849, A
c1441	32.6	1.9	670689	4	US-09-949-016-12505	Sequence 12505, A
c1442	32.6	1.9	670690	4	US-09-949-016-14207	Sequence 14207, A
1443	32.6	1.9	784019	4	US-09-949-016-14033	Sequence 14033, A
1444	32.6	1.9	828152	4	US-09-949-016-12777	Sequence 12777, A
1445	32.4	1.9	68	4	US-09-513-999C-21471	Sequence 21471, A
1446	32.4	1.9	181	4	US-09-354-147C-32	Sequence 32, Appl
c1447	32.4	1.9	601	4	US-09-949-016-20387	Sequence 20387, A
c1448	32.4	1.9	601	4	US-09-949-016-20388	Sequence 20388, A
c1449	32.4	1.9	601	4	US-09-949-016-20389	Sequence 20389, A
1450	32.4	1.9	601	4	US-09-949-016-26669	Sequence 26669, A
1451	32.4	1.9	601	4	US-09-949-016-26671	Sequence 26671, A
1452	32.4	1.9	601	4	US-09-949-016-53714	Sequence 53714, A
c1453	32.4	1.9	601	4	US-09-949-016-89018	Sequence 89018, A
1454	32.4	1.9	601	4	US-09-949-016-95236	Sequence 95236, A
1455	32.4	1.9	601	4	US-09-949-016-95414	Sequence 95414, A
1456	32.4	1.9	601	4	US-09-949-016-95592	Sequence 95592, A
1457	32.4	1.9	601	4	US-09-949-016-95770	Sequence 95770, A
c1458	32.4	1.9	601	4	US-09-949-016-111594	Sequence 111594,
c1459	32.4	1.9	601	4	US-09-949-016-111742	Sequence 111742,
c1460	32.4	1.9	601	4	US-09-949-016-111888	Sequence 111888,
c1461	32.4	1.9	601	4	US-09-949-016-112033	Sequence 112033,
1462	32.4	1.9	601	4	US-09-949-016-149722	Sequence 149722,
1463	32.4	1.9	601	4	US-09-949-016-149724	Sequence 149724,
c1464	32.4	1.9	601	4	US-09-949-016-161552	Sequence 161552,
c1465	32.4	1.9	601	4	US-09-949-016-166474	Sequence 166474,
c1466	32.4	1.9	601	4	US-09-949-016-166475	Sequence 166475,
c1467	32.4	1.9	601	4	US-09-949-016-166476	Sequence 166476,
1468	32.4	1.9	601	4	US-09-949-016-171902	Sequence 171902,
c1469	32.4	1.9	601	4	US-09-949-016-175742	Sequence 175742,
c1470	32.4	1.9	601	4	US-09-949-016-175744	Sequence 175744,
c1471	32.4	1.9	601	4	US-09-949-016-175745	Sequence 175745,
c1472	32.4	1.9	601	4	US-09-949-016-175747	Sequence 175747,
c1473	32.4	1.9	601	4	US-09-949-016-175748	Sequence 175748,
c1474	32.4	1.9	601	4	US-09-949-016-175749	Sequence 175749,
1475	32.4	1.9	601	4	US-09-949-016-191529	Sequence 191529,
1476	32.4	1.9	601	4	US-09-949-016-191707	Sequence 191707,
1477	32.4	1.9	601	4	US-09-949-016-191885	Sequence 191885,
1478	32.4	1.9	601	4	US-09-949-016-192063	Sequence 192063,
c1479	32.4	1.9	1512	4	US-09-482-273-18	Sequence 18, Appl
1480	32.4	1.9	1750	4	US-09-668-097A-7	Sequence 7, Appli
1481	32.4	1.9	2448	4	US-09-949-016-4793	Sequence 4793, Ap
1482	32.4	1.9	17037	4	US-09-949-016-16535	Sequence 16535, A
c1483	32.4	1.9	30782	4	US-09-949-016-13724	Sequence 13724, A
1484	32.4	1.9	31074	4	US-09-949-016-12195	Sequence 12195, A
1485	32.4	1.9	31075	4	US-09-949-016-15951	Sequence 15951, A
c1486	32.4	1.9	31111	4	US-09-949-016-15628	Sequence 15628, A
c1487	32.4	1.9	56131	4	US-09-949-016-12944	Sequence 12944, A
1488	32.4	1.9	56551	4	US-09-949-016-12030	Sequence 12030, A
c1489	32.4	1.9	60002	4	US-09-949-016-12464	Sequence 12464, A
c1490	32.4	1.9	60003	4	US-09-949-016-13823	Sequence 13823, A
c1491	32.4	1.9	66213	4	US-09-949-016-11803	Sequence 11803, A
c1492	32.4	1.9	66213	4	US-09-949-016-16739	Sequence 16739, A
1493	32.4	1.9	68490	4	US-09-949-016-15849	Sequence 15849, A
1494	32.4	1.9	76221	4	US-09-949-016-12009	Sequence 12009, A
1495	32.4	1.9	76221	4	US-09-949-016-17053	Sequence 17053, A
c1496	32.4	1.9	76610	4	US-09-949-016-15521	Sequence 15521, A
c1497	32.4	1.9	87734	4	US-09-949-016-17521	Sequence 17521, A
c1498	32.4	1.9	106450	4	US-09-949-016-13873	Sequence 13873, A
c1499	32.4	1.9	110266	4	US-09-949-016-14913	Sequence 14913, A
c1500	32.4	1.9	110266	4	US-09-949-016-14914	Sequence 14914, A

ALIGNMENTS

RESULT 1
US-09-621-976-18060
; Sequence 18060, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18060
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18060

Query Match 30.7%; Score 522.2; DB 4; Length 552;
Best Local Similarity 98.6%; Pred. No. 2.8e-152;
Matches 547; Conservative 1; Mismatches 4; Indels 3; Gaps 2;

```
Qy      201 CTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTC 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCCCTGCACCCCTTC 60

Qy      261 CTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGA 320
            |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       61 CTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGA-GTGATTTGGATCCTGGCTGCAGA 119

Qy      321 TGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTA 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      120 TGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTCTTA 179

Qy      381 CCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATT 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 CCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATT 239

Qy      441 TGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTT 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 TGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTT 299

Qy      501 GGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGG 560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      300 GGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGG 359

Qy      561 TGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC 620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      360 TGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC 419

Qy      621 CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGT 680
            |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      420 CCCAGGKGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGT 479
```

```
Qy        681 ACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCT 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||  ||
Db        480 ACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCTCAGGG--CT 537

Qy        741 GGCTGTCCTGGGCAT 755
              ||||||||||||||||
Db        538 GGCTGTCCTGGGCAT 552


RESULT 2
US-09-313-294A-7148
; Sequence 7148, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ito, Laura Y.
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;  FILE REFERENCE:  PL-0017 US
;  CURRENT APPLICATION NUMBER: US/09/313,294A
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  7600
;  SOFTWARE:  PERL Program
; SEQ ID NO 7148
;   LENGTH: 297
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6476212 700381207H1
;   NAME/KEY: unsure
;   LOCATION: 2-3, 25, 40-41, 43-44, 52, 62, 69, 71, 77, 81, 93, 120, 192, 197, 200, 205
;   OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7148

  Query Match             13.1%;  Score 222.2;  DB 4;  Length 297;
  Best Local Similarity   87.9%;  Pred. No. 8.1e-59;
  Matches  261;  Conservative    0;  Mismatches   32;  Indels    4;  Gaps    3;

Qy        990 GCTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGT 1049
              |  |||||||||||||||||||| |||||||||||||  |  |||||| | ||||||
Db          1 GNNGGAAAAGCTTCAGGGGACATTNTTCTCCACAGAAGANNANNCCTCTAANCCTCTGGT 60

Qy       1050 ACAGAACT--ACCGAGCCCTTCAGCCTCTCAAT-CAGCGCATGGTCTTTGCTTCTTTCAT 1106
              | ||||||   |     | | ||||||||||| ||||||||||||||||||||||||
Db         61 ANAGAACTNANCGAGCNCTTNCAGCCTCTCAANCCAGCGCATGGTCTTTGCTTCTTTCAN 120

Qy       1107 CCAAGCAGGATCCTCGTATACCACAGGT-GAAATGCTGAGTCTAGGTGTAGGAATCTTGG 1165
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db         121 CCAAGCAGGATCCTCGTATACCACAGGTAGAAATGCTGAGTCTAGGTGTAGGAATCTTGG 180

Qy       1166 TTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGA 1225
              |||||||||| |||| || |||| |||| |||||||||||| ||||| ||||||||||
Db         181 TTGGCTGTCTCNGCCTNCTNCTGGNTGTTNATTTCATTGCTANAAAGANTCGGAAGAAGA 240

Qy       1226 GGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCAT 1282
              |||||||||| |||||| ||||||||| || |||||||||||||||||||| ||||
Db         241 GGCTGGAAAATCGAAAGNGTGTGGTCTACANCTCAGCACAAGCCACGACTGANGCAT 297


RESULT 3
US-08-276-919-1
; Sequence 1, Application US/08276919
; Patent No. 5589579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,919
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelligan, Mark C.
;      REGISTRATION NUMBER:  36,389
;      REFERENCE/DOCKET NUMBER:  B35792
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1104 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  32..1093
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  119..1093
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1013..1024
;      OTHER INFORMATION:  /note= "phosphorylation site
;      OTHER INFORMATION:  recognized by protein kinase C and other kinases"
US-08-276-919-1

  Query Match             12.6%;  Score 213.6;  DB 1;  Length 1104;
  Best Local Similarity   53.9%;  Pred. No. 8.8e-56;
  Matches  488;  Conservative    0;  Mismatches  409;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||    |  ||   |  || | |  |   || |  |||   |  ||
Db         37 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 96

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||     |||     | ||||| |||   || ||  ||||  || |
Db         97 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 156

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              |||  |       |||||   ||||||   |       ||||| ||||| ||  | || |
Db        157 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 216

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |   | |||| |   |  |  | ||  ||  ||| || ||  | | | |
Db        217 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 276

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   ||||  |||||||||||  ||||| | ||    ||||||||
Db        277 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 336

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |    || || |          ||    ||  | ||||| ||||||||||
Db        337 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 396

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |      |||     || || || |||     ||| | |  |  |       ||
Db        397 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 456

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
```

```
Db        457 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 516

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785

Db        517 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 573

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845

Db        574 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 633

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905

Db        634 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 693

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965

Db        694 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 753

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023

Db        754 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 813

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079

Db        814 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 873

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139

Db        874 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 933

Qy       1140 GCTGAG 1145

Db        934 TCTGGG 939

RESULT 4
US-08-776-088-1
; Sequence 1, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1104 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  32..1093
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  119..1093
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1013..1024
;      OTHER INFORMATION:  /note= "phosphorylation site
;      OTHER INFORMATION:  recognized by protein kinase C and other kina..."
US-08-776-088-1

  Query Match           12.6%;  Score 213.6;  DB 1;  Length 1104;
  Best Local Similarity  53.9%;  Pred. No. 8.8e-56;
  Matches  488;  Conservative    0;  Mismatches  409;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305

Db         37 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 96

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365

Db         97 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 156

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425

Db        157 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 216

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485

Db        217 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 276

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545

Db        277 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 336

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605

Db        337 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 396

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665

Db        397 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 456

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725

Db        457 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 516

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785

Db        517 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 573

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845

Db        574 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 633

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905

Db        634 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 693

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965

Db        694 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 753

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023

Db        754 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 813

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
```

```
Db        814 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 873

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139

Db        874 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 933

Qy       1140 GCTGAG 1145

Db        934 TCTGGG 939
```

RESULT 5
US-09-325-320-1
; Sequence 1, Application US/09325320
; Patent No. 6117981
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06101
; CURRENT APPLICATION NUMBER: US/09/325,320
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1093)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (119)..(1093)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1013)..(1024)
; OTHER INFORMATION: phosphorylation site recognized by protein kinase
; OTHER INFORMATION: C and other kinases
US-09-325-320-1

Query Match 12.6%; Score 213.6; DB 3; Length 1104;
Best Local Similarity 53.9%; Pred. No. 8.8e-56;
Matches 488; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305

Db         37 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 96

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365

Db         97 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 156

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425

Db        157 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 216

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485

Db        217 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 276

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545

Db        277 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 336

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605

Db        337 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 396

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665

Db        397 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 456

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725

Db        457 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 516

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785

Db        517 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 573

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845

Db        574 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 633

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905

Db        634 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 693

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965

Db        694 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 753

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023

Db        754 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 813

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079

Db        814 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 873

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139

Db        874 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 933

Qy       1140 GCTGAG 1145

Db        934 TCTGGG 939
```

RESULT 6
US-09-585-109-1
; Sequence 1, Application US/09585109
; Patent No. 6242204
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06104
; CURRENT APPLICATION NUMBER: US/09/585,109
; CURRENT FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(1093)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (119)..(1093)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1013)..(1024)
; OTHER INFORMATION: phosphorylation site recognized by protein kinase
; OTHER INFORMATION: C and other kinases
US-09-585-109-1

Query Match 12.6%; Score 213.6; DB 3; Length 1104;
Best Local Similarity 53.9%; Pred. No. 8.8e-56;
Matches 488; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||    |  ||   |  || | |    |   || |   |||   |  ||
Db         37 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 96

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||     |||    | ||||| |||   || ||  ||||  || |
Db         97 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 156

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              ||| |      |||||   ||||||   |      ||||| ||||| ||  | || |
Db        157 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 216

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |.  | |||| |     | | | ||  ||  ||| || ||  | | | |
Db        217 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 276

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   |||| ||||||||||||  ||||| | ||     |||||||
Db        277 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 336

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |     || || |          ||     ||  | ||||| ||||||||||
Db        337 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 396

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |          |||    || || || |||    ||| | |  |  |       ||
Db        397 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 456

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
              ||||| |||||||| |||||| |||| ||    |||     |   ||    ||     |
Db        457 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 516

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
              | | |  | ||||| ||||||||||    | || |||||| ||||      |    |||
Db        517 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 573

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
              | |||||  | ||  | ||||| | ||  | || | | ||||  ||| |  | |
Db        574 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 633

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
              || ||    |||||| |   |||||||| || |   |   |   | || | ||||||
Db        634 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 693

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
              |   || || || || || |||||||| |||  | ||||||||||||||||||     |
Db        694 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 753

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
              || |||||   ||| ||||||     |  ||    |  ||| || ||||
Db        754 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 813

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
                  || ||     || | |      || |  | |||| |||      | |||    || |
Db        814 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 873

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
              | || |  |||| |   | || |||  |||||    |  ||     | |  ||||    |
Db        874 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 933

Qy       1140 GCTGAG 1145
                 ||| |
Db        934 TCTGGG 939


RESULT 7
PCT-US95-09145A-1
; Sequence 1, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1104 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  32..1093
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  119..1093
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1013..1024
;      OTHER INFORMATION:  /note= "phosphorylation site
;      OTHER INFORMATION:  recognized by protein kinase C and other kina..."
PCT-US95-09145A-1

  Query Match             12.6%;  Score 213.6;  DB 5;  Length 1104;
  Best Local Similarity   53.9%;  Pred. No. 8.8e-56;
  Matches  488;  Conservative    0;  Mismatches  409;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||    |  ||   |  || | |    |   || |   |||   |  ||
Db         37 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 96

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||     |||    | ||||| |||   || ||  ||||  || |
Db         97 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 156

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              ||| |      |||||   ||||||   |      ||||| ||||| ||  | || |
Db        157 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 216

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |.  | |||| |     | | | ||  ||  ||| || ||  | | | |
Db        217 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 276

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   |||| ||||||||||||  ||||| | ||     |||||||
Db        277 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 336

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |     || || |          ||     ||  | ||||| ||||||||||
Db        337 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 396

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |          |||    || || || |||    ||| | |  |  |       ||
Db        397 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 456
```

```
Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
Db        457 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 516

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
Db        517 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 573

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
Db        574 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 633

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
Db        634 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 693

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
Db        694 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 753

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        754 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 813

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        814 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 873

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
Db        874 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 933

Qy       1140 GCTGAG 1145
Db        934 TCTGGG 939
```

```
RESULT 8
US-08-776-088-5
; Sequence 5, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2134 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  116..1177
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  203..1177
US-08-776-088-5

  Query Match            12.6%;  Score 213.6;  DB 1;  Length 2134;
  Best Local Similarity  53.9%;  Pred. No. 1.3e-55;
  Matches  488;  Conservative    0;  Mismatches  409;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
Db        121 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 180

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
Db        181 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 240

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
Db        241 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 300

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
Db        301 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 360

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
Db        361 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 420

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
Db        421 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 480

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
Db        481 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 540

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
Db        541 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 600

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
Db        601 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 657

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
Db        658 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 717

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
Db        718 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 777

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
Db        778 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 837

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        838 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 897

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        898 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 957

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
```

```
Db        958 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 1017

Qy       1140 GCTGAG 1145
Db       1018 TCTGGG 1023
```

RESULT 9
PCT-US95-09145A-5
; Sequence 5, Application PC/TUS9509145A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09145A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: John A. Harre
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35792CIPPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..1177
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 203..1177
PCT-US95-09145A-5

Query Match 12.6%; Score 213.6; DB 5; Length 2134;
Best Local Similarity 53.9%; Pred. No. 1.3e-55;
Matches 488; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
Db        121 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 180

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
Db        181 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 240

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
Db        241 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 300

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
Db        301 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 360

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
Db        361 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 420

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
Db        421 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 480

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
Db        481 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 540

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
Db        541 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 600

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
Db        601 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 657

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
Db        658 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 717

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
Db        718 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 777

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
Db        778 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 837

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        838 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 897

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        898 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 957

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
Db        958 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 1017

Qy       1140 GCTGAG 1145
Db       1018 TCTGGG 1023
```

RESULT 10
US-09-949-016-4029
; Sequence 4029, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4029
; LENGTH: 2774
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4029

Query Match 12.6%; Score 213.6; DB 4; Length 2774;
Best Local Similarity 53.9%; Pred. No. 1.5e-55;
Matches 488; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||     |  ||    | || | |     |   || |  |||   |  ||
Db        121 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 180

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||      |||     | ||||| |||   || ||  ||||  || |
Db        181 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 240

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              |||  |      |||||   ||||||    |     |||||  |||||  ||  | || |
Db        241 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 300

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |    | ||||  |      |  |  | ||  ||  ||| || ||  | | | |
Db        301 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 360

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   ||||  ||||||||||||  |||||  | ||     ||||||||
Db        361 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 420

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |    || || |      ||    ||  | ||||| ||||||||||
Db        421 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 480

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |           |||    || || || |||    ||| | |  |    |      ||
Db        481 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 540

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
              |||||  |||||||| |||||| |||| ||    |||     |   ||     ||     |
Db        541 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 600

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
              | | |  | |||||  ||||||||||    | || ||||||  ||||     |    |||
Db        601 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 657

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
              | |||||  | ||  | ||||||  | ||  | || | | | ||||  |||  |  | |
Db        658 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 717

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
              || ||   ||||||  |   |||||||||| ||  |    |   |  | || | ||||||
Db        718 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 777

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
              |   || || || || || |||||||||  |||  | ||||||||||||||||||     |
Db        778 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 837

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
                  || |||||   ||| ||||||        |  ||    | ||| || ||||
Db        838 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 897

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
                  || ||    || | |      || | |  |||| |||    | |||    || |
Db        898 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 957

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
              | || |  |||| |   | || |||  |||||    |  ||    | |  ||||    |
Db        958 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 1017

Qy       1140 GCTGAG 1145
                 ||| |
Db       1018 TCTGGG 1023
```

RESULT 11
US-09-949-016-172
; Sequence 172, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-172

Query Match 12.6%; Score 213.6; DB 4; Length 2775;
Best Local Similarity 53.9%; Pred. No. 1.5e-55;
Matches 488; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||     |  ||    | || | |     |   || |  |||   |  ||
Db        121 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 180

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||      |||     | ||||| |||   || ||  ||||  || |
Db        181 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 240

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              |||  |      |||||   ||||||    |     |||||  |||||  ||  | || |
Db        241 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 300

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |    | ||||  |      |  |  | ||  ||  ||| || ||  | | | |
Db        301 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 360

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   ||||  ||||||||||||  |||||  | ||     ||||||||
Db        361 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 420

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |    || || |      ||    ||  | ||||| ||||||||||
Db        421 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 480

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |           |||    || || || |||    ||| | |  |    |      ||
Db        481 GGGGAACCCGAATGACCCGCACGGCTCTGAGCACACCGTCAGCGGACAGCACTTCGCCGC 540

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
              |||||  |||||||| |||||| |||| ||    |||     |   ||     ||     |
Db        541 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGCCAGCACTGCCAGCAA 600

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
              | | |  | |||||  ||||||||||    | || ||||||  ||||     |    |||
Db        601 CAAGTCAGAAGGCCTCGCTGTCCTGGCTGTTCTCATTGAGATGGG---CTCCTTCAATCC 657

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
              | |||||  | ||  | ||||||  | ||  | || | | | ||||  |||  |  | |
Db        658 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 717

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
              || ||   ||||||  |   |||||||||| ||  |    |   |  | || | ||||||
Db        718 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 777

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
              |   || || || || || |||||||||  |||  | ||||||||||||||||||     |
Db        778 CCGGGGGTCCCTGACCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 837
```

```
Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        838 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 897

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        898 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 957

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
Db        958 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 1017

Qy       1140 GCTGAG 1145
Db       1018 TCTGGG 1023
```

RESULT 12
US-08-479-328-1
; Sequence 1, Application US/08479328
; Patent No. 5698396
; GENERAL INFORMATION:
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
; TITLE OF INVENTION: And Molecules Identified Thereby
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,328
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5698396man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2679 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double-stranded
; TOPOLOGY: linear
US-08-479-328-1

Query Match 12.4%; Score 211; DB 1; Length 2679;
Best Local Similarity 53.6%; Pred. No. 9.8e-55;
Matches 486; Conservative 0; Mismatches 411; Indels 9; Gaps 2;

```
Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
Db         13 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 72

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
Db         73 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 132

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
Db        133 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 192

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
Db        193 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 252

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
Db        253 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 312

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
Db        313 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 372

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
Db        373 GGGGAACCCGAATGACCCGCACGGCTCTGAGCATACCGTCAGCGGACAGCACTTCTCCGC 432

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
Db        433 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGACAGNACTGCCAGCAA 492

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
Db        493 CAAGTCAGAAGACCTCGCTGTCCTGGGTGCTCTCATTGAGATGGG---CTCCTTCAATCC 549

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
Db        550 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 609

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
Db        610 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 669

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
Db        670 CCGGGGGTCCCTGATCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 729

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        730 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 789

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        790 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 849

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
Db        850 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 909

Qy       1140 GCTGAG 1145
Db        910 TCTGGG 915
```

RESULT 13
US-08-761-119-1
; Sequence 1, Application US/08761119
; Patent No. 5798264
; GENERAL INFORMATION:
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
; TITLE OF INVENTION: And Molecules Identified Thereby
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,119
;      FILING DATE:  6-DECEMBER-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/479,328
;      FILING DATE:  07-JUNE-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5798264man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5410.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2679 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double-stranded
;      TOPOLOGY:  linear
US-08-761-119-1

  Query Match            12.4%;  Score 211;  DB 1;  Length 2679;
  Best Local Similarity   53.6%;  Pred. No. 9.8e-55;
  Matches  486;  Conservative    0;  Mismatches  411;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||    |  ||   |  || |  |    |  || |   |||   |  ||
Db         13 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 72

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
              | || |||  |||     |||     | ||||| |||   || ||  ||||  || |
Db         73 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 132

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
              |||  |       |||||   ||||||   |       ||||| ||||| ||  | || |
Db        133 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 192

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
              ||||   |    | |||| |     |  |  | ||  ||  ||| || ||  | | | |
Db        193 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 252

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
              || || | |||  ||   ||||  ||||||||||||  ||||| | ||     ||||||||
Db        253 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 312

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
              | || |  |    || || |         ||    ||  | ||||| ||||||||||
Db        313 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 372

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
              |||  |       |||    || || || ||     ||| | |  |  |  |  |  ||
Db        373 GGGGAACCCGAATGACCCGCACGGCTCTGAGCATACCGTCAGCGGACAGCACTTCTCCGC 432

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
              |||||  |||||||| |||||| |||| ||     |||      |   ||    ||     |
Db        433 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGACAGNACTGCCAGCAA 492

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
              | | |  | | ||| ||||||||||    || |||||| ||||      |    |||
Db        493 CAAGTCAGAAGACCTCGCTGTCCTGGGTGCTCTCATTGAGATGGG---CTCCTTCAATCC 549

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
              | ||||| | ||  | ||||||| | ||  | || | | | ||||  ||| |  | |
Db        550 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 609

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
              || ||    |||||| |    |||||||||| ||  |    |    |    | || | ||||||
Db        610 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 669

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
              |   || || || |  || |||||||| |||  | ||||||||||||||||||    |
Db        670 CCGGGGGTCCCTGATCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 729

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
                  || |||||   ||| ||||||       |  ||    |  ||| || ||||
Db        730 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 789

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
                  || ||    || | |      || |  | |||| |||    | |||     || |
Db        790 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 849

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
              | || |  |||| |   | || |||  |||||    |  ||    | |  ||||    |
Db        850 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 909

Qy       1140 GCTGAG 1145
                 |||
Db        910 TCTGGG 915


RESULT 14
US-08-668-128B-1
; Sequence 1, Application US/08668128B
; Patent No. 5840568
;  GENERAL INFORMATION:
;    APPLICANT:  Pfreundschuh, Michael
;    TITLE OF INVENTION:  Hodgkin's Disease Associated Molecules And
;    TITLE OF INVENTION:  Uses Thereof
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/668,128B
;      FILING DATE:  21-JUNE-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/644,116
;      FILING DATE:  10-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/580,980
;      FILING DATE:  03-JANUARY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/479,328
;      FILING DATE:  07-JUNE-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5840568man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5441
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2679 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double-stranded
;      TOPOLOGY:  linear
US-08-668-128B-1

  Query Match            12.4%;  Score 211;  DB 2;  Length 2679;
  Best Local Similarity   53.6%;  Pred. No. 9.8e-55;
  Matches  486;  Conservative    0;  Mismatches  411;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
              ||   ||| ||    |  ||   |  || |  |    |  || |   |||   |  ||
Db         13 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 72
```

```
Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
Db         73 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 132

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
Db        133 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 192

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
Db        193 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 252

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
Db        253 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 312

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
Db        313 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 372

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
Db        373 GGGGAACCCGAATGACCCGCACGGCTCTGAGCATACCGTCAGCGGACAGCACTTCTCCGC 432

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
Db        433 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGACAGNACTGCCAGCAA 492

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785
Db        493 CAAGTCAGAAGACCTCGCTGTCCTGGGTGCTCTCATTGAGATGGG---CTCCTTCAATCC 549

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845
Db        550 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 609

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905
Db        610 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 669

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965
Db        670 CCGGGGGTCCCTGATCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 729

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023
Db        730 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 789

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079
Db        790 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 849

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139
Db        850 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 909

Qy       1140 GCTGAG 1145
Db        910 TCTGGG 915


RESULT 15
US-08-905-445-1
; Sequence 1, Application US/08905445
; Patent No. 5864015
;  GENERAL INFORMATION:
;    APPLICANT:  Pfreundschuh, Michael
;    TITLE OF INVENTION:  Hodgkin's Disease Associated Molecules And
;    TITLE OF INVENTION:  Uses Thereof
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,445
;      FILING DATE:  04-AUG-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/668,128
;      FILING DATE:  21-JUNE-1996
;      APPLICATION NUMBER:  08/644,116
;      FILING DATE:  10-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/580,980
;      FILING DATE:  03-JANUARY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/479,328
;      FILING DATE:  07-JUNE-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5864015man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5441
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2679 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double-stranded
;      TOPOLOGY:  linear
US-08-905-445-1

  Query Match            12.4%;  Score 211;  DB 2;  Length 2679;
  Best Local Similarity  53.6%;  Pred. No. 9.8e-55;
  Matches  486;  Conservative    0;  Mismatches  411;  Indels    9;  Gaps    2;

Qy        246 CCCCTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTG 305
Db         13 CCGGCGCAGCCTGCACGCGGCGGCCGTGCTCCTGCTGGTGATCTTAAAGGAACAGCCTTC 72

Qy        306 GATCCTGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCA 365
Db         73 CAGCCCGGCCCCAGTGAACGGTTCCAAGTGGACTTATTTTGGTCCTGATGGGGAGAATAG 132

Qy        366 TTGGCCAGCCTCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGAC 425
Db        133 CTGGTCCAAGAAGTACCCGTCGTGTGGGGGCCTGCTGCAGTCCCCCATAGACCTGCACAG 192

Qy        426 AGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCC 485
Db        193 TGACATCCTCCAGTATGACGCCAGCCTCACGCCCCTCGAGTTCCAAGGCTACAATCTGTC 252

Qy        486 TGGCACCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTC 545
Db        253 TGCCAACAAGCAGTTTCTCCTGACCAACAATGGCCATTCAGTGAAGCTGAACCTGCCCTC 312

Qy        546 TACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTG 605
Db        313 GGACATGCACATCCAGGGCCTCCAGTCTCGCTACAGTGCCACGCAGCTGCACCTGCACTG 372

Qy        606 GGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGC 665
Db        373 GGGGAACCCGAATGACCCGCACGGCTCTGAGCATACCGTCAGCGGACAGCACTTCTCCGC 432

Qy        666 AGAGCTCCACATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGA 725
```

```
Db        433 CGAGCTGCACATTGTCCATTATAACTCAGACCTTTATCCTGACGACAGNACTGCCAGCAA 492

Qy        726 GAGGCCTCAGGGCCTGGCTGTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATAT 785

Db        493 CAAGTCAGAAGACCTCGCTGTCCTGGGTGCTCTCATTGAGATGGG---CTCCTTCAATCC 549

Qy        786 AGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC 845

Db        550 GTCCTATGACAAGATCTTCAGTCACCTTCAACATGTAAAGTACAAAGGCCAGGAAGCATT 609

Qy        846 AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTA 905

Db        610 CGTCCCGGGATTCAACATTGAAGAGCTGCTTCCGGAGAGGACCGCTGAATATTACCGCTA 669

Qy        906 CAATGGCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAG 965

Db        670 CCGGGGGTCCCTGATCACACCCCCTTGCAACCCCACTGTGCTCTGGACAGTTTTCCGAAA 729

Qy        966 AAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACA-- 1023

Db        730 CCCCGTGCAAATTTCCCAGGAGCAGCTGCTGGCTTTGGAGACAGCCCTGTACTGCACACA 789

Qy       1024 ----GAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAA 1079

Db        790 CATGGACGACCCTTCCCCCAGAGAAATGATCAACAACTTCCGGCAGGTCCAGAAGTTCGA 849

Qy       1080 TCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAAT 1139

Db        850 TGAGAGGCTGGTATACACCTCCTTCTCCCAAGTGCAAGTCTGTACTGCGGCAGGACTGAG 909

Qy       1140 GCTGAG 1145

Db        910 TCTGGG 915
```

Search completed: April 30, 2005, 03:59:14
Job time : 403 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2005, 00:26:37 ; Search time 969 Seconds
(without alignments)
10686.434 Million cell updates/sec

Perfect score: 1701
Sequence: 1 gagactgcagagggagataa.....aaattaaagtttctgacttt 1701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
521	1700	99.9	1701	16	US-10-174-587-267	Sequence 267, App
589	1700	99.9	1701	16	US-10-063-742-73	Sequence 73, Appl
665	1700	99.9	1701	16	US-10-013-909A-422	Sequence 422, App
733	1700	99.9	1701	19	US-10-972-317-73	Sequence 73, Appl
734	1496	87.9	1657	18	US-10-467-903-19	Sequence 19, Appl
735	1486.6	87.4	1673	17	US-10-378-029-4	Sequence 4, Appli
736	1201.4	70.6	1537	10	US-09-892-877-19	Sequence 19, Appl
737	1201.4	70.6	1537	10	US-09-948-783-19	Sequence 19, Appl
738	1172.8	68.9	1434	17	US-10-264-237-653	Sequence 653, App
739	954.8	56.1	999	10	US-09-989-442-14	Sequence 14, Appl
740	795.6	46.8	1624	15	US-10-205-194-50	Sequence 50, Appl
741	482.4	28.4	11470	17	US-10-264-237-2859	Sequence 2859, Ap
742	420.6	24.7	561	10	US-09-989-442-62	Sequence 62, Appl
743	401.2	23.6	406	10	US-09-918-995-34673	Sequence 34673, A
744	267.8	15.7	458	9	US-09-867-701-1442	Sequence 1442, Ap
745	245	14.4	295	18	US-10-425-115-21930	Sequence 21930, A
746	213.6	12.6	2771	17	US-10-240-425-381	Sequence 381, App
747	213.6	12.6	2771	18	US-10-723-860-3224	Sequence 3224, Ap
748	213.6	12.6	2771	19	US-10-278-698-170	Sequence 170, App
749	213.6	12.6	2771	19	US-10-278-698-686	Sequence 686, App
750	213.6	12.6	2775	17	US-10-172-118-575	Sequence 575, App
751	213.6	12.6	2775	17	US-10-295-027-295	Sequence 295, App
752	213.6	12.6	2775	17	US-10-342-887-575	Sequence 575, App
753	213.6	12.6	2775	18	US-10-648-593-87	Sequence 87, Appl
754	213.6	12.6	3171	10	US-09-814-353-21734	Sequence 21734, A
755	202.4	11.9	3151	18	US-10-723-860-7224	Sequence 7224, Ap
c 756	181.4	10.7	661	13	US-10-027-632-29488	Sequence 29488, A
c 757	181.4	10.7	661	17	US-10-027-632-29488	Sequence 29488, A
c 758	181.4	10.7	697	13	US-10-027-632-98244	Sequence 98244, A
c 759	181.4	10.7	697	17	US-10-027-632-98244	Sequence 98244, A
760	146	8.6	2556	17	US-10-108-260A-1531	Sequence 1531, Ap
761	126.6	7.4	528	19	US-10-696-639-2389	Sequence 2389, Ap
762	118.4	7.0	1399	18	US-10-795-933-1	Sequence 1, Appli
763	118.4	7.0	1519	15	US-10-102-524-1695	Sequence 1695, Ap
764	118.4	7.0	1522	9	US-09-772-719-1	Sequence 1, Appli
765	118.4	7.0	1522	10	US-09-967-237-1	Sequence 1, Appli
766	118.4	7.0	1522	18	US-10-795-933-5	Sequence 5, Appli
767	118.4	7.0	1522	18	US-10-888-694-1	Sequence 1, Appli
768	118.4	7.0	1522	19	US-10-921-590-1	Sequence 1, Appli
769	118.4	7.0	1552	9	US-09-954-456-89	Sequence 89, Appl
770	118.4	7.0	1552	9	US-09-954-456-726	Sequence 726, App
771	118.4	7.0	1552	10	US-09-960-706-1080	Sequence 1080, Ap
772	118.4	7.0	1552	10	US-09-873-367C-516	Sequence 516, App
773	118.4	7.0	1552	11	US-09-968-007A-213	Sequence 213, App
774	118.4	7.0	1552	15	US-10-301-822-11	Sequence 11, Appl
775	118.4	7.0	1552	17	US-10-465-572-9	Sequence 9, Appli
776	118.4	7.0	1552	17	US-10-172-118-574	Sequence 574, App
777	118.4	7.0	1552	17	US-10-388-360-291	Sequence 291, App
778	118.4	7.0	1552	17	US-10-295-027-305	Sequence 305, App
779	118.4	7.0	1552	17	US-10-295-027-1022	Sequence 1022, Ap
780	118.4	7.0	1552	17	US-10-342-887-574	Sequence 574, App
781	118.4	7.0	1552	18	US-10-734-564-71	Sequence 71, Appl
782	118.4	7.0	1552	18	US-10-723-860-460	Sequence 460, App
783	118.4	7.0	1552	19	US-10-921-590-70	Sequence 70, Appl
784	118.4	7.0	1552	19	US-10-848-755A-94	Sequence 94, Appl
785	118.4	7.0	1552	19	US-10-843-641A-516	Sequence 516, App
786	118.4	7.0	1552	19	US-10-843-641A-3116	Sequence 3116, Ap
787	118.4	7.0	1552	19	US-10-843-641A-3753	Sequence 3753, Ap
788	118.4	7.0	1552	19	US-10-843-641A-6683	Sequence 6683, Ap
789	118.4	7.0	1658	18	US-10-723-860-5135	Sequence 5135, Ap
790	118.4	7.0	1833	9	US-09-783-708-2	Sequence 2, Appli
791	117.2	6.9	5787	19	US-10-887-553A-434	Sequence 434, App
792	117.2	6.9	6687	18	US-10-723-860-5795	Sequence 5795, Ap
793	111.8	6.6	1965	19	US-10-921-590-79	Sequence 79, Appl
794	94.4	5.5	1006	17	US-10-287-226-355	Sequence 355, App
795	91.2	5.4	1316	9	US-09-795-651-77	Sequence 77, Appl
796	90.8	5.3	5052	18	US-10-795-933-23	Sequence 23, Appl
797	81.8	4.8	1023	17	US-10-433-802-19	Sequence 19, Appl
798	81.8	4.8	3564	17	US-10-108-260A-639	Sequence 639, App
799	81.8	4.8	3564	19	US-10-753-267-7	Sequence 7, Appli
800	79.8	4.7	586	19	US-10-921-590-73	Sequence 73, Appl
801	72.2	4.2	331	17	US-10-242-535A-11940	Sequence 11940, A
802	72.2	4.2	331	17	US-10-085-783A-11940	Sequence 11940, A
c 803	69.8	4.1	296	15	US-10-102-524-697	Sequence 697, App
804	68.2	4.0	6801	15	US-10-205-219-120	Sequence 120, App
805	67.8	4.0	1136	17	US-10-287-226-353	Sequence 353, App
806	67.6	4.0	1248	17	US-10-220-120-4	Sequence 4, Appli
c 807	66.6	3.9	304	9	US-09-777-564-348	Sequence 348, App
c 808	66.6	3.9	304	14	US-10-015-219-348	Sequence 348, App
809	66.4	3.9	1508	15	US-10-084-817-11	Sequence 11, Appl
810	65.2	3.8	1053	17	US-10-388-934-93	Sequence 93, Appl
c 811	64.4	3.8	297	9	US-09-777-564-592	Sequence 592, App
c 812	64.4	3.8	297	14	US-10-015-219-592	Sequence 592, App
813	63.8	3.8	911	15	US-10-069-434-4	Sequence 4, Appli
814	63.4	3.7	1201	9	US-09-917-800A-1677	Sequence 1677, Ap

815	63.4	3.7	1201	17	US-10-388-934-507	Sequence 507, App
816	59	3.5	60	10	US-09-908-975-9140	Sequence 9140, Ap
817	58.8	3.5	305	9	US-09-777-564-8	Sequence 8, Appli
818	58.8	3.5	305	14	US-10-015-219-8	Sequence 8, Appli
819	58.8	3.5	988	9	US-09-917-800A-1676	Sequence 1676, Ap
820	58.4	3.4	1233	15	US-10-106-698-360	Sequence 360, App
821	58.4	3.4	1244	9	US-09-981-353-79	Sequence 79, Appl
822	58.4	3.4	1244	15	US-10-235-994-23	Sequence 23, Appl
823	58.4	3.4	2785	9	US-09-802-674-3	Sequence 3, Appli
824	58.4	3.4	2785	16	US-10-393-892-31	Sequence 31, Appl
825	58.4	3.4	2785	16	US-10-394-382-31	Sequence 31, Appl
826	58.4	3.4	2826	14	US-10-158-646-47	Sequence 47, Appl
827	56	3.3	1266	9	US-09-938-270B-2	Sequence 2, Appli
828	56	3.3	2286	17	US-10-363-616-5	Sequence 5, Appli
829	56	3.3	2357	18	US-10-723-860-1121	Sequence 1121, Ap
830	53.2	3.1	1224	19	US-10-764-420-2184	Sequence 2184, Ap
831	53	3.1	423	10	US-09-918-995-37075	Sequence 37075, A
832	52.8	3.1	1007	17	US-10-425-114-16438	Sequence 16438, A
833	52.2	3.1	65	10	US-09-908-975-26220	Sequence 26220, A
834	52.2	3.1	3091	10	US-09-983-000A-1	Sequence 1, Appli
835	52.2	3.1	3091	19	US-10-652-981-1	Sequence 1, Appli
836	52.2	3.1	3340	17	US-10-295-027-1047	Sequence 1047, Ap
837	52.2	3.1	3350	18	US-10-723-860-950	Sequence 950, App
838	52.2	3.1	4220	17	US-10-295-027-1049	Sequence 1049, Ap
839	52.2	3.1	4347	17	US-10-295-027-1042	Sequence 1042, Ap
840	52.2	3.1	5343	17	US-10-295-027-375	Sequence 375, App
841	52.2	3.1	5367	17	US-10-295-027-373	Sequence 373, App
842	52.2	3.1	5367	17	US-10-295-027-1044	Sequence 1044, Ap
843	52.2	3.1	5481	17	US-10-295-027-379	Sequence 379, App
844	52.2	3.1	5481	17	US-10-295-027-1046	Sequence 1046, Ap
845	52.2	3.1	7941	9	US-09-954-456-1812	Sequence 1812, Ap
846	52.2	3.1	7941	9	US-09-816-703A-1	Sequence 1, Appli
847	52.2	3.1	7941	10	US-09-983-000A-5	Sequence 5, Appli
848	52.2	3.1	7941	17	US-10-295-027-381	Sequence 381, App
849	52.2	3.1	7941	19	US-10-843-641A-4839	Sequence 4839, Ap
850	52.2	3.1	7941	19	US-10-652-981-5	Sequence 5, Appli
851	52.2	3.1	7944	17	US-10-295-027-371	Sequence 371, App
852	52.2	3.1	7944	17	US-10-295-027-1043	Sequence 1043, Ap
853	52.2	3.1	8058	10	US-09-983-000A-3	Sequence 3, Appli
854	52.2	3.1	8058	19	US-10-652-981-3	Sequence 3, Appli
855	52.2	3.1	8292	18	US-10-723-860-5522	Sequence 5522, Ap
856	52	3.1	478	10	US-09-918-995-24749	Sequence 24749, A
857	51.8	3.0	3670	14	US-10-074-475-98	Sequence 98, Appl
858	51.8	3.0	128668	13	US-10-087-192-340	Sequence 340, App
859	51.2	3.0	1058	18	US-10-425-115-22694	Sequence 22694, A
860	50.8	3.0	457	18	US-10-437-963-50789	Sequence 50789, A
c 861	50.8	3.0	981	17	US-10-260-238-5746	Sequence 5746, Ap
862	50.8	3.0	1104	14	US-10-165-603-12	Sequence 12, Appl
863	50.8	3.0	1104	15	US-10-205-823-47	Sequence 47, Appl
864	50.8	3.0	1104	17	US-10-099-322-19	Sequence 19, Appl
865	50.8	3.0	1104	17	US-10-044-564-19	Sequence 19, Appl
866	50.8	3.0	1105	9	US-09-954-456-1229	Sequence 1229, Ap
867	50.8	3.0	1105	10	US-09-873-367C-168	Sequence 168, App
868	50.8	3.0	1105	19	US-10-843-641A-168	Sequence 168, App
869	50.8	3.0	1105	19	US-10-843-641A-4256	Sequence 4256, Ap
870	50.8	3.0	1237	9	US-09-981-353-67	Sequence 67, Appl
871	50.6	3.0	683	17	US-10-404-460-38	Sequence 38, Appl
872	50.6	3.0	4480	17	US-10-295-027-1048	Sequence 1048, Ap
c 873	50.4	3.0	198161	18	US-10-775-169-52	Sequence 52, Appl
c 874	50.4	3.0	198161	18	US-10-723-860-165	Sequence 165, App
c 875	50.4	3.0	3673778	16	US-10-312-841-1	Sequence 1, Appli
c 876	50.2	3.0	263744	16	US-10-229-834A-6	Sequence 6, Appli
877	50	2.9	1019	17	US-10-425-114-17952	Sequence 17952, A
878	50	2.9	1157	18	US-10-425-115-22706	Sequence 22706, A
c 879	49.6	2.9	23169	17	US-10-052-482-25	Sequence 25, Appl
c 880	49.2	2.9	125322	18	US-10-322-281-855	Sequence 855, App
c 881	49	2.9	119057	18	US-10-322-281-609	Sequence 609, App
882	48.6	2.9	203132	18	US-10-322-281-459	Sequence 459, App
883	48.4	2.8	5363	17	US-10-295-027-377	Sequence 377, App
884	48.4	2.8	5363	17	US-10-295-027-1045	Sequence 1045, Ap
c 885	48	2.8	448	18	US-10-674-124A-11813	Sequence 11813, A
886	47.4	2.8	2905	18	US-10-723-860-5655	Sequence 5655, Ap
c 887	47.2	2.8	3051	13	US-10-027-632-255985	Sequence 255985,
c 888	47.2	2.8	3051	17	US-10-027-632-255985	Sequence 255985,
c 889	47.2	2.8	47745	13	US-10-087-192-469	Sequence 469, App
890	47.2	2.8	115863	18	US-10-723-860-2504	Sequence 2504, Ap
891	47	2.8	256525	13	US-10-087-192-451	Sequence 451, App
892	46.8	2.8	262	18	US-10-674-124A-9475	Sequence 9475, Ap
893	46.8	2.8	3079	18	US-10-723-860-7526	Sequence 7526, Ap
894	46.6	2.7	323	18	US-10-357-930-1605	Sequence 1605, Ap
895	46.6	2.7	324	18	US-10-357-930-10774	Sequence 10774, A
896	46.4	2.7	453	9	US-09-960-352-1054	Sequence 1054, Ap
897	46.4	2.7	553	19	US-10-696-639-2008	Sequence 2008, Ap
898	46.4	2.7	684187	18	US-10-367-094-71	Sequence 71, Appl
899	46.2	2.7	354	18	US-10-674-124A-14397	Sequence 14397, A
c 900	46.2	2.7	1393	18	US-10-437-963-84546	Sequence 84546, A
901	46.2	2.7	185555	13	US-10-087-192-1999	Sequence 1999, Ap
902	46.2	2.7	225734	18	US-10-322-696-13	Sequence 13, Appl
c 903	46	2.7	307	18	US-10-674-124A-17571	Sequence 17571, A
904	46	2.7	1318	18	US-10-437-963-43421	Sequence 43421, A
905	46	2.7	157044	13	US-10-087-192-565	Sequence 565, App
906	45.8	2.7	368	18	US-10-674-124A-4468	Sequence 4468, Ap
907	45.8	2.7	1523	9	US-09-954-456-287	Sequence 287, App
908	45.8	2.7	1523	9	US-09-880-107-3844	Sequence 3844, Ap
909	45.8	2.7	1523	10	US-09-873-367C-825	Sequence 825, App
910	45.8	2.7	1523	11	US-09-968-007A-473	Sequence 473, App
911	45.8	2.7	1523	19	US-10-843-641A-825	Sequence 825, App
912	45.8	2.7	1523	19	US-10-843-641A-3314	Sequence 3314, Ap
913	45.8	2.7	1523	19	US-10-843-641A-6943	Sequence 6943, Ap
914	45.8	2.7	1551	15	US-10-102-524-1753	Sequence 1753, Ap
915	45.8	2.7	1551	17	US-10-172-118-423	Sequence 423, App
916	45.8	2.7	1551	17	US-10-342-887-423	Sequence 423, App
917	45.8	2.7	1608	18	US-10-723-860-6345	Sequence 6345, Ap
918	45.8	2.7	1723	9	US-09-925-299-172	Sequence 172, App
919	45.8	2.7	1723	10	US-09-925-299-172	Sequence 172, App
920	45.8	2.7	1755	14	US-10-158-646-46	Sequence 46, Appl
921	45.8	2.7	1755	16	US-10-240-965-199	Sequence 199, App
922	45.8	2.7	1886	10	US-09-814-353-21737	Sequence 21737, A
923	45.8	2.7	2391	10	US-09-822-846-103	Sequence 103, App
924	45.8	2.7	4742	18	US-10-357-930-21009	Sequence 21009, A
925	45.8	2.7	4742	18	US-10-357-930-23623	Sequence 23623, A
926	45.8	2.7	4742	18	US-10-357-930-26850	Sequence 26850, A
927	45.8	2.7	4742	18	US-10-357-930-29511	Sequence 29511, A
c 928	45.8	2.7	115223	18	US-10-322-281-773	Sequence 773, App
929	45.6	2.7	605	9	US-09-988-292-17	Sequence 17, Appl
930	45.6	2.7	605	18	US-10-776-601-17	Sequence 17, Appl
931	45.6	2.7	1122	17	US-10-425-114-26486	Sequence 26486, A
932	45.6	2.7	1128	17	US-10-425-114-21260	Sequence 21260, A
933	45.6	2.7	1180	18	US-10-425-115-16732	Sequence 16732, A
934	45.6	2.7	1272	18	US-10-425-115-16731	Sequence 16731, A
935	45.4	2.7	153740	18	US-10-322-696-85	Sequence 85, Appl
c 936	45.4	2.7	659158	9	US-09-771-208-20	Sequence 20, Appl
937	45.2	2.7	1077	18	US-10-335-053-76	Sequence 76, Appl
938	45.2	2.7	91141	13	US-10-087-192-649	Sequence 649, App
939	45.2	2.7	344548	13	US-10-087-192-334	Sequence 334, App
976	45	2.6	45	16	US-10-013-909A-427	Sequence 427, App
c1006	45	2.6	256	18	US-10-674-124A-4703	Sequence 4703, Ap
c1007	45	2.6	286	18	US-10-674-124A-15178	Sequence 15178, A
1008	45	2.6	570	18	US-10-425-115-5311	Sequence 5311, Ap
1009	44.8	2.6	1108	17	US-10-038-854-7	Sequence 7, Appli
1010	44.8	2.6	32963	13	US-10-087-192-1801	Sequence 1801, Ap
1011	44.6	2.6	531	18	US-10-437-963-20239	Sequence 20239, A
1012	44.6	2.6	600	9	US-09-864-761-7218	Sequence 7218, Ap
1013	44.6	2.6	31312	18	US-10-322-281-709	Sequence 709, App
1014	44.6	2.6	69327	9	US-09-777-921A-3	Sequence 3, Appli
1015	44.6	2.6	69327	17	US-10-698-489-3	Sequence 3, Appli
c1016	44.6	2.6	133955	13	US-10-087-192-1984	Sequence 1984, Ap
c1017	44.4	2.6	7340	17	US-10-052-482-26	Sequence 26, Appl
1018	44.4	2.6	74868	14	US-10-175-523-67	Sequence 67, Appl
c1019	44.4	2.6	344548	13	US-10-087-192-334	Sequence 334, App
1020	44.2	2.6	174	18	US-10-674-124A-4076	Sequence 4076, Ap
1021	44.2	2.6	1759	9	US-09-981-353-116	Sequence 116, App
1022	44.2	2.6	1759	14	US-10-116-802-234	Sequence 234, App
1023	44.2	2.6	43103	19	US-10-741-600-17772	Sequence 17772, A
c1024	44	2.6	75164	18	US-10-388-838-11	Sequence 11, Appl
1025	44	2.6	140152	18	US-10-684-422-66	Sequence 66, Appl

c1026	43.8	2.6	282	18	US-10-674-124A-8108	Sequence 8108, Ap
1027	43.8	2.6	337	18	US-10-674-124A-22631	Sequence 22631, A
1028	43.8	2.6	5403	10	US-09-902-563-3	Sequence 3, Appli
1029	43.8	2.6	5403	15	US-10-096-255-3	Sequence 3, Appli
1030	43.8	2.6	37135	17	US-10-052-482-151	Sequence 151, App
1031	43.8	2.6	47856	13	US-10-087-192-157	Sequence 157, App
1032	43.6	2.6	224	18	US-10-674-124A-25046	Sequence 25046, A
c1033	43.6	2.6	42811	17	US-10-085-117-37	Sequence 37, Appl
1034	43.4	2.6	615	13	US-10-027-632-159212	Sequence 159212,
1035	43.4	2.6	615	17	US-10-027-632-159212	Sequence 159212,
1036	43.4	2.6	1056	18	US-10-767-701-7966	Sequence 7966, Ap
c1037	43.4	2.6	1133	14	US-10-198-846-7189	Sequence 7189, Ap
1038	43.4	2.6	251364	14	US-10-175-523-58	Sequence 58, Appl
1039	43.4	2.6	251364	14	US-10-175-523-61	Sequence 61, Appl
1040	43.4	2.6	251364	14	US-10-175-523-79	Sequence 79, Appl
1041	43.4	2.6	659158	9	US-09-771-208-20	Sequence 20, Appl
1042	43.2	2.5	313	18	US-10-674-124A-20730	Sequence 20730, A
1043	43.2	2.5	330	18	US-10-674-124A-10022	Sequence 10022, A
c1044	43.2	2.5	21230	13	US-10-087-192-601	Sequence 601, App
c1045	43.2	2.5	96598	11	US-09-997-722-127	Sequence 127, App
1046	43.2	2.5	188017	13	US-10-087-192-1951	Sequence 1951, Ap
c1047	43	2.5	201	19	US-10-741-600-63590	Sequence 63590, A
c1048	43	2.5	409	18	US-10-674-124A-12033	Sequence 12033, A
1049	43	2.5	984	14	US-10-160-501-28	Sequence 28, Appl
1050	43	2.5	1855	14	US-10-160-501-26	Sequence 26, Appl
1497	43	2.5	2531	19	US-10-931-886-33	Sequence 33, Appl
1499	43	2.5	2652	13	US-10-027-632-111629	Sequence 111629,
1500	43	2.5	2652	13	US-10-027-632-111630	Sequence 111630,

Search completed: April 30, 2005, 04:31:23
Job time : 999 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:31:00 ; Search time 176 Seconds
(without alignments)
980.515 Million cell updates/sec

Title: US-10-063-583-74
Perfect score: 1779
Sequence: 1 MLFSALLLEVIWILAADGGQ.....KRLENRKSVVFTSAQATTEA 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1779	100.0	337	1	CAHE_HUMAN	Q9ulx7 homo sapien
2	1500	84.3	337	1	CAHE_MOUSE	Q9wvt6 mus musculu
3	698	39.2	355	1	CAHC_RABIT	Q9mz30 oryctolagus
4	696.5	39.2	354	1	CAHC_HUMAN	O43570 homo sapien
5	690	38.8	354	1	CAHC_MOUSE	Q8ci85 mus musculu
6	684	38.4	344	2	Q8K2J1	Q8k2j1 mus musculu
7	562	31.6	459	1	CAH9_HUMAN	Q16790 homo sapien
8	561.5	31.6	437	1	CAH9_MOUSE	Q8vhb5 mus musculu
9	535.5	30.1	307	1	CAH6_SHEEP	P08060 ovis aries
10	533	30.0	525	2	Q6GQ30	Q6gq30 xenopus lae
11	530	29.8	319	1	CAH6_BOVIN	P18915 bos taurus
12	518.5	29.1	320	2	Q865C0	Q865c0 canis famil
13	498	28.0	308	1	CAH6_HUMAN	P23280 homo sapien
14	465	26.1	259	1	CAH2_TRIHK	Q8uwa5 tribolodon
15	460.5	25.9	309	2	Q6NWD3	Q6nwd3 brachydanio
16	458.5	25.8	717	2	Q8CIN0	Q8cin0 rattus norv
17	458.5	25.8	1168	2	Q8CIN1	Q8cin1 rattus norv
18	458.5	25.8	1397	2	Q8CIN2	Q8cin2 rattus norv
19	458.5	25.8	1426	2	Q8CIN3	Q8cin3 rattus norv
20	458.5	25.8	1442	1	PTPG_MOUSE	Q05909 mus musculu
21	456	25.6	260	2	Q6PFU7	Q6pfu7 brachydanio
22	452.5	25.4	1422	1	PTPG_CHICK	Q98936 gallus gall
23	451.5	25.4	1445	1	PTPG_HUMAN	P23470 homo sapien
24	451	25.4	263	2	Q6PBI7	Q6pbi7 brachydanio
25	450	25.3	306	2	Q7ZUE2	Q7zue2 brachydanio
26	447	25.1	317	1	CAH6_MOUSE	P18761 mus musculu
27	440	24.7	317	2	Q7TNG9	Q7tng9 mus musculu
28	440	24.7	325	2	Q80YB7	Q80yb7 mus musculu
29	427	24.0	314	2	Q6DBS1	Q6dbs1 brachydanio
30	423	23.8	309	1	CAH4_RAT	P48284 rattus norv
31	422.5	23.7	262	1	CAHD_HUMAN	Q8n1q1 homo sapien
32	421	23.7	264	2	Q811X4	Q811x4 mus musculu
33	420	23.6	259	1	CAH2_HUMAN	P00918 homo sapien
34	419.5	23.6	261	2	Q8JG56	Q8jg56 lepisosteus
35	419.5	23.6	308	1	CAH4_RABIT	P48283 oryctolagus
36	415	23.3	259	1	CAH2_CHICK	P07630 gallus gall
37	414.5	23.3	262	1	CAH1_MONDO	Q8hy33 monodelphis
38	413	23.2	259	1	CAH2_RABIT	P00919 oryctolagus
39	412.5	23.2	260	1	CAH1_SHEEP	P48282 ovis aries
40	411	23.1	260	2	Q68YC1	Q68yc1 oncorhynchu
41	411	23.1	264	1	CAH7_HUMAN	P43166 homo sapien
42	410	23.0	259	1	CAH2_BOVIN	P00921 bos taurus
43	409	23.0	306	2	Q63839	Q63839 mus sp. rec
44	407.5	22.9	255	1	CAH7_MOUSE	Q9erq8 mus musculu
45	406	22.8	259	1	CAH2_SHEEP	P00922 ovis aries
46	406	22.8	259	1	CAH3_HUMAN	P07451 homo sapien
47	404	22.7	259	1	CAH2_RAT	P27139 rattus norv
48	404	22.7	260	1	CAHZ_BRARE	Q92051 brachydanio
49	402.5	22.6	260	1	CAH1_HORSE	P00917 equus cabal
50	402	22.6	260	2	Q7TPE1	Q7tpe1 mus musculu
51	401.5	22.6	260	1	CAH1_MOUSE	P13634 mus musculu
52	401	22.5	259	2	Q6R4A2	Q6r4a2 oncorhynchu
53	400.5	22.5	297	2	Q6R4A1	Q6r4a1 oncorhynchu
54	399	22.4	312	2	Q7SYW3	Q7syw3 xenopus lae
55	398	22.4	305	1	CAH4_MOUSE	Q64444 mus musculu
56	397	22.3	258	2	Q6JRS3	Q6jrs3 oreochromis
57	397	22.3	259	1	CAH2_MOUSE	P00920 mus musculu
58	396	22.3	309	2	Q6WLH6	Q6wlh6 anopheles g
59	395	22.2	260	2	Q6DUZ8	Q6duz8 gekko japon
60	393	22.1	259	1	CAH3_MOUSE	P16015 mus musculu
61	392	22.0	330	2	Q7Q823	Q7q823 anopheles g
62	391.5	22.0	262	1	CAHD_MOUSE	Q9d6n1 mus musculu
63	390.5	22.0	304	1	CAH5_RAT	P43165 rattus norv
64	389.5	21.9	263	2	Q6DCX9	Q6dcx9 xenopus lae
65	389	21.9	259	1	CAH3_RAT	P14141 rattus norv
66	387	21.8	259	1	CAH3_HORSE	P07450 equus cabal
67	386.5	21.7	260	1	CAH1_MACMU	P00916 macaca mula
68	386	21.7	2316	1	PTPZ_RAT	Q62656 rattus norv
69	385.5	21.7	260	1	CAH1_MACNE	P35217 macaca nemestrina
70	384.5	21.6	260	1	CAH1_GORGO	Q7m316 gorilla gor
71	382.5	21.5	299	1	CAH5_MOUSE	P23589 mus musculu
72	382	21.5	429	2	Q8C4M8	Q8c4m8 mus musculu
73	381	21.4	298	2	Q8WRV4	Q8wrv4 aedes aegyp
74	380.5	21.4	260	1	CAH1_HUMAN	P00915 homo sapien
75	380.5	21.4	312	1	CAH4_HUMAN	P22748 homo sapien
76	379.5	21.3	1457	2	Q6IRM3	Q6irm3 xenopus lae
77	379	21.3	305	1	CAH5_HUMAN	P35218 homo sapien
78	379	21.3	324	1	CAHF_MOUSE	Q99n23 mus musculu
79	378.5	21.3	260	1	CAH1_PANTR	Q7m317 pan troglod
80	378	21.2	260	2	Q7T2K6	Q7t2k6 oncorhynchu
81	377.5	21.2	503	2	Q6DC74	Q6dc74 brachydanio
82	376.5	21.2	310	1	CAH5_CAEEL	Q10462 caenorhabdi
83	374	21.0	261	2	Q9XZG6	Q9xzg6 anthopleura
84	371.5	20.9	1576	2	Q9I908	Q9i908 xenopus lae
85	371.5	20.9	2271	2	Q9I909	Q9i909 xenopus lae
86	371	20.9	1612	2	Q9WUT8	Q9wut8 mus musculu
87	370	20.8	312	1	CAH4_BOVIN	Q95323 bos taurus
88	365	20.5	1005	2	O76043	O76043 homo sapien
89	365	20.5	2314	1	PTPZ_HUMAN	P23471 homo sapien
90	364	20.5	260	2	Q8AVG8	Q8avg8 xenopus lae
91	363	20.4	289	1	CAH8_HUMAN	P35219 homo sapien
92	363	20.4	290	1	CAH8_MOUSE	P28651 mus musculu
93	363	20.4	328	2	Q7QKJ5	Q7qkj5 anopheles g
94	362	20.3	335	2	Q9VTU8	Q9vtu8 drosophila
95	358	20.1	260	2	Q7ZYU6	Q7zyu6 xenopus lae
96	357.5	20.1	311	2	Q6NLI8	Q6nli8 drosophila
97	357.5	20.1	311	2	Q9VB76	Q9vb76 drosophila
98	356	20.0	597	2	Q810U6	Q810u6 mus musculu
99	352.5	19.8	318	2	Q6NTY3	Q6nty3 xenopus lae
100	351.5	19.8	323	2	Q7QBY2	Q7qby2 anopheles g
101	347	19.5	261	2	Q71UK2	Q71uk2 mus musculu
102	344	19.3	317	2	Q66HG6	Q66hg6 rattus norv
103	343.5	19.3	317	1	CA5B_HUMAN	Q9y2d0 homo sapien
104	343	19.3	208	2	Q86YU0	Q86yu0 homo sapien

105	343	19.3	317	1	CA5B_MOUSE	Q9qza0	mus musculu
106	342.5	19.3	243	2	Q8MPH8	Q8mph8	riftia pach
107	340	19.1	235	1	CAH1_RABIT	P07452	oryctolagus
108	336.5	18.9	331	2	Q6GQN2	Q6gqn2	brachydanio
109	336.5	18.9	352	2	Q7QJJ8	Q7qjj8	anopheles g
110	330.5	18.6	270	2	Q9V396	Q9v396	drosophila
111	324.5	18.2	251	2	Q811E8	Q811e8	mus musculu
112	324.5	18.2	288	2	Q7QLL3	Q7qll3	anopheles g
113	323.5	18.2	327	2	Q9W316	Q9w316	drosophila
114	319.5	18.0	246	1	CAH3_CAEEL	Q27504	caenorhabdi
115	318	17.9	321	2	Q9W3P7	Q9w3p7	drosophila
116	318	17.9	322	2	Q9VD19	Q9vd19	drosophila
117	317	17.8	305	2	Q7SZR2	Q7szr2	brachydanio
118	316.5	17.8	266	2	Q7QBY3	Q7qby3	anopheles g
119	312.5	17.6	275	2	Q8P3S8	Q8p3s8	xanthomonas
120	312	17.5	328	1	CAHA_HUMAN	Q9ns85	homo sapien
121	312	17.5	328	1	CAHA_MACFA	Q9n085	macaca fasc
122	312	17.5	328	1	CAHA_MOUSE	P61215	mus musculu
123	312	17.5	334	2	Q68D28	Q68d28	homo sapien
124	308.5	17.3	238	2	Q87G15	Q87g15	vibrio para
125	305	17.1	192	2	Q9DCT3	Q9dct3	mus musculu
126	302.5	17.0	235	2	Q9V9Y8	Q9v9y8	drosophila
127	300	16.9	304	2	Q6NZJ2	Q6nzj2	mus musculu
128	299	16.8	282	2	Q7PRN8	Q7prn8	anopheles g
129	294.5	16.6	376	2	Q7PQV5	Q7pqv5	anopheles g
130	292.5	16.4	257	2	Q6WLH5	Q6wlh5	anopheles g
131	291.5	16.4	328	1	CAHB_MOUSE	O70354	mus musculu
132	289.5	16.3	304	2	Q9VH26	Q9vh26	drosophila
133	288.5	16.2	240	2	Q8D412	Q8d412	vibrio vuln
134	288.5	16.2	328	1	CAHB_HUMAN	O75493	homo sapien
135	288.5	16.2	328	2	Q811X3	Q811x3	rattus norv
136	286.5	16.1	249	2	Q7Q9S6	Q7q9s6	anopheles g
137	285.5	16.0	249	2	Q7PTT6	Q7ptt6	anopheles g
138	284.5	16.0	257	2	Q7MFI3	Q7mfi3	vibrio vuln
139	283.5	15.9	328	1	CAHB_SHEEP	Q95203	ovis aries
140	283.5	15.9	328	2	Q866X7	Q866x7	bos taurus
141	282	15.9	252	2	Q6NBN4	Q6nbn4	rhodopseudo
142	281	15.8	241	2	Q6LM17	Q6lm17	photobacter
143	280.5	15.8	275	2	Q9KFW1	Q9kfw1	bacillus ha
144	280	15.7	292	2	Q7QEE7	Q7qee7	anopheles g
145	278.5	15.7	285	2	Q9Q8Z4	Q9q8z4	rabbit fibr
146	276.5	15.5	255	2	Q9XDX8	Q9xdx8	rhodopseudo
147	275.5	15.5	239	2	Q87JM7	Q87jm7	vibrio para
148	275.5	15.5	337	1	CAH2_CAEEL	Q18932	caenorhabdi
149	273	15.3	331	2	Q866X6	Q866x6	sus scrofa
150	272.5	15.3	252	1	CAH_NEIGO	Q50940	neisseria g
151	272.5	15.3	286	2	Q9Q8L7	Q9q8l7	myxoma viru
152	267.5	15.0	304	1	CAHH_VARV	P33065	variola vir
153	267.5	15.0	304	2	Q8QMV3	Q8qmv3	cowpox viru
154	267.5	15.0	304	2	Q66218	Q66218	cowpox viru
155	267.5	15.0	304	2	Q76Q02	Q76q02	variola min
156	267.5	15.0	304	2	Q9JFA1	Q9jfa1	vaccinia vi
157	267	15.0	264	1	CAH_ANASP	P94170	anabaena sp
158	266.5	15.0	146	2	Q6UIR8	Q6uir8	macaca mula
159	266.5	15.0	199	2	Q9V9Y6	Q9v9y6	drosophila
160	266.5	15.0	304	1	CAHH_VACCC	P20508	vaccinia vi
161	266.5	15.0	304	2	Q80DX3	Q80dx3	cowpox viru
162	264.5	14.9	246	1	CAH_KLEPN	O52535	klebsiella
163	263.5	14.8	244	2	Q6DAJ6	Q6daj6	erwinia car
164	263.5	14.8	304	1	CAHH_VACCV	P04195	vaccinia vi
165	263.5	14.8	304	2	Q6RZI9	Q6rzi9	rabbitpox v
166	263.5	14.8	304	2	Q76ZR9	Q76zr9	vaccinia vi
167	263	14.8	250	2	Q989K6	Q989k6	rhizobium l
168	262.5	14.8	304	2	Q8JLB8	Q8jlb8	ectromelia
169	262	14.7	266	2	Q6EPY7	Q6epy7	oryza sativ
170	261.5	14.7	304	2	Q8V2R1	Q8v2r1	camelpox vi
171	261.5	14.7	304	2	Q90197	Q90197	monkeypox v
172	261.5	14.7	304	2	Q66281	Q66281	camelpox vi
173	261.5	14.7	304	2	Q775T1	Q775t1	camelpox vi
174	261	14.7	250	2	Q8KJM6	Q8kjm6	rhizobium l
175	260.5	14.6	279	2	Q8MZG0	Q8mzg0	drosophila
176	260	14.6	303	2	Q83439	Q83439	ectromelia
177	259.5	14.6	272	2	Q8MTV2	Q8mtv2	drosophila
178	259.5	14.6	304	2	O57211	O57211	vaccinia vi
179	259.5	14.6	304	2	Q8V4Y0	Q8v4y0	monkeypox v
180	259.5	14.6	332	2	Q9W2Q2	Q9w2q2	drosophila
181	258.5	14.5	146	2	Q6UIR9	Q6uir9	pan troglod
182	257.5	14.5	239	2	Q9KMP6	Q9kmp6	vibrio chol
183	257.5	14.5	279	2	Q8IMV4	Q8imv4	drosophila
184	255	14.3	256	2	Q8CVC3	Q8cvc3	streptococc
185	253	14.2	272	2	Q9M519	Q9m519	dioscorea a
186	252.5	14.2	244	1	CAH_ERWCA	O52538	erwinia car
187	250.5	14.1	265	2	Q82WQ7	Q82wq7	nitrosomona
188	250	14.1	291	2	Q89VB0	Q89vb0	bradyrhizob
189	249.5	14.0	235	2	Q9V9Y7	Q9v9y7	drosophila
190	247.5	13.9	200	2	Q7LZP1	Q7lzp1	galeocerdo
191	247.5	13.9	235	2	Q8WQD8	Q8wqd8	caenorhabdi
192	247.5	13.9	280	2	Q21614	Q21614	caenorhabdi
193	246	13.8	247	2	Q7VHP3	Q7vhp3	helicobacte
194	245	13.8	365	1	CAH1_CAEEL	Q20781	caenorhabdi
195	244.5	13.7	241	2	Q7QMK6	Q7qmk6	anopheles g
196	241	13.5	275	2	Q6Z9S4	Q6z9s4	oryza sativ
197	235	13.2	250	2	Q9W3C8	Q9w3c8	drosophila
198	235	13.2	252	2	Q9CJT6	Q9cjt6	pasteurella
199	235	13.2	272	2	Q75N35	Q75n35	dioscorea p
200	233	13.1	589	1	CAH_DUNSA	P54212	dunaliella
201	230.5	13.0	249	2	Q931C3	Q931c3	rhizobium m
202	229.5	12.9	225	2	Q8MS01	Q8ms01	drosophila
203	229	12.9	268	2	Q75N34	Q75n34	dioscorea p
204	229	12.9	271	2	Q8PFA4	Q8pfa4	xanthomonas
205	227.5	12.8	224	2	Q9MZT3	Q9mzt3	megaderma l
206	227.5	12.8	273	2	Q9M4Z0	Q9m4z0	dioscorea a
207	226.5	12.7	273	2	Q39695	Q39695	dioscorea c
208	226.5	12.7	275	2	Q8L817	Q81817	arabidopsis
209	224.5	12.6	273	2	Q9M501	Q9m501	dioscorea a
210	218.5	12.3	274	2	Q84UV8	Q84uv8	nicotiana l
211	218	12.3	276	2	Q7XVG9	Q7xvg9	oryza sativ
212	218	12.3	498	2	Q9SP18	Q9sp18	dunaliella
213	217.5	12.2	276	2	Q8GTK1	Q8gtk1	oryza sativ
214	217	12.2	284	2	O04846	O04846	arabidopsis
215	217	12.2	498	2	Q84UY1	Q84uy1	dunaliella
216	215.5	12.1	248	2	Q9SL34	Q9sl34	arabidopsis
217	213	12.0	276	2	Q6YZ80	Q6yz80	oryza sativ
218	211.5	11.9	275	2	Q6Z9S0	Q6z9s0	oryza sativ
219	211	11.9	224	2	Q65RJ8	Q65rj8	mannheimia
220	209.5	11.8	259	2	O93587	O93587	platichthys
221	208.5	11.7	211	2	Q88U15	Q88u15	lactobacill
222	207	11.6	142	2	O60420	O60420	homo sapien
223	207	11.6	277	2	Q6YZ76	Q6yz76	oryza sativ
224	206.5	11.6	555	2	Q84NF2	Q84nf2	dunaliella
225	205	11.5	110	2	Q7SXQ8	Q7sxq8	pseudopleur
226	204.5	11.5	348	2	O64462	O64462	chlorella s
227	202.5	11.4	555	2	Q9SE49	Q9se49	dunaliella
228	200	11.2	197	2	Q8BPV2	Q8bpv2	mus musculu
229	200	11.2	269	2	Q7QFC1	Q7qfc1	anopheles g
230	199.5	11.2	263	2	Q9LN00	Q9ln00	arabidopsis
231	198	11.1	527	2	Q8MS78	Q8ms78	drosophila
232	197.5	11.1	277	2	Q9FYE3	Q9fye3	arabidopsis
233	193	10.8	319	2	O02637	O02637	caenorhabdi
234	189	10.6	237	2	P95828	P95828	synechococc
235	187.5	10.5	310	2	Q39588	Q39588	chlamydomon
236	183	10.3	188	2	Q940K9	Q940k9	arabidopsis
237	182	10.2	210	2	Q7USW3	Q7usw3	rhodopirell
238	181	10.2	247	2	Q9ZK30	Q9zk30	helicobacte
239	180.5	10.1	196	2	Q6IDD8	Q6idd8	drosophila
240	178	10.0	197	2	Q8IMV3	Q8imv3	drosophila
241	177.5	10.0	2254	2	Q9LN02	Q9ln02	arabidopsis
242	175.5	9.9	279	2	Q7QGP5	Q7qgp5	anopheles g
243	173	9.7	232	2	Q834E4	Q834e4	enterococcu
244	173	9.7	325	2	Q9SWA2	Q9swa2	acetabulari
245	172.5	9.7	315	2	Q9SWA1	Q9swa1	acetabulari
246	171.5	9.6	315	2	Q9SWA0	Q9swa0	acetabulari
247	169.5	9.5	150	2	Q9SUB5	Q9sub5	arabidopsis
248	165.5	9.3	179	2	Q8N4G4	Q8n4g4	homo sapien
249	164	9.2	260	2	Q9SUB4	Q9sub4	arabidopsis
250	163.5	9.2	447	2	Q27908	Q27908	pinctada fu

251	160.5	9.0	377	1	CAH1_CHLRE	P20507	chlamydomon
252	159.5	9.0	380	1	CAH2_CHLRE	P24258	chlamydomon
253	155	8.7	134	2	Q7PLY8	Q7ply8	anopheles g
254	151.5	8.5	288	2	Q7XZ98	Q7xz98	griffithsia
255	144.5	8.1	233	2	Q722A7	Q722a7	listeria mo
256	143.5	8.1	233	2	Q8Y8T3	Q8y8t3	listeria mo
257	143.5	8.1	360	2	Q7S607	Q7s607	neurospora
258	139.5	7.8	233	2	Q92DK6	Q92dk6	listeria in
259	135	7.6	229	2	Q6Z9S3	Q6z9s3	oryza sativ
260	133.5	7.5	81	2	Q8CEY0	Q8cey0	mus musculu
261	131.5	7.4	144	2	Q9SMD6	Q9smd6	laminaria d
262	131	7.4	96	2	Q67UA6	Q67ua6	oryza sativ
263	128	7.2	568	2	Q9NL38	Q9nl38	pinctada ma
264	124.5	7.0	291	2	Q9W2R0	Q9w2r0	drosophila
265	124	7.0	131	2	Q7QEE8	Q7qee8	anopheles g
266	117	6.6	128	2	Q7Q0Z5	Q7q0z5	anopheles g
267	112	6.3	350	2	Q9FM99	Q9fm99	arabidopsis
268	111.5	6.3	99	2	Q8BT66	Q8bt66	mus musculu
269	107.5	6.0	728	2	Q7RRH6	Q7rrh6	plasmodium
270	105.5	5.9	1439	1	PTPK_HUMAN	Q15262	homo sapien
271	105	5.9	1440	2	Q68DT8	Q68dt8	homo sapien
272	105	5.9	1440	2	Q86WJ2	Q86wj2	homo sapien
273	104	5.8	626	2	Q6GUK9	Q6guk9	scophthalmu
274	103.5	5.8	844	2	Q8C462	Q8c462	mus musculu
275	103.5	5.8	1457	1	PTPK_MOUSE	P35822	mus musculu
276	103	5.8	223	2	Q67UA4	Q67ua4	oryza sativ
277	103	5.8	838	2	Q9H9B9	Q9h9b9	homo sapien
278	103	5.8	2472	2	Q66YK6	Q66yk6	homo sapien
279	103	5.8	2472	2	Q6PRU2	Q6pru2	homo sapien
280	102.5	5.8	450	2	Q9KWE6	Q9kwe6	agrobacteri
281	101	5.7	574	2	Q7S2M5	Q7s2m5	neurospora
282	100.5	5.6	1627	2	Q7R446	Q7r446	giardia lam
283	100.5	5.6	1751	2	Q8ML44	Q8ml44	drosophila
284	100.5	5.6	1776	2	Q9V6E1	Q9v6e1	drosophila
285	100.5	5.6	2061	2	O77025	O77025	drosophila
286	100.5	5.6	2062	2	Q8ML45	Q8ml45	drosophila
287	100	5.6	530	2	Q6EAV2	Q6eav2	norovirus g
288	100	5.6	1423	2	Q6NL96	Q6nl96	drosophila
289	100	5.6	1423	2	Q9W1A0	Q9w1a0	drosophila
290	99	5.6	202	2	O25798	O25798	helicobacte
291	99	5.6	626	2	Q6GUK8	Q6guk8	scophthalmu
292	98	5.5	517	2	Q9JH41	Q9jh41	norwalk-lik
293	98	5.5	530	2	Q83884	Q83884	norwalk vir
294	98	5.5	530	2	Q9QT39	Q9qt39	human calic
295	97.5	5.5	82	2	Q670P3	Q670p3	meriones un
296	97	5.5	518	1	FXH1_XENLA	P70056	xenopus lae
297	97	5.5	544	2	Q8NC97	Q8nc97	homo sapien
298	97	5.5	545	2	Q9H4M6	Q9h4m6	homo sapien
299	97	5.5	613	2	Q8WV49	Q8wv49	homo sapien
300	97	5.5	613	2	Q6UVY6	Q6uvy6	homo sapien
301	96	5.4	374	2	Q9FPP8	Q9fpp8	calendula o
302	96	5.4	1751	2	O17143	O17143	drosophila
303	96	5.4	1773	2	O17142	O17142	drosophila
304	95.5	5.4	337	2	Q7KLX2	Q7klx2	drosophila
305	95.5	5.4	338	2	Q9U9Q4	Q9u9q4	drosophila
306	95.5	5.4	461	2	Q99UQ1	Q99uq1	staphylococ
307	95.5	5.4	461	2	Q7A601	Q7a601	staphylococ
308	95.5	5.4	823	1	YRR2_CAEEL	Q09345	caenorhabdi
309	95.5	5.4	1288	2	Q9STV0	Q9stv0	arabidopsis
310	95	5.3	335	2	Q9Y4U3	Q9y4u3	homo sapien
311	95	5.3	694	2	Q9H4Z7	Q9h4z7	homo sapien
312	95	5.3	810	1	Z33A_HUMAN	Q06730	homo sapien
313	95	5.3	3695	1	LMA5_HUMAN	O15230	homo sapien
314	95	5.3	3695	2	Q8TDF8	Q8tdf8	homo sapien
315	94.5	5.3	266	2	O87725	O87725	clostridium
316	94.5	5.3	785	2	Q9J0X4	Q9j0x4	pig-tailed
317	94.5	5.3	1278	2	Q84W86	Q84w86	arabidopsis
318	94	5.3	707	2	Q7NH00	Q7nh00	gloeobacter
319	93.5	5.3	435	2	Q6GHL8	Q6ghl8	staphylococ
320	93.5	5.3	887	2	Q6G2Z4	Q6g2z4	bartonella
321	93	5.2	241	2	Q7XZA2	Q7xza2	griffithsia
322	93	5.2	535	2	Q6T277	Q6t277	aplysia pun
323	93	5.2	734	1	YHU9_YEAST	P32900	saccharomyc
324	92.5	5.2	539	2	Q8CFW3	Q8cfw3	mus musculu
325	92.5	5.2	760	2	Q73M24	Q73m24	treponema d
326	92.5	5.2	1197	1	CAM1_BRARE	Q90478	brachydanio
327	92	5.2	314	2	Q8WPH8	Q8wph8	theileria a
328	92	5.2	546	2	Q7YQK0	Q7yqk0	bos taurus
329	92	5.2	549	2	Q8VHX1	Q8vhx1	mus musculu
330	92	5.2	626	2	Q6PW23	Q6pw23	epinephelus
331	92	5.2	811	2	Q9V5J1	Q9v5j1	drosophila
332	92	5.2	824	2	Q8MKX0	Q8mkx0	drosophila
333	92	5.2	1509	1	GSR1_HUMAN	Q9nzm4	homo sapien
334	91.5	5.1	326	2	Q71VR1	Q71vr1	listeria mo
335	91.5	5.1	401	2	Q972I0	Q972i0	sulfolobus
336	91.5	5.1	414	2	Q87CB0	Q87cb0	xylella fas
337	91.5	5.1	435	2	Q8NX17	Q8nx17	staphylococ
338	91.5	5.1	435	2	Q6G9Z6	Q6g9z6	staphylococ
339	91.5	5.1	454	2	Q6NE86	Q6ne86	neurospora
340	91.5	5.1	550	2	Q9TYQ2	Q9tyq2	caenorhabdi
341	91.5	5.1	676	2	Q6CTC4	Q6ctc4	kluyveromyc
342	91.5	5.1	743	2	Q8SXC8	Q8sxc8	drosophila
343	91	5.1	131	2	Q7XZ72	Q7xz72	griffithsia
344	91	5.1	549	2	Q8VI41	Q8vi41	mus musculu
345	91	5.1	631	2	Q84RX6	Q84rx6	oryza sativ
346	91	5.1	862	2	Q6H535	Q6h535	oryza sativ
347	90.5	5.1	326	2	Q8Y3I5	Q8y3i5	listeria mo
348	90.5	5.1	368	1	Y974_HAEIN	P44087	haemophilus
349	90.5	5.1	464	2	Q7XR50	Q7xr50	oryza sativ
350	90.5	5.1	727	2	Q8TF81	Q8tf81	aspergillus
351	90	5.1	354	2	Q90ZI0	Q90zi0	xenopus lae
352	90	5.1	389	2	Q66KH2	Q66kh2	xenopus lae
353	90	5.1	475	2	Q7MDT5	Q7mdt5	vibrio vuln
354	90	5.1	476	2	Q6KYX2	Q6kyx2	picrophilus
355	90	5.1	534	2	Q6T276	Q6t276	aplysia pun
356	90	5.1	622	2	Q9I9J5	Q9i9j5	hippoglossu
357	90	5.1	623	2	Q98990	Q98990	salmo salar
358	90	5.1	623	2	Q98991	Q98991	salmo salar
359	90	5.1	1003	2	Q74Z42	Q74z42	ashbya goss
360	90	5.1	1064	2	Q8DIP1	Q8dip1	synechococc
361	90	5.1	1765	2	Q7US49	Q7us49	rhodopirell
362	89.5	5.0	326	2	Q926Q8	Q926q8	listeria in
363	89.5	5.0	353	2	Q9Y998	Q9y998	aeropyrum p
364	89.5	5.0	394	2	Q8K368	Q8k368	mus musculu
365	89.5	5.0	495	2	Q94E28	Q94e28	oryza sativ
366	89.5	5.0	646	2	Q8JH68	Q8jh68	brachydanio
367	89.5	5.0	1019	2	Q8BJK6	Q8bjk6	mus musculu
368	89.5	5.0	1187	2	Q6QB10	Q6qb10	homo sapien
369	89.5	5.0	2377	1	CCAG_HUMAN	O43497	homo sapien
370	89	5.0	517	2	Q6T275	Q6t275	aplysia pun
371	89	5.0	538	2	Q8N0R6	Q8n0r6	turbo marmo
372	89	5.0	746	1	AD18_MACFA	Q95194	macaca fasc
373	89	5.0	824	2	Q966U9	Q966u9	drosophila
374	89	5.0	1032	2	Q05645	Q05645	schistosoma
375	89	5.0	2069	2	Q9Y1Y9	Q9y1y9	ephydatia f
376	88.5	5.0	522	1	SNX1_MOUSE	Q9wv80	mus musculu
377	88.5	5.0	620	2	Q7T3I5	Q7t3i5	paralichthy
378	88.5	5.0	743	2	Q9W502	Q9w502	drosophila
379	88.5	5.0	744	2	O46076	O46076	drosophila
380	88.5	5.0	1071	2	Q758E3	Q758e3	ashbya goss
381	88.5	5.0	1142	2	Q8LL91	Q8ll91	chlamydomon
382	88.5	5.0	1187	1	TYK2_HUMAN	P29597	homo sapien
383	88	4.9	239	2	Q82VZ5	Q82vz5	nitrosomona
384	88	4.9	569	2	Q6P3G2	Q6p3g2	brachydanio
385	88	4.9	623	2	Q91197	Q91197	oncorhynchu
386	88	4.9	786	2	Q9RZL4	Q9rzl4	deinococcus
387	88	4.9	829	2	Q6P3Z8	Q6p3z8	mus musculu
388	88	4.9	830	1	GCL2_MOUSE	Q9jhd2	mus musculu
389	88	4.9	994	2	Q7ZZ40	Q7zz40	brachydanio
390	88	4.9	1018	2	Q8EDB9	Q8edb9	shewanella
391	87.5	4.9	478	2	Q7PXD6	Q7pxd6	anopheles g
392	87.5	4.9	554	2	O77709	O77709	bos taurus
393	87.5	4.9	885	1	SYA_CHLTE	Q8kg04	chlorobium
394	87.5	4.9	934	2	Q63DJ0	Q63dj0	bacillus ce
395	87.5	4.9	934	2	Q6HL13	Q6hl13	bacillus th
396	87.5	4.9	1176	2	Q6BU13	Q6bu13	debaryomyce

397	87.5	4.9	1342	2	Q64N18	Q64n18 bacteroides
398	87	4.9	276	2	Q88CL4	Q88cl4 pseudomonas
399	87	4.9	482	2	Q90WB5	Q90wb5 anas platyr
400	87	4.9	486	2	O09243	O09243 simian t-ly
401	87	4.9	623	2	Q98992	Q98992 salmo salar
402	87	4.9	669	2	Q707I9	Q707i9 escherichia
403	87	4.9	935	2	Q7M7P8	Q7m7p8 wolinella s
404	87	4.9	936	2	Q84LG6	Q84lg6 oryza sativ
405	87	4.9	1220	2	Q12465	Q12465 saccharomyc
406	87	4.9	2481	2	Q6GQA5	Q6gqa5 xenopus lae
407	86.5	4.9	280	2	Q8D034	Q8d034 yersinia pe
408	86.5	4.9	299	2	Q7PRQ9	Q7prq9 anopheles g
409	86.5	4.9	301	2	Q8ZGF7	Q8zgf7 yersinia pe
410	86.5	4.9	306	1	UCP1_MOUSE	P12242 mus musculu
411	86.5	4.9	312	2	Q8YSI6	Q8ys16 anabaena sp
412	86.5	4.9	522	1	SNX1_RAT	Q99n27 rattus norv
413	86.5	4.9	537	1	ICA1_MOUSE	P13597 mus musculu
414	86.5	4.9	669	2	Q8FAN9	Q8fan9 escherichia
415	86.5	4.9	684	2	Q95P18	Q95p18 palinurus v
416	86.5	4.9	785	2	Q8BUE9	Q8bue9 mus musculu
417	86.5	4.9	855	2	Q8CY44	Q8cy44 bifidobacte
418	86.5	4.9	892	2	Q9TSZ6	Q9tsz6 canis famil
419	86.5	4.9	934	2	Q81ST0	Q81st0 bacillus an
420	86	4.8	235	2	Q35594	Q35594 physarum po
421	86	4.8	307	2	Q9ER18	Q9er18 phodopus su
422	86	4.8	454	2	Q87HA7	Q87ha7 vibrio para
423	86	4.8	487	2	Q8D6X8	Q8d6x8 vibrio vuln
424	86	4.8	530	2	Q83876	Q83876 norwalk vir
425	86	4.8	545	2	O80567	O80567 arabidopsis
426	86	4.8	602	2	Q6J724	Q6j724 rattus norv
427	86	4.8	628	1	NR43_RAT	P51179 rattus norv
428	86	4.8	659	2	Q7MWY5	Q7mwy5 porphyromon
429	86	4.8	867	2	Q68CR3	Q68cr3 homo sapien
430	86	4.8	1065	2	Q6FPC4	Q6fpc4 candida gla
431	86	4.8	1117	1	YDVG_SCHPO	O14232 schizosacch
432	86	4.8	1243	1	WNK4_HUMAN	Q96j92 homo sapien
433	86	4.8	2301	2	Q9ATK5	Q9atk5 chlamydomon
434	85.5	4.8	364	2	Q8MHU3	Q8mhu3 sus scrofa
435	85.5	4.8	377	2	Q20892	Q20892 caenorhabdi
436	85.5	4.8	450	2	Q8TGY3	Q8tgy3 methanopyru
437	85.5	4.8	474	2	Q8WNV0	Q8wnv0 macaca fasc
438	85.5	4.8	483	1	POK9_HUMAN	P63134 homo sapien
439	85.5	4.8	532	2	Q8PHC6	Q8phc6 xanthomonas
440	85.5	4.8	545	2	Q7QWJ9	Q7qwj9 giardia lam
441	85.5	4.8	655	2	Q7TT26	Q7tt26 mus musculu
442	85.5	4.8	807	1	GCR_PAROL	O73673 paralichthy
443	85.5	4.8	959	1	POK3_HUMAN	Q9wjr5 homo sapien
444	85.5	4.8	3194	2	Q9ZLM3	Q9zlm3 helicobacte
445	85.5	4.8	5369	2	Q9R9J0	Q9r9j0 bacillus su
446	85	4.8	200	2	Q9K3L0	Q9k3l0 streptomyce
447	85	4.8	262	2	Q881M4	Q881m4 pseudomonas
448	85	4.8	286	1	DHA2_MYCBO	P64304 mycobacteri
449	85	4.8	286	1	DHA2_MYCTU	P64303 mycobacteri
450	85	4.8	332	2	Q9ZIH2	Q9zih2 pseudomonas
451	85	4.8	384	2	Q9LMC3	Q9lmc3 arabidopsis
452	85	4.8	615	2	Q6CXI2	Q6cxi2 kluyveromyc
453	85	4.8	621	1	MX_ONCMY	Q91192 oncorhynchu
454	85	4.8	660	2	Q6TKV3	Q6tkv3 escherichia
455	85	4.8	2481	1	FINC_XENLA	Q91740 xenopus lae
456	84.5	4.7	263	1	COLI_ACITR	P87352 a corticotr
457	84.5	4.7	301	2	Q6C4U9	Q6c4u9 yarrowia li
458	84.5	4.7	326	2	Q97FN7	Q97fn7 clostridium
459	84.5	4.7	363	2	Q9H5G9	Q9h5g9 homo sapien
460	84.5	4.7	438	2	Q9SNB3	Q9snb3 arabidopsis
461	84.5	4.7	465	2	Q7PQU8	Q7pqu8 anopheles g
462	84.5	4.7	505	1	FXO4_HUMAN	P98177 homo sapien
463	84.5	4.7	509	2	Q8NDG0	Q8ndg0 homo sapien
464	84.5	4.7	512	2	Q6PEZ8	Q6pez8 homo sapien
465	84.5	4.7	591	2	Q9U261	Q9u261 caenorhabdi
466	84.5	4.7	594	2	Q8U6T4	Q8u6t4 agrobacteri
467	84.5	4.7	656	2	Q6YF16	Q6yf16 rattus norv
468	84.5	4.7	731	2	Q6NAL9	Q6nal9 rhodopseudo
469	84.5	4.7	753	2	Q9P6Y6	Q9p6y6 neurospora
470	84.5	4.7	813	2	Q6DG00	Q6dg00 brachydanio
471	84.5	4.7	956	1	POK6_HUMAN	P63133 homo sapien
472	84.5	4.7	1014	1	PK10_HUMAN	P10266 homo sapien
473	84.5	4.7	1041	2	Q6C9C9	Q6c9c9 yarrowia li
474	84.5	4.7	1161	2	Q7EYN1	Q7eyn1 oryza sativ
475	84.5	4.7	1459	1	PK12_HUMAN	P63135 homo sapien
476	84.5	4.7	1612	2	Q83DF0	Q83df0 coxiella bu
477	84.5	4.7	1756	2	Q12193	Q12193 saccharomyc
478	84.5	4.7	1947	2	Q84SE8	Q84se8 oryza sativ
479	84	4.7	322	2	O62322	O62322 caenorhabdi
480	84	4.7	327	2	Q75EZ0	Q75ez0 ashbya goss
481	84	4.7	341	2	Q7RB31	Q7rb31 plasmodium
482	84	4.7	505	2	Q90Y45	Q90y45 brachydanio
483	84	4.7	505	2	Q7SXK7	Q7sxk7 brachydanio
484	84	4.7	510	2	Q7SG07	Q7sg07 neurospora
485	84	4.7	521	2	Q802U6	Q802u6 brachydanio
486	84	4.7	535	2	Q6IWZ0	Q6iwz0 aplysia cal
487	84	4.7	598	2	Q754U5	Q754u5 ashbya goss
488	84	4.7	824	2	Q82CB7	Q82cb7 streptomyce
489	84	4.7	937	2	Q821X3	Q821x3 chlamydophi
490	84	4.7	976	1	EPA1_HUMAN	P21709 homo sapien
491	84	4.7	1073	2	Q6CLP8	Q6clp8 kluyveromyc
492	84	4.7	1269	2	Q6U7I5	Q6u7i5 brachydanio
493	84	4.7	1297	2	Q759H0	Q759h0 ashbya goss
494	84	4.7	1446	2	Q7TP07	Q7tp07 rattus norv
495	84	4.7	2841	1	NF1_MOUSE	Q04690 mus musculu
496	83.5	4.7	306	1	UCP1_RAT	P04633 rattus norv
497	83.5	4.7	312	2	Q9RI89	Q9ri89 streptomyce
498	83.5	4.7	361	2	Q8HX62	Q8hx62 sus scrofa
499	83.5	4.7	389	2	Q9KMQ0	Q9kmq0 vibrio chol
500	83.5	4.7	409	2	Q752K9	Q752k9 ashbya goss
501	83.5	4.7	433	2	Q8N7D8	Q8n7d8 homo sapien
502	83.5	4.7	443	2	Q88HV2	Q88hv2 pseudomonas
503	83.5	4.7	535	2	Q6C3S3	Q6c3s3 yarrowia li
504	83.5	4.7	539	2	O95196	O95196 homo sapien
505	83.5	4.7	566	2	Q71M39	Q71m39 homo sapien
506	83.5	4.7	651	2	Q7QAK9	Q7qak9 anopheles g
507	83.5	4.7	732	2	Q46767	Q46767 escherichia
508	83.5	4.7	758	1	YA93_SCHPO	Q09782 schizosacch
509	83.5	4.7	779	2	Q8IJU6	Q8iju6 plasmodium
510	83.5	4.7	798	2	Q6LL21	Q6ll21 photobacter
511	83.5	4.7	812	1	POK7_HUMAN	Q9qc07 homo sapien
512	83.5	4.7	939	2	Q8FBI6	Q8fb16 escherichia
513	83.5	4.7	954	1	PK17_HUMAN	P63136 homo sapien
514	83.5	4.7	1011	2	O74839	O74839 schizosacch
515	83.5	4.7	1011	2	Q75MD7	Q75md7 homo sapien
516	83.5	4.7	1100	2	Q8CCT8	Q8cct8 mus musculu
517	83.5	4.7	1112	2	Q7T1J8	Q7t1j8 tetraodon n
518	83.5	4.7	1259	1	AUT2_HUMAN	Q8wxx7 homo sapien
519	83.5	4.7	1796	2	Q9Y1M4	Q9y1m4 lymnaea sta
520	83.5	4.7	1951	2	Q9Y1M5	Q9y1m5 lymnaea sta
521	83.5	4.7	2332	2	Q6ALH4	Q6alh4 desulfotale
522	83.5	4.7	5085	1	PCLO_RAT	Q9jks6 rattus norv
523	83	4.7	309	2	Q8JJP9	Q8jjp9 porcine lym
524	83	4.7	344	1	QUEA_LACPL	Q88v04 lactobacill
525	83	4.7	362	2	Q39897	Q39897 glycine max
526	83	4.7	373	2	Q8S0H0	Q8s0h0 oryza sativ
527	83	4.7	380	2	O42600	O42600 xenopus lae
528	83	4.7	424	2	Q8BYL5	Q8byl5 mus musculu
529	83	4.7	448	2	Q7M998	Q7m998 wolinella s
530	83	4.7	498	1	YAOI_SCHPO	Q10097 schizosacch
531	83	4.7	537	2	Q6PE66	Q6pe66 mus musculu
532	83	4.7	675	2	Q654G8	Q654g8 oryza sativ
533	83	4.7	715	2	Q6UXJ9	Q6uxj9 homo sapien
534	83	4.7	731	2	Q76MG4	Q76mg4 mus musculu
535	83	4.7	739	1	AD18_HUMAN	Q9y3q7 homo sapien
536	83	4.7	765	1	BAR1_MOUSE	O70445 mus musculu
537	83	4.7	791	2	Q9KU26	Q9ku26 vibrio chol
538	83	4.7	1005	2	Q7NNY2	Q7nny2 gloeobacter
539	83	4.7	1032	2	Q8WZZ2	Q8wzz2 neurospora
540	83	4.7	1032	2	Q7RWZ4	Q7rwz4 neurospora
541	83	4.7	1102	2	Q9LVP0	Q9lvp0 arabidopsis
542	83	4.7	1235	1	KPB2_MOUSE	Q8bwj3 mus musculu

543	83	4.7	1344	2	Q93YQ1	Q93yq1 arabidopsis
544	83	4.7	1384	2	Q9SR85	Q9sr85 arabidopsis
545	83	4.7	1756	2	Q12269	Q12269 saccharomyc
546	83	4.7	1902	2	Q9Y878	Q9y878 coccidioide
547	83	4.7	2425	2	Q95MJ0	Q95mj0 tupaia glis
548	82.5	4.6	202	2	Q888I1	Q888i1 pseudomonas
549	82.5	4.6	291	1	CDK2_ENTHI	Q04770 entamoeba h
550	82.5	4.6	306	1	UCP1_MESAU	P04575 mesocricetu
551	82.5	4.6	320	2	Q9RBW0	Q9rbw0 pseudomonas
552	82.5	4.6	357	2	Q9FJ18	Q9fj18 arabidopsis
553	82.5	4.6	378	2	Q6K1Z6	Q6k1z6 oryza sativ
554	82.5	4.6	482	2	Q6MZR3	Q6mzr3 homo sapien
555	82.5	4.6	635	2	Q7T2M3	Q7t2m3 carassius a
556	82.5	4.6	650	2	Q6BLX3	Q6blx3 debaryomyce
557	82.5	4.6	652	2	Q6BKX5	Q6bkx5 debaryomyce
558	82.5	4.6	716	2	Q8LM77	Q8lm77 oryza sativ
559	82.5	4.6	755	2	Q9HAK5	Q9hak5 homo sapien
560	82.5	4.6	793	2	Q94BY0	Q94by0 arabidopsis
561	82.5	4.6	838	2	Q9K6W8	Q9k6w8 bacillus ha
562	82.5	4.6	912	2	Q9SSD8	Q9ssd8 arabidopsis
563	82.5	4.6	934	2	Q73AV1	Q73av1 bacillus ce
564	82.5	4.6	987	2	Q8SXJ5	Q8sxj5 drosophila
565	82.5	4.6	987	2	Q9V9Q2	Q9v9q2 drosophila
566	82.5	4.6	1119	2	Q9N4C3	Q9n4c3 caenorhabdi
567	82.5	4.6	1221	2	Q7QEC9	Q7qec9 anopheles g
568	82.5	4.6	1413	2	Q6YNQ7	Q6ynq7 botrytis vi
569	82.5	4.6	1511	2	Q7R203	Q7r203 giardia lam
570	82.5	4.6	1749	2	Q99337	Q99337 saccharomyc
571	82.5	4.6	1755	2	Q03612	Q03612 saccharomyc
572	82.5	4.6	1755	2	Q03619	Q03619 saccharomyc
573	82.5	4.6	1755	2	Q12088	Q12088 saccharomyc
574	82.5	4.6	1755	2	Q12141	Q12141 saccharomyc
575	82.5	4.6	1755	2	Q12273	Q12273 saccharomyc
576	82.5	4.6	1755	2	Q92393	Q92393 saccharomyc
577	82.5	4.6	1756	2	Q12316	Q12316 saccharomyc
578	82.5	4.6	1793	2	O13535	O13535 saccharomyc
579	82.5	4.6	4019	2	Q9VJB4	Q9vjb4 drosophila
580	82	4.6	187	2	Q9VI77	Q9vi77 drosophila
581	82	4.6	344	2	Q9RRC5	Q9rrc5 deinococcus
582	82	4.6	359	2	Q8HT39	Q8ht39 isopterygiu
583	82	4.6	403	2	Q8TEL7	Q8tel7 homo sapien
584	82	4.6	429	2	Q9ZL62	Q9zl62 helicobacte
585	82	4.6	433	2	Q6NRA9	Q6nra9 xenopus lae
586	82	4.6	445	2	Q80UY3	Q80uy3 mus musculu
587	82	4.6	447	2	Q87EH5	Q87eh5 xylella fas
588	82	4.6	462	2	Q8QGE4	Q8qge4 xiphophorus
589	82	4.6	506	2	Q6N090	Q6n090 homo sapien
590	82	4.6	539	2	Q6CBK6	Q6cbk6 yarrowia li
591	82	4.6	541	2	Q8HT49	Q8ht49 plagiotheci
592	82	4.6	605	2	Q62224	Q62224 mus musculu
593	82	4.6	667	1	YYAE_BACSU	P37519 bacillus su
594	82	4.6	791	2	Q7XP28	Q7xp28 oryza sativ
595	82	4.6	865	2	Q8XY19	Q8xy19 ralstonia s
596	82	4.6	888	1	SYA_RHILO	Q98nq5 rhizobium l
597	82	4.6	977	2	Q62269	Q62269 mus musculu
598	82	4.6	991	2	Q62223	Q62223 mus musculu
599	82	4.6	1014	2	Q68D69	Q68d69 homo sapien
600	82	4.6	1178	1	DSRA_MOUSE	Q99mu3 mus musculu
601	82	4.6	1195	2	Q6BKG7	Q6bkg7 debaryomyce
602	82	4.6	1203	2	Q6ZQ56	Q6zq56 mus musculu
603	82	4.6	1234	1	NPHN_RAT	Q9r044 rattus norv
604	82	4.6	1252	2	Q9JIX2	Q9jix2 rattus norv
605	82	4.6	1302	1	NRG_DROME	P20241 drosophila
606	82	4.6	1413	2	Q7QFK9	Q7qfk9 anopheles g
607	82	4.6	1442	2	Q92735	Q92735 homo sapien
608	82	4.6	1553	2	Q8HZK3	Q8hzk3 sus scrofa
609	82	4.6	1766	2	Q25668	Q25668 plasmodium
610	82	4.6	2588	2	Q8YTR5	Q8ytr5 anabaena sp
611	82	4.6	3616	2	Q7PPF9	Q7ppf9 anopheles g
612	82	4.6	4823	2	O93321	O93321 fugu rubrip
613	82	4.6	5085	2	Q70LM4	Q70lm4 bacillus br
614	81.5	4.6	299	2	Q6AGG2	Q6agg2 leifsonia x
615	81.5	4.6	306	2	Q6F1E0	Q6f1e0 mesoplasma
616	81.5	4.6	307	2	Q8K404	Q8k404 dicrostonyx
617	81.5	4.6	310	1	END4_STRAW	Q82ag6 streptomyce
618	81.5	4.6	358	1	YVAA_BACSU	O32223 bacillus su
619	81.5	4.6	372	2	Q9FPP7	Q9fpp7 calendula o
620	81.5	4.6	400	2	Q26837	Q26837 trypanosoma
621	81.5	4.6	453	2	Q8PW50	Q8pw50 methanosarc
622	81.5	4.6	456	1	NX3B_BOVIN	Q28143 bos taurus
623	81.5	4.6	496	2	Q64SC7	Q64sc7 bacteroides
624	81.5	4.6	522	2	Q6CER2	Q6cer2 yarrowia li
625	81.5	4.6	582	2	Q7QCS2	Q7qcs2 anopheles g
626	81.5	4.6	606	2	Q9XAJ2	Q9xaj2 streptomyce
627	81.5	4.6	616	2	Q6LUB7	Q6lub7 photobacter
628	81.5	4.6	656	1	P137_MOUSE	Q60865 mus musculu
629	81.5	4.6	695	2	Q7N978	Q7n978 photorhabdu
630	81.5	4.6	743	2	Q95RK9	Q95rk9 drosophila
631	81.5	4.6	747	2	Q9DSJ3	Q9dsj3 human immun
632	81.5	4.6	775	2	Q8BQW3	Q8bqw3 mus musculu
633	81.5	4.6	855	2	Q9ZS83	Q9zs83 lycopersico
634	81.5	4.6	949	2	Q97DN1	Q97dn1 clostridium
635	81.5	4.6	956	1	POK5_HUMAN	P63132 homo sapien
636	81.5	4.6	969	1	PK20_HUMAN	Q9uqg0 homo sapien
637	81.5	4.6	994	2	Q9Y489	Q9y489 homo sapien
638	81.5	4.6	1066	2	Q8CK35	Q8ck35 streptomyce
639	81.5	4.6	1076	2	Q26154	Q26154 plasmodium
640	81.5	4.6	1139	2	Q9BHF4	Q9bhf4 leishmania
641	81.5	4.6	1153	2	Q6A1Q0	Q6a1q0 drosophila
642	81.5	4.6	1153	2	Q9V6J8	Q9v6j8 drosophila
643	81.5	4.6	1155	2	Q7KR63	Q7kr63 drosophila
644	81.5	4.6	1301	2	Q7Q1L3	Q7q1l3 anopheles g
645	81.5	4.6	1346	2	Q7KR62	Q7kr62 drosophila
646	81.5	4.6	1351	2	Q7YU89	Q7yu89 drosophila
647	81.5	4.6	1394	2	Q6GPQ1	Q6gpq1 xenopus lae
648	81.5	4.6	1560	2	Q871B2	Q871b2 neurospora
649	81.5	4.6	1709	2	Q93H59	Q93h59 streptomyce
650	81.5	4.6	1755	1	YJZ7_YEAST	P47098 saccharomyc
651	81.5	4.6	2061	2	Q8NJI8	Q8nj18 monascus an
652	81.5	4.6	2317	2	Q962X1	Q962x1 paramecium
653	81	4.6	297	1	RPOF_STRAU	P37970 streptomyce
654	81	4.6	312	2	Q8WPJ1	Q8wpj1 theileria a
655	81	4.6	312	2	Q7Z285	Q7z285 theileria s
656	81	4.6	313	2	Q8WPI8	Q8wpi8 theileria a
657	81	4.6	347	2	Q8UKN8	Q8ukn8 agrobacteri
658	81	4.6	348	2	Q88LQ3	Q88lq3 pseudomonas
659	81	4.6	359	2	O62489	O62489 caenorhabdi
660	81	4.6	379	2	Q8HT44	Q8ht44 pylaisia in
661	81	4.6	401	2	Q26719	Q26719 trypanosoma
662	81	4.6	401	2	Q7JPZ0	Q7jpz0 trypanosoma
663	81	4.6	401	2	Q7KPI7	Q7kpi7 trypanosoma
664	81	4.6	409	2	Q8VZK6	Q8vzk6 arabidopsis
665	81	4.6	411	1	LCYB_SYNP7	Q55276 synechococc
666	81	4.6	429	2	Q6P2D5	Q6p2d5 homo sapien
667	81	4.6	438	2	Q6ACB0	Q6acb0 leifsonia x
668	81	4.6	449	2	O53390	O53390 m probable
669	81	4.6	449	2	Q7TWP1	Q7twp1 mycobacteri
670	81	4.6	460	2	Q9ZR27	Q9zr27 perilla fru
671	81	4.6	462	2	Q98ES9	Q98es9 rhizobium l
672	81	4.6	479	2	Q9HHK3	Q9hhk3 halobacteri
673	81	4.6	539	2	Q6FT15	Q6ft15 candida gla
674	81	4.6	543	2	Q44235	Q44235 anabaena sp
675	81	4.6	543	2	Q7A2D7	Q7a2d7 anabaena sp
676	81	4.6	626	2	Q6TN15	Q6tn15 siniperca c
677	81	4.6	640	2	Q6A6I8	Q6a6i8 propionibac
678	81	4.6	642	2	Q64TA9	Q64ta9 bacteroides
679	81	4.6	642	2	Q7ZX03	Q7zx03 xenopus lae
680	81	4.6	705	2	Q8CAL4	Q8cal4 mus musculu
681	81	4.6	706	2	Q8CBZ9	Q8cbz9 mus musculu
682	81	4.6	787	2	Q8CFV2	Q8cfv2 mus musculu
683	81	4.6	791	1	YJD1_SCHPO	O74504 schizosacch
684	81	4.6	793	2	O70246	O70246 mus musculu
685	81	4.6	800	2	Q6Y9I6	Q6y9i6 human immun
686	81	4.6	803	2	Q9UNY1	Q9uny1 homo sapien
687	81	4.6	807	2	Q8CW69	Q8cw69 escherichia
688	81	4.6	892	2	Q9Y6F6	Q9y6f6 homo sapien

689	81	4.6	939	2	Q7SD71	Q7sd71	neurospora
690	81	4.6	942	2	Q6FSW6	Q6fsw6	candida gla
691	81	4.6	1007	2	Q8WX70	Q8wx70	homo sapien
692	81	4.6	1187	2	Q28613	Q28613	oryctolagus
693	81	4.6	1189	2	Q8YTD1	Q8ytd1	anabaena sp
694	81	4.6	1389	2	Q6DRM6	Q6drm6	brachydanio
695	81	4.6	1604	2	Q07793	Q07793	saccharomyc
696	81	4.6	1755	2	Q12414	Q12414	saccharomyc
697	81	4.6	1793	2	Q8TEP3	Q8tep3	homo sapien
698	81	4.6	2325	2	Q7Z7A1	Q7z7a1	homo sapien
699	81	4.6	3317	2	Q9RAH2	Q9rah2	nostoc sp.
700	81	4.6	5457	2	Q83VS1	Q83vs1	pseudomonas
701	80.5	4.5	248	2	Q9FFB5	Q9ffb5	arabidopsis
702	80.5	4.5	253	1	CAL_ARATH	Q39081	arabidopsis
703	80.5	4.5	264	2	Q9W7F6	Q9w7f6	polyodon sp
704	80.5	4.5	268	1	NAGB_BORBU	O30564	borrelia bu
705	80.5	4.5	272	2	Q7PYS9	Q7pys9	anopheles g
706	80.5	4.5	277	2	Q6DDE0	Q6dde0	xenopus lae
707	80.5	4.5	298	2	Q7VGJ7	Q7vgj7	helicobacte
708	80.5	4.5	300	2	Q8GAM7	Q8gam7	arthrobacte
709	80.5	4.5	306	1	ARC2_DEIRA	Q9ry72	deinococcus
710	80.5	4.5	318	2	Q88H49	Q88h49	pseudomonas
711	80.5	4.5	331	2	Q82UE7	Q82ue7	nitrosomona
712	80.5	4.5	364	2	Q860U5	Q860u5	sus scrofa
713	80.5	4.5	379	2	Q6QPZ1	Q6qpz1	lactococcus
714	80.5	4.5	381	1	PRC1_CORGL	Q8nsh7	corynebacte
715	80.5	4.5	398	2	Q725A2	Q725a2	listeria mo
716	80.5	4.5	406	2	Q96U68	Q96u68	neurospora
717	80.5	4.5	417	2	Q7WUA1	Q7wua1	cycloclasti
718	80.5	4.5	418	2	Q72TH6	Q72th6	leptospira
719	80.5	4.5	418	2	Q8F1T7	Q8f1t7	leptospira
720	80.5	4.5	448	1	NCAP_CVBEN	Q91a22	bovine coro
721	80.5	4.5	448	1	NCAP_CVBLU	Q8v432	bovine coro
722	80.5	4.5	448	2	Q6W358	Q6w358	human enter
723	80.5	4.5	472	1	PEDA_STRPY	Q9a0m0	streptococc
724	80.5	4.5	472	2	Q8P1N3	Q8p1n3	streptococc
725	80.5	4.5	480	2	Q8C901	Q8c901	mus musculu
726	80.5	4.5	493	1	SYK_OCEIH	Q8eu10	oceanobacil
727	80.5	4.5	509	2	Q39658	Q39658	cucumis sat
728	80.5	4.5	523	2	Q6ZMP1	Q6zmp1	homo sapien
729	80.5	4.5	551	2	Q981W0	Q981w0	rhizobium l
730	80.5	4.5	600	2	Q8FPD5	Q8fpd5	corynebacte
731	80.5	4.5	602	2	Q78WQ9	Q78wq9	mus musculu
732	80.5	4.5	602	2	Q8BS83	Q8bs83	mus musculu
733	80.5	4.5	602	2	Q9CRC8	Q9crc8	mus musculu
734	80.5	4.5	615	2	Q6ZBS2	Q6zbs2	oryza sativ
735	80.5	4.5	619	2	Q8MT81	Q8mt81	drosophila
736	80.5	4.5	625	2	Q9FMD7	Q9fmd7	arabidopsis
737	80.5	4.5	632	2	Q6GN05	Q6gn05	xenopus lae
738	80.5	4.5	707	2	Q6IMN3	Q6imn3	mus musculu
739	80.5	4.5	708	2	O80461	O80461	arabidopsis
740	80.5	4.5	708	2	Q8RY67	Q8ry67	arabidopsis
741	80.5	4.5	735	2	Q7QK26	Q7qk26	anopheles g
742	80.5	4.5	748	1	TAP1_GORGO	Q28433	gorilla gor
743	80.5	4.5	748	2	Q6QWC0	Q6qwc0	homo sapien
744	80.5	4.5	769	2	Q6BQM4	Q6bqm4	debaryomyce
745	80.5	4.5	775	2	Q99LI8	Q99li8	mus musculu
746	80.5	4.5	775	2	Q61691	Q61691	mus musculu
747	80.5	4.5	809	2	Q7P7P1	Q7p7p1	fusobacteri
748	80.5	4.5	813	2	Q7Q3Q5	Q7q3q5	anopheles g
749	80.5	4.5	851	2	O65384	O65384	arabidopsis
750	80.5	4.5	857	1	ENV_HV2KR	Q74126	human immun
751	80.5	4.5	857	2	Q8A5N4	Q8a5n4	bacteroides
752	80.5	4.5	860	2	Q6CJJ8	Q6cjj8	kluyveromyc
753	80.5	4.5	888	2	Q6C2Y0	Q6c2y0	yarrowia li
754	80.5	4.5	899	1	GLND_AZOVI	P36223	azotobacter
755	80.5	4.5	1077	2	Q9U209	Q9u209	caenorhabdi
756	80.5	4.5	1157	2	Q8BWE0	Q8bwe0	mus musculu
757	80.5	4.5	1226	2	Q9W1D6	Q9w1d6	drosophila
758	80.5	4.5	1483	2	Q756W3	Q756w3	ashbya goss
759	80.5	4.5	1885	2	Q8TGV2	Q8tgv2	exophiala d
760	80.5	4.5	3197	2	Q9W1D5	Q9w1d5	drosophila
761	80	4.5	259	2	Q8N7Q0	Q8n7q0	homo sapien
762	80	4.5	272	2	Q7TSA8	Q7tsa8	mus musculu
763	80	4.5	312	2	Q82X59	Q82x59	nitrosomona
764	80	4.5	329	2	Q8FS99	Q8fs99	corynebacte
765	80	4.5	345	2	Q6N2X3	Q6n2x3	rhodopseudo
766	80	4.5	362	2	Q93XA2	Q93xa2	phaseolus v
767	80	4.5	393	2	Q8VEH6	Q8veh6	mus musculu
768	80	4.5	409	2	Q821L0	Q82110	chlamydophi
769	80	4.5	456	2	Q73UB1	Q73ub1	mycobacteri
770	80	4.5	490	2	Q6BEL6	Q6bel6	chromohalob
771	80	4.5	503	2	Q8ZDZ1	Q8zdz1	yersinia pe
772	80	4.5	521	2	Q6NZD2	Q6nzd2	mus musculu
773	80	4.5	545	1	ICA1_RAT	Q00238	rattus norv
774	80	4.5	553	2	Q7S9I1	Q7s9i1	neurospora
775	80	4.5	572	2	Q7S3D6	Q7s3d6	neurospora
776	80	4.5	594	2	Q923I8	Q923i8	rattus norv
777	80	4.5	611	2	Q94KS4	Q94ks4	hordeum vul
778	80	4.5	628	1	RA21_SCHPO	P30776	schizosacch
779	80	4.5	629	2	Q7ZTW7	Q7ztw7	brachydanio
780	80	4.5	631	1	LIB3_HUMAN	O75022	homo sapien
781	80	4.5	635	2	Q91196	Q91196	oncorhynchu
782	80	4.5	637	2	Q9R9G3	Q9r9g3	pseudomonas
783	80	4.5	705	2	Q9SH29	Q9sh29	arabidopsis
784	80	4.5	718	2	Q6C9L7	Q6c917	yarrowia li
785	80	4.5	725	1	TAP1_RAT	P36370	rattus norv
786	80	4.5	725	2	P97559	P97559	rattus norv
787	80	4.5	725	2	P97560	P97560	rattus norv
788	80	4.5	725	2	P97561	P97561	rattus norv
789	80	4.5	725	2	P97949	P97949	rattus norv
790	80	4.5	729	2	Q9CUM1	Q9cum1	mus musculu
791	80	4.5	774	2	Q84MG3	Q84mg3	oryza sativ
792	80	4.5	780	2	Q9SL06	Q9sl06	arabidopsis
793	80	4.5	814	1	COLA_VIBAL	P43154	vibrio algi
794	80	4.5	817	2	Q6PGX9	Q6pgx9	brachydanio
795	80	4.5	865	2	Q8I759	Q8i759	paramecium
796	80	4.5	893	2	Q6PAS4	Q6pas4	mus musculu
797	80	4.5	968	2	Q9HCM7	Q9hcm7	homo sapien
798	80	4.5	1051	2	Q9YQX8	Q9yqx8	ranid herpe
799	80	4.5	1062	2	Q6BU75	Q6bu75	debaryomyce
800	80	4.5	1235	1	KPB2_RABIT	P46018	oryctolagus
801	80	4.5	1237	2	Q64B63	Q64b63	uncultured
802	80	4.5	1367	2	Q8S664	Q8s664	oryza sativ
803	80	4.5	1367	2	Q7XFV1	Q7xfv1	oryza sativ
804	80	4.5	1516	1	MY52_SCHPO	O94477	schizosacch
805	80	4.5	1939	2	Q8TKB8	Q8tkb8	methanosarc
806	79.5	4.5	280	2	Q8L192	Q8l192	rhodococcus
807	79.5	4.5	292	2	Q675V3	Q675v3	oikopleura
808	79.5	4.5	386	2	Q6P561	Q6p561	mus musculu
809	79.5	4.5	386	2	Q80ZF4	Q80zf4	rattus norv
810	79.5	4.5	391	2	Q6IRE4	Q6ire4	rattus norv
811	79.5	4.5	401	2	Q9NJ13	Q9nj13	trypanosoma
812	79.5	4.5	435	1	PURA_SPICI	P52150	spiroplasma
813	79.5	4.5	448	1	NCAP_CVBLS	Q9qar1	bovine coro
814	79.5	4.5	459	2	Q8SQR9	Q8sqr9	encephalito
815	79.5	4.5	464	2	Q8EGF9	Q8egf9	shewanella
816	79.5	4.5	477	2	Q8RE83	Q8re83	fusobacteri
817	79.5	4.5	477	2	Q9QF42	Q9qf42	human immun
818	79.5	4.5	499	2	O46559	O46559	oryctolagus
819	79.5	4.5	511	2	Q9GRK5	Q9grk5	leishmania
820	79.5	4.5	512	2	Q9MA38	Q9ma38	arabidopsis
821	79.5	4.5	528	1	PRPR_ECOLI	P77743	escherichia
822	79.5	4.5	537	1	CAB2_AQUAE	O67233	aquifex aeo
823	79.5	4.5	540	2	P92025	P92025	culex quinq
824	79.5	4.5	540	2	Q23733	Q23733	culex quinq
825	79.5	4.5	540	2	Q8WQ88	Q8wq88	culex pipie
826	79.5	4.5	540	2	Q8WQ89	Q8wq89	culex pipie
827	79.5	4.5	569	2	Q69013	Q69013	human endog
828	79.5	4.5	597	2	Q8BZP3	Q8bzp3	mus musculu
829	79.5	4.5	622	2	Q9YNA0	Q9yna0	sheep pulmo
830	79.5	4.5	639	2	Q67UU1	Q67uu1	oryza sativ
831	79.5	4.5	685	2	Q95P17	Q95p17	palinurus v
832	79.5	4.5	727	2	Q755T3	Q755t3	ashbya goss
833	79.5	4.5	748	1	TAP1_HUMAN	Q03518	h antigen p
834	79.5	4.5	748	2	Q6QWC1	Q6qwc1	homo sapien

835	79.5	4.5	768	2	Q7N1Z2	Q7n1z2	photorhabdu
836	79.5	4.5	773	2	Q96JU8	Q96ju8	homo sapien
837	79.5	4.5	784	2	Q82VK9	Q82vk9	nitrosomona
838	79.5	4.5	808	2	Q96CP4	Q96cp4	homo sapien
839	79.5	4.5	815	1	PYGO_DROME	Q9v9w8	drosophila
840	79.5	4.5	855	2	O50024	O50024	lycopersico
841	79.5	4.5	855	2	Q7DLS4	Q7dls4	lycopersico
842	79.5	4.5	887	1	SYA_AGRT5	Q8ue87	agrobacteri
843	79.5	4.5	890	2	Q9LQ11	Q9lq11	arabidopsis
844	79.5	4.5	905	2	O84057	O84057	chlamydia t
845	79.5	4.5	911	2	Q96UD5	Q96ud5	neurospora
846	79.5	4.5	931	2	Q6CB39	Q6cb39	yarrowia li
847	79.5	4.5	941	2	Q7RVW5	Q7rvw5	neurospora
848	79.5	4.5	967	2	Q76IN1	Q76in1	tetraodon n
849	79.5	4.5	977	2	Q8YXF9	Q8yxf9	anabaena sp
850	79.5	4.5	1066	1	PUM2_HUMAN	Q8tb72	homo sapien
851	79.5	4.5	1067	2	Q64ZI7	Q64zi7	bacteroides
852	79.5	4.5	1104	2	Q8BHQ4	Q8bhq4	mus musculu
853	79.5	4.5	1286	1	PATC_DROME	P18502	drosophila
854	79.5	4.5	1293	2	Q8IWF1	Q8iwf1	homo sapien
855	79.5	4.5	1307	2	O43138	O43138	aspergillus
856	79.5	4.5	1456	2	Q6C4S5	Q6c4s5	yarrowia li
857	79.5	4.5	1474	2	Q19106	Q19106	caenorhabdi
858	79.5	4.5	1541	2	Q6ZQE2	Q6zqe2	mus musculu
859	79.5	4.5	1639	2	Q7Z3K8	Q7z3k8	homo sapien
860	79.5	4.5	1724	2	P91019	P91019	caenorhabdi
861	79.5	4.5	1745	2	Q14675	Q14675	homo sapien
862	79.5	4.5	1755	1	YJZ9_YEAST	P47100	saccharomyc
863	79.5	4.5	1788	2	Q6NV66	Q6nv66	mus musculu
864	79.5	4.5	1928	2	Q8D674	Q8d674	vibrio vuln
865	79.5	4.5	1997	2	Q6CWA6	Q6cwa6	kluyveromyc
866	79.5	4.5	2013	2	Q8VHZ8	Q8vhz8	rattus norv
867	79.5	4.5	2013	2	Q9ERC8	Q9erc8	mus musculu
868	79.5	4.5	2148	2	Q6CNJ6	Q6cnj6	kluyveromyc
869	79.5	4.5	2854	2	Q6G5H5	Q6g5h5	bartonella
870	79	4.4	192	2	Q52607	Q52607	plasmid ti.
871	79	4.4	227	2	Q92PB7	Q92pb7	rhizobium m
872	79	4.4	324	2	Q9HX84	Q9hx84	pseudomonas
873	79	4.4	354	1	PON2_MOUSE	Q62086	mus musculu
874	79	4.4	368	2	Q30838	Q30838	ovis aries
875	79	4.4	377	2	Q90ZH9	Q90zh9	xenopus lae
876	79	4.4	377	2	Q6PAE5	Q6pae5	xenopus lae
877	79	4.4	394	2	Q99MB4	Q99mb4	rattus norv
878	79	4.4	400	2	Q8WPS5	Q8wps5	trypanosoma
879	79	4.4	425	2	Q82SG4	Q82sg4	nitrosomona
880	79	4.4	441	2	O80587	O80587	arabidopsis
881	79	4.4	447	2	Q9PEH5	Q9peh5	xylella fas
882	79	4.4	454	2	Q6ST69	Q6st69	human rhino
883	79	4.4	467	2	Q716M3	Q716m3	mycobacteri
884	79	4.4	483	2	Q6WNR9	Q6wnr9	pichia angu
885	79	4.4	486	2	O70644	O70644	simian t-ly
886	79	4.4	502	2	Q8DP24	Q8dp24	streptococc
887	79	4.4	503	2	Q7V551	Q7v551	prochloroco
888	79	4.4	505	2	Q9IAT1	Q9iat1	oncorhynchu
889	79	4.4	532	2	Q82GN0	Q82gn0	streptomyce
890	79	4.4	535	2	Q6I7K9	Q6i7k9	vibrio chol
891	79	4.4	568	2	Q62K19	Q62k19	burkholderi
892	79	4.4	568	2	Q63TS8	Q63ts8	burkholderi
893	79	4.4	583	2	Q722T4	Q722t4	listeria mo
894	79	4.4	626	2	Q90ZT2	Q90zt2	brachydanio
895	79	4.4	636	2	Q7RUH9	Q7ruh9	neurospora
896	79	4.4	639	2	Q9DSJ6	Q9dsj6	human immun
897	79	4.4	649	2	Q75HQ6	Q75hq6	oryza sativ
898	79	4.4	650	2	Q23707	Q23707	cancer magi
899	79	4.4	672	2	Q6DAD2	Q6dad2	erwinia car
900	79	4.4	721	2	Q8A3V3	Q8a3v3	bacteroides
901	79	4.4	732	2	Q27480	Q27480	caenorhabdi
902	79	4.4	735	2	Q8K4N4	Q8k4n4	mus musculu
903	79	4.4	768	1	BAR1_RAT	Q9qzh2	rattus norv
904	79	4.4	784	1	SX15_DROME	P40657	drosophila
905	79	4.4	789	1	VIB4_AGRTU	P05353	agrobacteri
906	79	4.4	814	2	O70162	O70162	mus musculu
907	79	4.4	819	2	Q04525	Q04525	prevotella
908	79	4.4	845	2	Q6DKG3	Q6dkg3	homo sapien
909	79	4.4	881	2	Q8D6X3	Q8d6x3	vibrio vuln
910	79	4.4	897	2	Q6PUB6	Q6pub6	anopheles g
911	79	4.4	1014	2	Q6ZU41	Q6zu41	homo sapien
912	79	4.4	1023	2	Q8TDN0	Q8tdn0	homo sapien
913	79	4.4	1087	2	Q6P3G1	Q6p3g1	brachydanio
914	79	4.4	1153	2	Q6BIP2	Q6bip2	debaryomyce
915	79	4.4	1195	2	Q9A2J6	Q9a2j6	caulobacter
916	79	4.4	1417	2	Q7YU09	Q7yu09	drosophila
917	79	4.4	1432	1	DAK1_HUMAN	P53355	homo sapien
918	79	4.4	1621	2	Q9VIK7	Q9vik7	drosophila
919	79	4.4	1764	2	Q86WC0	Q86wc0	homo sapien
920	79	4.4	1809	1	DLG5_HUMAN	Q8tdm6	homo sapien
921	79	4.4	1829	1	Y296_HUMAN	O15015	homo sapien
922	79	4.4	1832	2	Q8IVD8	Q8ivd8	homo sapien
923	79	4.4	1967	2	Q7S752	Q7s752	neurospora
924	79	4.4	2011	2	Q871L5	Q87115	neurospora
925	79	4.4	2343	2	O18806	O18806	canis famil
926	79	4.4	2839	1	NF1_HUMAN	P21359	homo sapien
927	79	4.4	3119	1	HD_MOUSE	P42859	mus musculu
928	79	4.4	3412	2	Q87PW3	Q87pw3	vibrio para
929	79	4.4	5060	2	Q9K5M1	Q9k5m1	anabaena ci
930	79	4.4	5183	1	PCLO_HUMAN	Q9y6v0	homo sapien
931	78.5	4.4	160	2	Q760Q2	Q760q2	macrobdella
932	78.5	4.4	189	2	Q9V3E3	Q9v3e3	drosophila
933	78.5	4.4	213	2	Q9PTQ5	Q9ptq5	oryzias lat
934	78.5	4.4	233	2	Q7NVB9	Q7nvb9	chromobacte
935	78.5	4.4	249	2	Q6WQW9	Q6wqw9	bos taurus
936	78.5	4.4	257	2	O77710	O77710	bos taurus
937	78.5	4.4	258	2	Q7VH45	Q7vh45	helicobacte
938	78.5	4.4	266	1	TYSY_MYCLE	Q9cbw0	mycobacteri
939	78.5	4.4	286	2	O42290	O42290	gallus gall
940	78.5	4.4	286	2	O57342	O57342	coturnix co
941	78.5	4.4	286	2	Q8AWH8	Q8awh8	gallus gall
942	78.5	4.4	321	2	Q6TY50	Q6ty50	hydrangea m
943	78.5	4.4	327	2	Q72UP1	Q72up1	leptospira
944	78.5	4.4	327	2	Q8F0B3	Q8f0b3	leptospira
945	78.5	4.4	350	2	Q94GH5	Q94gh5	oryza sativ
946	78.5	4.4	352	2	Q8SPA8	Q8spa8	sus scrofa
947	78.5	4.4	364	2	Q9TSW2	Q9tsw2	sus scrofa
948	78.5	4.4	374	2	Q65HD4	Q65hd4	bacillus li
949	78.5	4.4	379	2	Q9HT99	Q9ht99	pseudomonas
950	78.5	4.4	381	2	Q86BN4	Q86bn4	drosophila
951	78.5	4.4	391	1	T101_MOUSE	Q61187	mus musculu
952	78.5	4.4	394	2	Q84MI5	Q84mi5	lycopersico
953	78.5	4.4	398	2	Q8YAQ6	Q8yaq6	listeria mo
954	78.5	4.4	398	2	Q92FQ0	Q92fq0	listeria in
955	78.5	4.4	399	2	O43935	O43935	trichomonas
956	78.5	4.4	399	2	Q9TSW1	Q9tsw1	sus scrofa
957	78.5	4.4	403	2	Q74E25	Q74e25	geobacter s
958	78.5	4.4	406	2	Q94I47	Q94i47	oryza sativ
959	78.5	4.4	420	2	Q7QIT4	Q7qit4	anopheles g
960	78.5	4.4	436	2	Q40121	Q40121	lycopersico
961	78.5	4.4	442	2	Q8ERI7	Q8eri7	oceanobacil
962	78.5	4.4	448	1	NCAP_CVBM	P10527	bovine coro
963	78.5	4.4	448	1	NCAP_CVBOK	P26020	bovine coro
964	78.5	4.4	448	1	NCAP_CVBQ	P59712	bovine coro
965	78.5	4.4	450	2	Q8TT49	Q8tt49	methanosarc
966	78.5	4.4	450	2	Q983I2	Q983i2	rhizobium l
967	78.5	4.4	465	2	Q8K848	Q8k848	streptococc
968	78.5	4.4	467	2	Q878G9	Q878g9	streptococc
969	78.5	4.4	479	1	DLDH_TRYBB	Q04933	trypanosoma
970	78.5	4.4	480	2	Q9H951	Q9h951	homo sapien
971	78.5	4.4	480	2	Q7N072	Q7n072	photorhabdu
972	78.5	4.4	481	2	Q8BNG3	Q8bng3	mus musculu
973	78.5	4.4	512	2	Q9JU05	Q9ju05	neisseria m
974	78.5	4.4	520	2	Q8RM50	Q8rm50	xanthobacte
975	78.5	4.4	537	2	Q8Y6R0	Q8y6r0	listeria mo
976	78.5	4.4	567	2	Q88C09	Q88c09	pseudomonas
977	78.5	4.4	591	2	Q70AD5	Q70ad5	spalax juda
978	78.5	4.4	606	2	Q70AD4	Q70ad4	spalax juda
979	78.5	4.4	608	1	GLMS_YERPE	Q8z9s8	y glucosami
980	78.5	4.4	608	1	SAV_DROME	Q9vcr6	drosophila

981	78.5	4.4	609	2	Q663R1	Q663r1	yersinia ps
982	78.5	4.4	614	2	Q6MQH0	Q6mqh0	bdellovibri
983	78.5	4.4	617	1	GLMS_METMA	Q8q038	m glucosami
984	78.5	4.4	627	1	NR43_MOUSE	Q9qzb6	mus musculu
985	78.5	4.4	635	2	Q7T2P0	Q7t2p0	ictalurus p
986	78.5	4.4	667	2	Q6C222	Q6c222	yarrowia li
987	78.5	4.4	675	1	PPK_HELPY	O25654	helicobacte
988	78.5	4.4	691	2	Q9VML1	Q9vml1	drosophila
989	78.5	4.4	707	2	Q6TEP7	Q6tep7	brachydanio
990	78.5	4.4	772	1	NFL1_HUMAN	Q14494	h nuclear f
991	78.5	4.4	772	2	Q91013	Q91013	gallus gall
992	78.5	4.4	773	2	Q98R04	Q98r04	mycoplasma
993	78.5	4.4	791	2	Q8NF22	Q8nf22	homo sapien
994	78.5	4.4	837	1	GCL2_HUMAN	Q92830	homo sapien
995	78.5	4.4	837	2	Q8N1A2	Q8n1a2	homo sapien
996	78.5	4.4	917	2	Q88MC3	Q88mc3	pseudomonas
997	78.5	4.4	928	2	Q9H8E3	Q9h8e3	homo sapien
998	78.5	4.4	952	2	Q7UYM2	Q7uym2	rhodopirell
999	78.5	4.4	981	2	Q8MQI1	Q8mqi1	drosophila
1000	78.5	4.4	1027	2	Q98FR6	Q98fr6	rhizobium l
1001	78.5	4.4	1040	2	Q8S5G8	Q8s5g8	oryza sativ
1002	78.5	4.4	1082	2	Q8K0I6	Q8k0i6	mus musculu
1003	78.5	4.4	1084	2	Q9NVI1	Q9nvi1	homo sapien
1004	78.5	4.4	1099	2	Q69ZK7	Q69zk7	mus musculu
1005	78.5	4.4	1311	2	Q9C6E3	Q9c6e3	arabidopsis
1006	78.5	4.4	1316	2	Q8A692	Q8a692	bacteroides
1007	78.5	4.4	1529	2	Q84KC2	Q84kc2	hordeum vul
1008	78.5	4.4	2294	2	Q9VUB7	Q9vub7	drosophila
1009	78.5	4.4	2310	2	Q9W2U7	Q9w2u7	drosophila
1010	78.5	4.4	3358	1	PGCV_MOUSE	Q62059	mus musculu
1011	78	4.4	131	2	Q87637	Q87637	chimpanzee
1012	78	4.4	187	2	Q8T3P7	Q8t3p7	drosophila
1013	78	4.4	198	2	Q7U0B9	Q7u0b9	mycobacteri
1014	78	4.4	222	2	Q8GQ91	Q8gq91	pseudomonas
1015	78	4.4	266	2	Q73VZ2	Q73vz2	mycobacteri
1016	78	4.4	314	2	Q8WPH7	Q8wph7	theileria a
1017	78	4.4	333	2	Q8XCD2	Q8xcd2	escherichia
1018	78	4.4	354	2	Q97I04	Q97i04	clostridium
1019	78	4.4	355	2	Q8QZ03	Q8qz03	rana tigrin
1020	78	4.4	355	2	Q6GZS4	Q6gzs4	frog virus
1021	78	4.4	376	2	O81484	O81484	arabidopsis
1022	78	4.4	382	2	Q8HT46	Q8ht46	stereophyll
1023	78	4.4	386	2	Q92ES3	Q92es3	listeria in
1024	78	4.4	389	2	Q87GL9	Q87gl9	vibrio para
1025	78	4.4	400	1	MKK2_HUMAN	P49137	homo sapien
1026	78	4.4	437	2	Q6SA23	Q6sa23	human coron
1027	78	4.4	444	2	Q7P6M2	Q7p6m2	fusobacteri
1028	78	4.4	448	1	NCAP_CVHOC	P33469	human coron
1029	78	4.4	448	2	Q9UFP1	Q9ufp1	homo sapien
1030	78	4.4	448	2	Q696P4	Q696p4	human coron
1031	78	4.4	448	2	Q6TNF5	Q6tnf5	human coron
1032	78	4.4	453	2	Q9A9H6	Q9a9h6	caulobacter
1033	78	4.4	480	2	Q96CP5	Q96cp5	homo sapien
1034	78	4.4	492	1	CATA_SOLAP	O24339	soldanella
1035	78	4.4	494	2	Q6BQM5	Q6bqm5	debaryomyce
1036	78	4.4	502	2	Q6ZPM9	Q6zpm9	mus musculu
1037	78	4.4	529	2	Q8WUV6	Q8wuv6	homo sapien
1038	78	4.4	548	2	Q9D2X9	Q9d2x9	mus musculu
1039	78	4.4	556	2	Q817Q3	Q817q3	bacillus ce
1040	78	4.4	557	2	Q633X3	Q633x3	bacillus ce
1041	78	4.4	557	2	Q72ZV5	Q72zv5	bacillus ce
1042	78	4.4	557	2	Q81LC0	Q81lc0	bacillus an
1043	78	4.4	557	2	Q6HD55	Q6hd55	bacillus th
1044	78	4.4	561	2	Q6Z4T7	Q6z4t7	oryza sativ
1045	78	4.4	584	2	Q6A024	Q6a024	mus musculu
1046	78	4.4	592	2	Q9R194	Q9r194	mus musculu
1047	78	4.4	620	2	Q89TU9	Q89tu9	bradyrhizob
1048	78	4.4	630	2	Q7M0C7	Q7m0c7	cricetidae
1049	78	4.4	634	2	Q6GQ19	Q6gq19	xenopus lae
1050	78	4.4	639	2	Q7W0T0	Q7w0t0	bordetella
1051	78	4.4	639	2	Q7W2I1	Q7w2i1	bordetella
1052	78	4.4	639	2	Q7WRF1	Q7wrf1	bordetella
1053	78	4.4	669	2	Q6YY15	Q6yy15	oryza sativ
1054	78	4.4	670	2	Q9BTT3	Q9btt3	homo sapien
1055	78	4.4	672	2	Q9NFR6	Q9nfr6	homarus ame
1056	78	4.4	674	2	Q891P8	Q891p8	clostridium
1057	78	4.4	681	2	Q6XCH2	Q6xch2	uncultured
1058	78	4.4	685	2	Q9DGC0	Q9dgc0	cyprinus ca
1059	78	4.4	685	2	Q9DGC1	Q9dgc1	cyprinus ca
1060	78	4.4	694	2	Q8A3X0	Q8a3x0	bacteroides
1061	78	4.4	760	2	Q8ILX2	Q8ilx2	plasmodium
1062	78	4.4	788	2	Q9RPH0	Q9rph0	salmonella
1063	78	4.4	807	1	YCDS_ECOLI	P75907	escherichia
1064	78	4.4	827	2	Q8BTW6	Q8btw6	mus musculu
1065	78	4.4	844	2	Q922D4	Q922d4	m sporulati
1066	78	4.4	852	2	Q89607	Q89607	human immun
1067	78	4.4	890	2	Q8XE40	Q8xe40	escherichia
1068	78	4.4	1044	2	Q97GN9	Q97gn9	clostridium
1069	78	4.4	1099	1	SGA2_HUMAN	O43295	homo sapien
1070	78	4.4	1099	1	SGA2_MOUSE	Q812a2	mus musculu
1071	78	4.4	1147	2	Q8X0Y3	Q8x0y3	neurospora
1072	78	4.4	1176	1	CND1_YEAST	Q06156	saccharomyc
1073	78	4.4	1185	2	Q6BT72	Q6bt72	debaryomyce
1074	78	4.4	1203	2	Q7QEK6	Q7qek6	anopheles g
1075	78	4.4	1311	2	Q81Z00	Q81z00	bacillus an
1076	78	4.4	1448	2	Q6MVR0	Q6mvr0	neurospora
1077	78	4.4	1449	2	Q8LSR0	Q8lsr0	oryza sativ
1078	78	4.4	1622	1	U13B_RAT	Q62769	rattus norv
1079	78	4.4	1654	1	PCFB_HUMAN	O94913	homo sapien
1080	78	4.4	1798	2	Q8KGY8	Q8kgy8	rhizobium l
1081	78	4.4	2219	2	Q88WI9	Q88wi9	lactobacill
1082	78	4.4	2373	2	Q8CUZ9	Q8cuz9	oceanobacil
1083	78	4.4	2788	2	Q7WRX9	Q7wrx9	anabaena ci
1084	78	4.4	2966	2	Q8IIK5	Q8iik5	plasmodium
1085	78	4.4	6084	2	Q87ID8	Q87id8	vibrio para
1086	77.5	4.4	151	2	Q97263	Q97263	human immun
1087	77.5	4.4	171	2	O50145	O50145	thermus the
1088	77.5	4.4	201	2	Q9CQZ8	Q9cqz8	m mus muscu
1089	77.5	4.4	211	1	WFD1_MOUSE	Q9esh5	mus musculu
1090	77.5	4.4	214	2	Q74J54	Q74j54	lactobacill
1091	77.5	4.4	280	1	YW55_CAUCR	Q9a3e9	caulobacter
1092	77.5	4.4	297	2	Q9U2D6	Q9u2d6	caenorhabdi
1093	77.5	4.4	314	2	Q76EH4	Q76eh4	polarella g
1094	77.5	4.4	318	2	Q8ZR34	Q8zr34	salmonella
1095	77.5	4.4	334	2	Q7QEI8	Q7qei8	anopheles g
1096	77.5	4.4	364	2	Q8SPA3	Q8spa3	sus scrofa
1097	77.5	4.4	372	1	3BHD_HORSE	O46516	e 3 beta-hy
1098	77.5	4.4	372	2	Q8XUY7	Q8xuy7	ralstonia s
1099	77.5	4.4	388	2	O02359	O02359	caenorhabdi
1100	77.5	4.4	391	2	Q7TSE5	Q7tse5	rattus norv
1101	77.5	4.4	394	2	P73510	P73510	synechocyst
1102	77.5	4.4	395	2	Q9VD68	Q9vd68	drosophila
1103	77.5	4.4	429	2	Q7V4W8	Q7v4w8	prochloroco
1104	77.5	4.4	468	2	Q8TH06	Q8th06	pyrococcus
1105	77.5	4.4	476	2	Q6S4V7	Q6s4v7	leishmania
1106	77.5	4.4	476	2	Q70AS6	Q70as6	streptomyce
1107	77.5	4.4	483	2	Q74M67	Q74m67	nanoarchaeu
1108	77.5	4.4	486	2	Q65NC2	Q65nc2	bacillus li
1109	77.5	4.4	492	2	Q6B153	Q6b153	saccharomyc
1110	77.5	4.4	498	2	Q8NAG0	Q8nag0	homo sapien
1111	77.5	4.4	498	2	Q9BT92	Q9bt92	homo sapien
1112	77.5	4.4	516	2	Q9JZ08	Q9jz08	neisseria m
1113	77.5	4.4	526	2	Q80ZG1	Q80zg1	rattus norv
1114	77.5	4.4	537	2	Q922B3	Q922b3	mus musculu
1115	77.5	4.4	566	1	HCYB_PONLE	P83180	pontastacus
1116	77.5	4.4	566	2	Q7ABQ2	Q7abq2	escherichia
1117	77.5	4.4	566	2	Q8XBE5	Q8xbe5	escherichia
1118	77.5	4.4	581	2	Q8TV69	Q8tv69	methanopyru
1119	77.5	4.4	613	2	Q8LH06	Q8lh06	oryza sativ
1120	77.5	4.4	630	2	Q9RKS4	Q9rks4	streptomyce
1121	77.5	4.4	631	2	Q41493	Q41493	solanum tub
1122	77.5	4.4	641	2	Q86SD2	Q86sd2	ciona intes
1123	77.5	4.4	645	2	Q7UEW8	Q7uew8	rhodopirell
1124	77.5	4.4	645	2	Q9F2W6	Q9f2w6	streptomyce
1125	77.5	4.4	649	2	Q6W5F4	Q6w5f4	oryza sativ
1126	77.5	4.4	682	2	Q7VF32	Q7vf32	helicobacte

1127	77.5	4.4	693	2	O96680	O96680	drosophila
1128	77.5	4.4	700	2	Q9XDN9	Q9xdn9	salmonella
1129	77.5	4.4	716	1	HGFL_MOUSE	P26928	mus musculu
1130	77.5	4.4	716	2	Q91XG8	Q91xg8	mus musculu
1131	77.5	4.4	721	2	Q6MBG6	Q6mbg6	parachlamyd
1132	77.5	4.4	733	2	Q8T806	Q8t806	dictyosteli
1133	77.5	4.4	734	1	PSAB_PHYPA	Q8mfa2	physcomitre
1134	77.5	4.4	746	2	Q9FLR6	Q9flr6	arabidopsis
1135	77.5	4.4	778	2	Q8NDW3	Q8ndw3	homo sapien
1136	77.5	4.4	784	2	Q6P5Z3	Q6p5z3	homo sapien
1137	77.5	4.4	788	2	Q8Z578	Q8z578	salmonella
1138	77.5	4.4	802	2	Q8A9F2	Q8a9f2	bacteroides
1139	77.5	4.4	810	2	Q8T3J2	Q8t3j2	drosophila
1140	77.5	4.4	811	2	Q9VK54	Q9vk54	drosophila
1141	77.5	4.4	880	2	P91643	P91643	drosophila
1142	77.5	4.4	944	1	YMH6_YEAST	Q03631	saccharomyc
1143	77.5	4.4	952	2	Q8MRN5	Q8mrn5	drosophila
1144	77.5	4.4	963	1	IRE2_HUMAN	P48200	homo sapien
1145	77.5	4.4	1008	2	Q65UE7	Q65ue7	mannheimia
1146	77.5	4.4	1012	2	Q9LKZ4	Q9lkz4	glycine max
1147	77.5	4.4	1063	2	Q8PWB2	Q8pwb2	methanosarc
1148	77.5	4.4	1172	2	Q7QSR2	Q7qsr2	giardia lam
1149	77.5	4.4	1176	1	SYLC_HUMAN	Q9p2j5	homo sapien
1150	77.5	4.4	1222	2	Q8IZU8	Q8izu8	homo sapien
1151	77.5	4.4	1307	2	Q8JFF7	Q8jff7	xenopus lae
1152	77.5	4.4	1334	2	Q7XPD5	Q7xpd5	oryza sativ
1153	77.5	4.4	1387	1	RPOB_XANCP	Q8pc56	xanthomonas
1154	77.5	4.4	1428	1	TOP2_YEAST	P06786	saccharomyc
1155	77.5	4.4	1428	2	Q8TF86	Q8tf86	saccharomyc
1156	77.5	4.4	1428	2	Q8TG43	Q8tg43	saccharomyc
1157	77.5	4.4	1428	2	Q8TG44	Q8tg44	saccharomyc
1158	77.5	4.4	1428	2	Q8TG46	Q8tg46	saccharomyc
1159	77.5	4.4	1428	2	Q8TG47	Q8tg47	saccharomyc
1160	77.5	4.4	1428	2	Q8TG53	Q8tg53	saccharomyc
1161	77.5	4.4	1428	2	Q8TG56	Q8tg56	saccharomyc
1162	77.5	4.4	1541	2	Q7SBV4	Q7sbv4	neurospora
1163	77.5	4.4	1550	2	Q87U34	Q87u34	pseudomonas
1164	77.5	4.4	1694	2	Q7SEZ4	Q7sez4	neurospora
1165	77.5	4.4	5363	2	Q6YK40	Q6yk40	bacillus su
1166	77.5	4.4	8407	2	Q7RTM4	Q7rtm4	homo sapien
1167	77.5	4.4	8797	1	SNE1_HUMAN	Q8nf91	homo sapien
1168	77.5	4.4	9550	2	Q6W5P6	Q6w5p6	streptomyce
1169	77	4.3	64	2	Q670P2	Q670p2	meriones un
1170	77	4.3	192	2	Q96K18	Q96k18	homo sapien
1171	77	4.3	192	2	Q9NYS0	Q9nys0	homo sapien
1172	77	4.3	192	2	Q9BH04	Q9bh04	macaca fasc
1173	77	4.3	254	2	Q825Z3	Q825z3	streptomyce
1174	77	4.3	264	2	Q9PVG5	Q9pvg5	acipenser t
1175	77	4.3	268	2	Q9RC96	Q9rc96	bacillus ha
1176	77	4.3	289	2	Q6PA45	Q6pa45	xenopus lae
1177	77	4.3	296	2	Q87ZH5	Q87zh5	pseudomonas
1178	77	4.3	313	2	O59869	O59869	orpinomyces
1179	77	4.3	337	2	Q9RS00	Q9rs00	deinococcus
1180	77	4.3	343	2	Q6Q242	Q6q242	chlamydomon
1181	77	4.3	366	2	Q8K013	Q8k013	mus musculu
1182	77	4.3	376	2	Q9SLG8	Q9slg8	arabidopsis
1183	77	4.3	382	2	Q8HT42	Q8ht42	pylaisia po
1184	77	4.3	395	2	Q6BCG2	Q6bcg2	lysobacter
1185	77	4.3	401	2	Q9PRG7	Q9prg7	xenopus lae
1186	77	4.3	403	1	YD13_METJA	Q58709	methanococc
1187	77	4.3	407	2	Q961I3	Q961i3	drosophila
1188	77	4.3	412	2	Q9HS20	Q9hs20	halobacteri
1189	77	4.3	424	2	Q7S1F2	Q7s1f2	neurospora
1190	77	4.3	428	2	Q9X6P5	Q9x6p5	bacillus me
1191	77	4.3	450	2	Q8J1X7	Q8j1x7	fusarium cu
1192	77	4.3	453	2	Q6FSH0	Q6fsh0	candida gla
1193	77	4.3	454	2	Q8Q0D9	Q8q0d9	methanosarc
1194	77	4.3	455	1	HN4A_XENLA	Q91766	xenopus lae
1195	77	4.3	457	2	Q8BRI6	Q8bri6	mus musculu
1196	77	4.3	459	1	SUOX_CHICK	P07850	gallus gall
1197	77	4.3	464	2	Q7N297	Q7n297	photorhabdu
1198	77	4.3	466	2	Q8C916	Q8c916	mus musculu
1199	77	4.3	470	1	SOX8_CHICK	P57074	gallus gall
1200	77	4.3	487	2	Q8A0W6	Q8a0w6	bacteroides
1201	77	4.3	502	2	Q9HMB7	Q9hmb7	halobacteri
1202	77	4.3	503	2	Q66A19	Q66a19	yersinia ps
1203	77	4.3	516	2	Q8N870	Q8n870	homo sapien
1204	77	4.3	529	2	Q21093	Q21093	caenorhabdi
1205	77	4.3	530	2	Q6N069	Q6n069	homo sapien
1206	77	4.3	534	2	Q6G2A5	Q6g2a5	bartonella
1207	77	4.3	541	2	Q8HT22	Q8ht22	herzogiella
1208	77	4.3	544	2	Q8HT33	Q8ht33	hylocomium
1209	77	4.3	545	2	Q8HT47	Q8ht47	entodontops
1210	77	4.3	545	2	Q8HT48	Q8ht48	plagiotheci
1211	77	4.3	548	2	Q6BRL9	Q6brl9	debaryomyce
1212	77	4.3	548	2	Q8HT24	Q8ht24	isopterygio
1213	77	4.3	563	2	Q64EL8	Q64el8	uncultured
1214	77	4.3	568	2	Q90Y94	Q90y94	cyprinus ca
1215	77	4.3	568	2	Q90Y95	Q90y95	cyprinus ca
1216	77	4.3	583	2	Q87QD5	Q87qd5	vibrio para
1217	77	4.3	603	2	Q83QI8	Q83qi8	shigella fl
1218	77	4.3	608	2	Q7UBY0	Q7uby0	shigella fl
1219	77	4.3	608	2	Q7UD47	Q7ud47	shigella fl
1220	77	4.3	610	2	Q8GRA8	Q8gra8	vibrio para
1221	77	4.3	626	2	Q63G22	Q63g22	bacillus ce
1222	77	4.3	626	2	Q81V77	Q81v77	bacillus an
1223	77	4.3	626	2	Q6HNJ0	Q6hnj0	bacillus th
1224	77	4.3	627	2	Q73DM0	Q73dm0	bacillus ce
1225	77	4.3	653	2	Q8A6S5	Q8a6s5	bacteroides
1226	77	4.3	654	2	P92128	P92128	giardia lam
1227	77	4.3	657	1	HCYA_PANIN	P04254	panulirus i
1228	77	4.3	658	2	Q87P81	Q87p81	vibrio para
1229	77	4.3	677	1	ZBT5_HUMAN	O15062	homo sapien
1230	77	4.3	677	2	Q51544	Q51544	pseudomonas
1231	77	4.3	680	2	Q6BXZ2	Q6bxz2	debaryomyce
1232	77	4.3	691	2	Q6AJ36	Q6aj36	desulfotale
1233	77	4.3	703	1	NHR5_CAEEL	Q9na51	caenorhabdi
1234	77	4.3	717	2	Q9K7U5	Q9k7u5	bacillus ha
1235	77	4.3	747	2	Q9I524	Q9i524	pseudomonas
1236	77	4.3	751	2	Q7SBQ7	Q7sbq7	neurospora
1237	77	4.3	752	2	Q6C669	Q6c669	yarrowia li
1238	77	4.3	771	2	Q19380	Q19380	caenorhabdi
1239	77	4.3	773	2	O22178	O22178	arabidopsis
1240	77	4.3	775	2	Q6FVS9	Q6fvs9	candida gla
1241	77	4.3	829	2	Q8Z3Z1	Q8z3z1	salmonella
1242	77	4.3	860	2	Q96X26	Q96x26	yarrowia li
1243	77	4.3	860	2	Q6C7Q6	Q6c7q6	yarrowia li
1244	77	4.3	887	2	Q9VLV2	Q9vlv2	drosophila
1245	77	4.3	899	2	Q80TP9	Q80tp9	mus musculu
1246	77	4.3	915	2	Q7N7Z1	Q7n7z1	photorhabdu
1247	77	4.3	917	2	Q9VE20	Q9ve20	drosophila
1248	77	4.3	919	2	Q8SY59	Q8sy59	drosophila
1249	77	4.3	932	2	Q7KQY4	Q7kqy4	drosophila
1250	77	4.3	949	1	MRN2_HUMAN	Q9h816	homo sapien
1251	77	4.3	949	2	Q41524	Q41524	triticum ae
1252	77	4.3	986	2	Q7R328	Q7r328	giardia lam
1253	77	4.3	1021	2	O15451	O15451	homo sapien
1254	77	4.3	1086	2	Q8BY76	Q8by76	mus musculu
1255	77	4.3	1087	2	Q7ZU12	Q7zu12	brachydanio
1256	77	4.3	1111	2	Q9VGE4	Q9vge4	drosophila
1257	77	4.3	1130	2	Q8IZL8	Q8izl8	homo sapien
1258	77	4.3	1130	2	Q6NTE6	Q6nte6	homo sapien
1259	77	4.3	1191	1	NIFJ_RHORU	Q53046	rhodospiril
1260	77	4.3	1284	2	O15450	O15450	homo sapien
1261	77	4.3	1329	2	Q6BP33	Q6bp33	debaryomyce
1262	77	4.3	1386	2	Q6L067	Q6l067	picrophilus
1263	77	4.3	1429	2	Q6RCQ3	Q6rcq3	legionella
1264	77	4.3	1430	2	Q68CP8	Q68cp8	homo sapien
1265	77	4.3	1475	1	TRA2_CAEEL	P34709	caenorhabdi
1266	77	4.3	1489	2	Q6FV44	Q6fv44	candida gla
1267	77	4.3	1508	2	Q7RHF5	Q7rhf5	plasmodium
1268	77	4.3	1680	2	Q6IFU1	Q6ifu1	schistosoma
1269	77	4.3	2039	2	Q658K1	Q658k1	homo sapien
1270	77	4.3	2062	1	ANRZ_HUMAN	Q6ub98	homo sapien
1271	77	4.3	2147	2	Q6XHB0	Q6xhb0	dictyosteli
1272	77	4.3	2258	2	Q7TN96	Q7tn96	rattus norv

1273	77	4.3	2363	2	Q6ALH2	Q6alh2	desulfotale
1274	77	4.3	2367	2	Q7R607	Q7r607	giardia lam
1275	77	4.3	3108	2	Q6FWS9	Q6fws9	candida gla
1276	77	4.3	3866	1	HRX_MOUSE	P55200	mus musculu
1277	77	4.3	4128	1	PRKD_HUMAN	P78527	homo sapien
1278	77	4.3	4207	2	Q7R3Y5	Q7r3y5	giardia lam
1279	76.5	4.3	162	2	Q8JN37	Q8jn37	human parvo
1280	76.5	4.3	245	2	Q9LPC2	Q9lpc2	arabidopsis
1281	76.5	4.3	255	2	Q9SD08	Q9sd08	arabidopsis
1282	76.5	4.3	282	2	Q6NMZ5	Q6nmz5	arabidopsis
1283	76.5	4.3	301	2	Q82TE2	Q82te2	nitrosomona
1284	76.5	4.3	305	2	Q7SEU8	Q7seu8	neurospora
1285	76.5	4.3	309	2	Q8J2S2	Q8j2s2	pholiota na
1286	76.5	4.3	310	2	Q8K8H8	Q8k8h8	streptococc
1287	76.5	4.3	318	2	Q9NUW1	Q9nuw1	homo sapien
1288	76.5	4.3	318	2	Q7UFM0	Q7ufm0	rhodopirell
1289	76.5	4.3	335	1	YN9B_SCHPO	Q9y800	schizosacch
1290	76.5	4.3	339	2	Q6BKW5	Q6bkw5	debaryomyce
1291	76.5	4.3	361	2	O66979	O66979	aquifex aeo
1292	76.5	4.3	364	2	Q8MHU5	Q8mhu5	sus scrofa
1293	76.5	4.3	364	2	Q8SPB3	Q8spb3	sus scrofa
1294	76.5	4.3	364	2	Q860U6	Q860u6	sus scrofa
1295	76.5	4.3	366	2	Q9HQM4	Q9hqm4	halobacteri
1296	76.5	4.3	377	2	Q8HT51	Q8ht51	bartramia p
1297	76.5	4.3	382	2	Q63L98	Q63198	burkholderi
1298	76.5	4.3	390	2	Q9RYF4	Q9ryf4	deinococcus
1299	76.5	4.3	394	2	Q8JTB5	Q8jtb5	striped bas
1300	76.5	4.3	403	2	Q9W3D5	Q9w3d5	drosophila
1301	76.5	4.3	407	2	Q8FV20	Q8fv20	brucella su
1302	76.5	4.3	437	2	Q6F2N0	Q6f2n0	oryza sativ
1303	76.5	4.3	464	2	Q6P5B1	Q6p5b1	mus musculu
1304	76.5	4.3	486	2	Q55728	Q55728	synechocyst
1305	76.5	4.3	515	2	Q9H0F5	Q9h0f5	homo sapien
1306	76.5	4.3	518	2	Q7P1Y8	Q7p1y8	chromobacte
1307	76.5	4.3	518	2	Q8BI21	Q8bi21	mus musculu
1308	76.5	4.3	519	2	Q6GND0	Q6gnd0	xenopus lae
1309	76.5	4.3	526	2	Q89YC4	Q89yc4	bradyrhizob
1310	76.5	4.3	529	2	Q7RX67	Q7rx67	neurospora
1311	76.5	4.3	557	2	Q9J2L5	Q9j2l5	rhesus monk
1312	76.5	4.3	557	2	Q9WRT1	Q9wrt1	macaca mula
1313	76.5	4.3	563	2	Q8A264	Q8a264	bacteroides
1314	76.5	4.3	590	2	Q6BV74	Q6bv74	debaryomyce
1315	76.5	4.3	590	2	Q6U4B6	Q6u4b6	nilaparvata
1316	76.5	4.3	594	2	O73932	O73932	xenopus lae
1317	76.5	4.3	602	2	Q9DSK9	Q9dsk9	human immun
1318	76.5	4.3	623	2	Q95S21	Q95s21	drosophila
1319	76.5	4.3	649	1	P137_HUMAN	Q14444	homo sapien
1320	76.5	4.3	653	2	O53182	O53182	mycobacteri
1321	76.5	4.3	653	2	Q7TYJ5	Q7tyj5	mycobacteri
1322	76.5	4.3	656	2	Q9BV09	Q9bv09	homo sapien
1323	76.5	4.3	658	2	Q7D742	Q7d742	mycobacteri
1324	76.5	4.3	661	1	HCYC_PANIN	P80096	panulirus i
1325	76.5	4.3	662	2	P91331	P91331	caenorhabdi
1326	76.5	4.3	685	2	Q93HU7	Q93hu7	enterococcu
1327	76.5	4.3	694	2	Q6IMN7	Q6imn7	homo sapien
1328	76.5	4.3	701	1	Y363_BUCAI	P57444	buchnera ap
1329	76.5	4.3	702	1	DYI2_ANTCR	Q16959	anthocidari
1330	76.5	4.3	706	2	Q6BH82	Q6bh82	debaryomyce
1331	76.5	4.3	709	2	Q6IMN4	Q6imn4	homo sapien
1332	76.5	4.3	752	2	Q93NY7	Q93ny7	anaplasma p
1333	76.5	4.3	753	2	Q8V5A9	Q8v5a9	casphalia e
1334	76.5	4.3	760	2	Q8NHV6	Q8nhv6	homo sapien
1335	76.5	4.3	764	2	Q75DU5	Q75du5	ashbya goss
1336	76.5	4.3	784	2	O00146	O00146	homo sapien
1337	76.5	4.3	784	2	Q66K89	Q66k89	homo sapien
1338	76.5	4.3	786	2	Q8IMM8	Q8imm8	drosophila
1339	76.5	4.3	807	2	Q68DK8	Q68dk8	homo sapien
1340	76.5	4.3	817	2	Q9TVT4	Q9tvt4	drosophila
1341	76.5	4.3	817	2	Q9U441	Q9u441	drosophila
1342	76.5	4.3	817	2	Q9U442	Q9u442	drosophila
1343	76.5	4.3	817	2	Q9U443	Q9u443	drosophila
1344	76.5	4.3	817	2	Q9U444	Q9u444	drosophila
1345	76.5	4.3	826	2	Q9TXW6	Q9txw6	caenorhabdi
1346	76.5	4.3	830	2	Q9Y7T4	Q9y7t4	schizosacch
1347	76.5	4.3	845	2	Q7SNL8	Q7snl8	human immun
1348	76.5	4.3	847	2	Q6VZC4	Q6vzc4	canarypox v
1349	76.5	4.3	927	2	Q6Z720	Q6z720	oryza sativ
1350	76.5	4.3	933	2	Q9LKQ0	Q9lkq0	solanum tub
1351	76.5	4.3	943	2	Q44109	Q44109	actinomyces
1352	76.5	4.3	948	2	Q6UXY8	Q6uxy8	homo sapien
1353	76.5	4.3	1180	1	TYK2_MOUSE	Q9r117	mus musculu
1354	76.5	4.3	1181	2	Q8G6E4	Q8g6e4	bifidobacte
1355	76.5	4.3	1257	2	Q9VK28	Q9vk28	drosophila
1356	76.5	4.3	1660	2	Q9NKN0	Q9nkn0	leishmania
1357	76.5	4.3	1665	2	Q7PDL3	Q7pdl3	plasmodium
1358	76.5	4.3	1746	2	Q8WY19	Q8wy19	homo sapien
1359	76.5	4.3	2012	1	DSCA_HUMAN	O60469	homo sapien
1360	76.5	4.3	2166	2	Q8FGC1	Q8fgc1	escherichia
1361	76.5	4.3	2602	1	FLNB_MOUSE	Q80x90	mus musculu
1362	76.5	4.3	3580	2	Q65NK5	Q65nk5	bacillus li
1363	76.5	4.3	5363	2	Q70JZ9	Q70jz9	bacillus am
1364	76.5	4.3	7105	2	Q7PXW9	Q7pxw9	anopheles g
1365	76	4.3	175	1	HSLV_BUCBP	P59581	buchnera ap
1366	76	4.3	190	1	GPX2_RAT	P83645	rattus norv
1367	76	4.3	192	2	Q7NW84	Q7nw84	chromobacte
1368	76	4.3	203	2	Q9UNC0	Q9unc0	homo sapien
1369	76	4.3	223	2	Q66ED6	Q66ed6	yersinia ps
1370	76	4.3	223	2	Q8ZBN4	Q8zbn4	yersinia pe
1371	76	4.3	246	2	Q67NW9	Q67nw9	symbiobacte
1372	76	4.3	246	2	Q82K86	Q82k86	streptomyce
1373	76	4.3	247	2	Q7QRW8	Q7qrw8	giardia lam
1374	76	4.3	275	2	Q62EK0	Q62ek0	burkholderi
1375	76	4.3	313	2	Q8WPI9	Q8wpi9	theileria a
1376	76	4.3	324	2	Q8RXQ9	Q8rxq9	arabidopsis
1377	76	4.3	333	2	Q8BVC4	Q8bvc4	mus musculu
1378	76	4.3	351	2	Q9LSL1	Q9lsl1	arabidopsis
1379	76	4.3	355	2	Q9KCG8	Q9kcg8	bacillus ha
1380	76	4.3	359	2	Q8UZM5	Q8uzm5	squash yell
1381	76	4.3	364	2	Q8HT27	Q8ht27	calliergone
1382	76	4.3	368	2	Q45425	Q45425	bacillus su
1383	76	4.3	374	2	Q7RUL7	Q7rul7	neurospora
1384	76	4.3	379	2	Q8HT30	Q8ht30	neodolichom
1385	76	4.3	379	2	Q9AEW6	Q9aew6	pseudomonas
1386	76	4.3	383	2	Q64I77	Q64i77	reticuliter
1387	76	4.3	384	2	Q6NVS2	Q6nvs2	xenopus tro
1388	76	4.3	392	2	Q8IQC3	Q8iqc3	drosophila
1389	76	4.3	396	2	Q8T4A7	Q8t4a7	drosophila
1390	76	4.3	400	2	Q7NDC9	Q7ndc9	gloeobacter
1391	76	4.3	401	2	P72902	P72902	synechocyst
1392	76	4.3	402	2	Q72U35	Q72u35	leptospira
1393	76	4.3	408	2	Q9VSZ5	Q9vsz5	drosophila
1394	76	4.3	412	2	Q9PWC2	Q9pwc2	brachydanio
1395	76	4.3	431	2	Q6U7U0	Q6u7u0	crinipellis
1396	76	4.3	457	1	BAG4_HUMAN	O95429	homo sapien
1397	76	4.3	467	2	P91596	P91596	culex pipie
1398	76	4.3	468	2	Q7X7S8	Q7x7s8	oryza sativ
1399	76	4.3	473	2	Q8SQG8	Q8sqg8	bos taurus
1400	76	4.3	502	1	SYK_CLOTE	Q899g7	clostridium
1401	76	4.3	513	2	Q9I8V9	Q9i8v9	raja eglant
1402	76	4.3	527	2	Q8YNG9	Q8yng9	anabaena sp
1403	76	4.3	532	2	Q9K3W4	Q9k3w4	streptomyce
1404	76	4.3	540	2	Q8HT32	Q8ht32	pleurozium
1405	76	4.3	541	2	Q8HT31	Q8ht31	rhytidiadel
1406	76	4.3	548	2	Q8HT28	Q8ht28	brachytheci
1407	76	4.3	553	2	Q7UER7	Q7uer7	rhodopirell
1408	76	4.3	567	2	Q8T9L5	Q8t9l5	drosophila
1409	76	4.3	583	2	Q92E36	Q92e36	listeria in
1410	76	4.3	588	2	Q97N97	Q97n97	streptococc
1411	76	4.3	590	1	CHL1_ARATH	Q05085	arabidopsis
1412	76	4.3	596	2	Q9VB83	Q9vb83	drosophila
1413	76	4.3	598	2	Q97P64	Q97p64	streptococc
1414	76	4.3	598	2	Q8DNP6	Q8dnp6	streptococc
1415	76	4.3	609	1	FETA_HORSE	P49066	equus cabal
1416	76	4.3	618	2	Q9A5B1	Q9a5b1	caulobacter
1417	76	4.3	619	2	Q8N669	Q8n669	homo sapien
1418	76	4.3	619	2	Q96K58	Q96k58	homo sapien

1419	76	4.3	624	2	Q8DJF4	Q8djf4 synechococc
1420	76	4.3	627	2	Q81I02	Q81i02 bacillus ce
1421	76	4.3	630	2	Q8J130	Q8j130 aspergillus
1422	76	4.3	638	1	SCAD_PANTR	O46547 pan troglod
1423	76	4.3	664	2	Q8XUT4	Q8xut4 ralstonia s
1424	76	4.3	674	2	Q6CFU3	Q6cfu3 yarrowia li
1425	76	4.3	697	2	Q6QR57	Q6qr57 ictalurus p
1426	76	4.3	698	2	Q709D7	Q709d7 fusarium ox
1427	76	4.3	719	1	YP62_CAEEL	Q09437 caenorhabdi
1428	76	4.3	734	1	PSAB_ANTFO	Q85av8 anthoceros
1429	76	4.3	735	2	Q7S720	Q7s720 neurospora
1430	76	4.3	744	2	Q7MCR2	Q7mcr2 vibrio vuln
1431	76	4.3	745	2	Q82IG9	Q82ig9 streptomyce
1432	76	4.3	765	2	Q6FPT7	Q6fpt7 candida gla
1433	76	4.3	797	2	O43686	O43686 homo sapien
1434	76	4.3	797	2	Q9PWG5	Q9pwg5 anguilla ja
1435	76	4.3	798	2	Q7XVQ7	Q7xvq7 oryza sativ
1436	76	4.3	806	2	Q759C1	Q759c1 ashbya goss
1437	76	4.3	813	2	O76216	O76216 drosophila
1438	76	4.3	813	2	Q9VTZ1	Q9vtz1 drosophila
1439	76	4.3	835	2	Q8GFC9	Q8gfc9 photorhabdu
1440	76	4.3	842	2	Q8G451	Q8g451 bifidobacte
1441	76	4.3	845	2	Q9Y357	Q9y357 homo sapien
1442	76	4.3	895	1	DAG1_BOVIN	O18738 bos taurus
1443	76	4.3	899	2	Q80V48	Q80v48 mus musculu
1444	76	4.3	922	2	Q8SQF8	Q8sqf8 desmodus ro
1445	76	4.3	926	2	Q7MGB4	Q7mgb4 vibrio vuln
1446	76	4.3	926	2	Q8D4R0	Q8d4r0 vibrio vuln
1447	76	4.3	933	2	Q8SS39	Q8ss39 encephalito
1448	76	4.3	943	2	O85487	O85487 pseudomonas
1449	76	4.3	956	1	DDF1_HUMAN	Q9ulh1 h 130-kda p
1450	76	4.3	984	2	Q7XS42	Q7xs42 oryza sativ
1451	76	4.3	1021	2	Q9K5L6	Q9k516 actinoplane
1452	76	4.3	1032	2	Q7XMJ5	Q7xmj5 oryza sativ
1453	76	4.3	1042	2	Q55528	Q55528 synechocyst
1454	76	4.3	1064	2	Q63D05	Q63d05 bacillus ce
1455	76	4.3	1070	2	Q7XWY9	Q7xwy9 oryza sativ
1456	76	4.3	1073	1	MTR4_YEAST	P47047 saccharomyc
1457	76	4.3	1143	2	Q6P0N6	Q6p0n6 homo sapien
1458	76	4.3	1187	2	Q6NRX8	Q6nrx8 xenopus lae
1459	76	4.3	1332	2	Q7PQL0	Q7pql0 anopheles g
1460	76	4.3	1375	2	Q6ZSE6	Q6zse6 homo sapien
1461	76	4.3	1433	2	Q8L332	Q8l332 aphanizomen
1462	76	4.3	1486	2	Q7TPM1	Q7tpm1 mus musculu
1463	76	4.3	1565	2	Q8BXE5	Q8bxe5 m mus muscu
1464	76	4.3	1646	2	Q6CCJ0	Q6ccj0 yarrowia li
1465	76	4.3	2134	2	Q8CZT9	Q8czt9 yersinia pe
1466	76	4.3	2201	2	Q8ZHV3	Q8zhv3 yersinia pe
1467	76	4.3	2274	2	Q8DZ40	Q8dz40 streptococc
1468	76	4.3	2343	2	O62730	O62730 canis famil
1469	76	4.3	3060	1	BPEB_HUMAN	Q8wxk8 homo sapien
1470	76	4.3	3311	2	Q74QP0	Q74qp0 yersinia pe
1471	76	4.3	3886	2	Q666G1	Q666g1 yersinia ps
1472	76	4.3	5171	1	BPEA_HUMAN	O94833 homo sapien
1473	75.5	4.2	153	2	Q7R639	Q7r639 giardia lam
1474	75.5	4.2	214	2	Q9W7C9	Q9w7c9 oryzias lat
1475	75.5	4.2	246	1	PLA2_AERPE	Q9yan6 aeropyrum p
1476	75.5	4.2	251	2	Q8PJQ1	Q8pjq1 xanthomonas
1477	75.5	4.2	264	1	COLI_MACNE	P01201 m corticotr
1478	75.5	4.2	266	1	NAGB_YERPE	Q8zde1 yersinia pe
1479	75.5	4.2	266	2	Q66DC7	Q66dc7 yersinia ps
1480	75.5	4.2	266	2	Q6LTD4	Q6ltd4 photobacter
1481	75.5	4.2	267	2	Q87BA2	Q87ba2 xylella fas
1482	75.5	4.2	284	1	S4A1_MOUSE	P63046 mus musculu
1483	75.5	4.2	284	1	S4A1_RAT	P63047 rattus norv
1484	75.5	4.2	284	2	Q68EV3	Q68ev3 xenopus lae
1485	75.5	4.2	310	2	Q8P2B5	Q8p2b5 streptococc
1486	75.5	4.2	310	2	Q9A198	Q9a198 streptococc
1487	75.5	4.2	314	2	Q76EI3	Q76ei3 symbiodiniu
1488	75.5	4.2	315	2	Q9QNM7	Q9qnm7 sweet potat
1489	75.5	4.2	329	2	Q8F115	Q8f115 leptospira
1490	75.5	4.2	342	2	Q6D8T9	Q6d8t9 erwinia car
1491	75.5	4.2	356	2	Q9VNK5	Q9vnk5 drosophila
1492	75.5	4.2	360	2	Q89MA8	Q89ma8 bradyrhizob
1493	75.5	4.2	364	2	Q8HX60	Q8hx60 sus scrofa
1494	75.5	4.2	364	2	Q8MGX8	Q8mgx8 sus scrofa
1495	75.5	4.2	371	2	Q7P4W9	Q7p4w9 fusobacteri
1496	75.5	4.2	389	2	Q6DVN8	Q6dvn8 rhizopus or
1497	75.5	4.2	389	2	Q6GVZ9	Q6gvz9 rhizopus sp
1498	75.5	4.2	394	2	Q8LT17	Q8lt17 solanum tub
1499	75.5	4.2	394	2	Q9LKZ1	Q9lkz1 capsicum an
1500	75.5	4.2	422	2	Q7MJV2	Q7mjv2 vibrio vuln

ALIGNMENTS

RESULT 1
CAHE_HUMAN
ID CAHE_HUMAN STANDARD; PRT; 337 AA.
AC Q9ULX7; Q8NCF4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbonic anhydrase XIV precursor (EC 4.2.1.1) (Carbonate dehydratase
DE XIV) (CA-XIV) (UNQ690/PRO1335).
GN Name=CA14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99443874; PubMed=10512682; DOI=10.1006/geno.1999.5938;
RA Fujikawa-Adachi K., Nishimori I., Taguchi T., Onishi S.;
RT "Human carbonic anhydrase XIV (CA14): cDNA cloning, mRNA expression,
RT and mapping to chromosome 1.";
RL Genomics 61:74-81(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

```
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Lung, and Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: High expression in all parts of the central
CC       nervous system and lower expression in adult liver, heart, small
CC       intestine, colon, kidney, urinary bladder and skeletal muscle.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB025904; BAA85002.1; -.
DR   EMBL; AY358689; AAQ89052.1; -.
DR   EMBL; AK074765; BAC11191.1; -.
DR   EMBL; BC034412; AAH34412.1; -.
DR   HSSP; O43570; 1JD0.
DR   Genew; HGNC:1372; CA14.
DR   MIM; 604832; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004089; F:carbonate dehydratase activity; TAS.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; FALSE_NEG.
KW   Lyase; Signal; Transmembrane; Zinc.
FT   SIGNAL       1     15       Potential.
FT   CHAIN       16    337       Carbonic anhydrase XIV.
FT   DOMAIN      16    290       Extracellular (Potential).
FT   TRANSMEM   291    311       Potential.
FT   DOMAIN     312    337       Cytoplasmic (Potential).
FT   METAL      109    109       Zinc (catalytic) (By similarity).
FT   METAL      111    111       Zinc (catalytic) (By similarity).
FT   METAL      135    135       Zinc (catalytic) (By similarity).
FT   CARBOHYD   213    213       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT   229    229       V -> A (in Ref. 3).
SQ   SEQUENCE   337 AA;  37667 MW;  6E101C44EA70A700 CRC64;

  Query Match             100.0%;  Score 1779;  DB 1;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-140;
  Matches  337;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPD 60

Qy         61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120

Qy        121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Qy        181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Qy        241 LEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300

Qy        301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
              |||||||||||||||||||||||||||||||||||||
Db        301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337


RESULT 2
CAHE_MOUSE
ID   CAHE_MOUSE     STANDARD;      PRT;   337 AA.
AC   Q9WVT6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase XIV precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   XIV) (CA-XIV).
GN   Name=Ca14; Synonyms=Car14, Catm;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=99269110; PubMed=10336468; DOI=10.1074/jbc.274.22.15701;
RA   Mori K., Ogawa Y., Ebihara K., Tamura N., Tashiro K., Kuwahara T.,
RA   Mukoyama M., Sugawara A., Ozaki S., Tanaka I., Nakao K.;
RT   "Isolation and characterization of CA XIV, a novel membrane-bound
RT   carbonic anhydrase from mouse kidney.";
RL   J. Biol. Chem. 274:15701-15705(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```

```
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Most abundant in the kidney and heart,
CC       followed by the skeletal muscle, brain, lung and liver.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB005450; BAA78709.1; -.
DR   EMBL; BC046995; AAH46995.1; -.
DR   HSSP; O43570; 1JD0.
DR   MGD; MGI:1344341; Car14.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; FALSE_NEG.
KW   Lyase; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16    337       Carbonic anhydrase XIV.
FT   DOMAIN       16    290       Extracellular (Potential).
FT   TRANSMEM    291    311       Potential.
FT   DOMAIN      312    337       Cytoplasmic (Potential).
FT   METAL       109    109       Zinc (catalytic) (By similarity).
FT   METAL       111    111       Zinc (catalytic) (By similarity).
FT   METAL       135    135       Zinc (catalytic) (By similarity).
FT   CARBOHYD    213    213       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   337 AA;  37505 MW;  32F02F4DB78AC0C9 CRC64;

  Query Match             84.3%;  Score 1500;  DB 1;  Length 337;
  Best Local Similarity   84.0%;  Pred. No. 3.1e-117;
  Matches  283;  Conservative   23;  Mismatches   31;  Indels    0;  Gaps    0;

Qy          1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPD 60
              ||| ||||:| |||||||| ||||||||||||||| |||||| :|||||:|||||| ||||
Db          1 MLFFALLLKVTWILAADGGHHWTYEGPHGQDHWPTSYPECGGDAQSPINIQTDSVIFDPD 60

Qy         61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGG 120
              |||:||||||| |||||||||||||||||| ||:|||||||| |||||||||:||  |
Db         61 LPAVQPHGYDQLGTEPLDLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQRGSLEG 120

Qy        121 SEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
              |||||||||| ||||:||||| || ||||||::||||||||||||||:| ||:||||
Db        121 SEHQINSEATAAELHVVHYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR 180

Qy        181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
              |||:|:|||||||||::||| |:|| |:|||||||||||||||||||| ||:|||| |
Db        181 LHEIRYKDQKTSVPPFSVRELFPQQLEQFFRYNGSLTTPPCYQSVLWTVFNRRAQISMGQ 240

Qy        241 LEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
              ||||| || ||||:||: ||||||  |||||| :|||||||  ||||||| |||||| |
Db        241 LEKLQETLSSTEEDPSEPLVQNYRVPQPLNQRTIFASFIQAGPLYTTGEMLGLGVGILAG 300

Qy        301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
              ||||||||||||:||||||| ||||||||||:|||||

Db        301 CLCLLLAVYFIAQKIRKKRLGNRKSVVFTSARATTEA 337


RESULT 3
CAHC_RABIT
ID   CAHC_RABIT     STANDARD;      PRT;   355 AA.
AC   Q9MZ30;
DT   16-OCT-2001 (Rel. 40, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   XII) (CA-XII).
GN   Name=CA12;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney cortex;
RX   MEDLINE=22417091; PubMed=12388401; DOI=10.1152/ajprenal.00370.2001;
RA   Schwartz G.J., Kittelberger A.M., Watkins R.H., O'Reilly M.A.;
RT   "Carbonic anhydrase XII mRNA encodes a hydratase that is
RT   differentially expressed along the rabbit nephron.";
RL   Am. J. Physiol. 284:F399-F410(2003).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF263367; AAF91392.2; -.
DR   HSSP; O43570; 1JD0.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    355       Carbonic anhydrase XII.
FT   DOMAIN       25    303       Extracellular (Potential).
FT   TRANSMEM    304    324       Potential.
FT   DOMAIN      325    355       Cytoplasmic (Potential).
FT   METAL       119    119       Zinc (catalytic) (By similarity).
FT   METAL       121    121       Zinc (catalytic) (By similarity).
FT   METAL       145    145       Zinc (catalytic) (By similarity).
FT   DISULFID     50    230       By similarity.
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     80     80       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    162    162       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   355 AA;  39591 MW;  5B468580EBA437D5 CRC64;

  Query Match             39.2%;  Score 698;  DB 1;  Length 355;
  Best Local Similarity   43.8%;  Pred. No. 5.7e-50;
  Matches  145;  Conservative   58;  Mismatches  118;  Indels   10;  Gaps    7;

Qy         15 AADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGT 74
              |   | ||| |  |: |   || ||   |||||:  |:: :|  |  |: ||:
Db         25 APRNGSKWTYVGADGERSWFKKYPSCGGRLQSPIDLHGDTLQYDASLTPLEFQGYNVSAD 84

Qy         75 EPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAEL 134
              :  :| |:||:|:|:||  :|| ||| :| | ||||||| :  | |||| :  :   |||
Db         85 KQFNLTNDGHSVRLNLPPDMYLQGLPSRYTATQLHLHWGNRNDPYGSEHTVGGKQFAAEL 144
```

```
Qy        135 HIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVP 194
              |||||:||||  :| |: : :||||| :||| |    |  |: | | |  |::| |   :|
Db        145 HIVHYNSDSYPDISTASNKSEGLAVLAVLIEKGYF-NPYYDRIFSFLRYVKYKGQNVRIP 203

Qy        195 PFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-E 253
               ||: ||||::  :|:|| ||||||||| |||||||     || |||  ||  |: |  :
Db        204 TFNIEELLPEKPAEYYRYRGSLTTPPCYPSVLWTVFRNPVTISQEQLLALQTALYFTRAD 263

Qy        254 EPS-KLLVQNYRALQPLNQRMVFASF----IQAGSSYTTGEMLSLGV-GILVGCLCLLLA 307
              :|: : :: |:| :|    |:| |||    |  |:  : | :||: : |:|  |: | :
Db        264 DPAPREMINNFRPIQNFGVRLVHASFQEVQILPGTGLSVGIILSVALAGVLGICIVLAVC 323

Qy        308 VYFIARKIRKKRLENRKSVVFTSA-QATTEA 337
              ::|  ||   |: :| | |::  | :  |||
Db        324 IWFFRRKKGSKKGDN-KGVIYNPAIKMETEA 353
```

RESULT 4
CAHC_HUMAN
ID CAHC_HUMAN STANDARD; PRT; 354 AA.
AC O43570; Q9BWG2;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase
DE XII) (CA-XII) (Tumor antigen HOM-RCC-3.1.3).
GN Name=CA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=98301622; PubMed=9636197; DOI=10.1073/pnas.95.13.7608;
RA Tuereci O., Sahin U., Vollmar E., Siemer S., Goettert E., Seitz G.,
RA Parkkila A.-K., Shah G.N., Grubb J.H., Pfreundschuh M., Sly W.S.;
RT "Human carbonic anhydrase XII: cDNA cloning, expression, and
RT chromosomal localization of a carbonic anhydrase gene that is
RT overexpressed in some renal cell cancers.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=98445416; PubMed=9770531; DOI=10.1073/pnas.95.21.12596;
RA Ivanov S.V., Kuzmin I., Wei M.-H., Pack S., Geil L., Johnson B.E.,
RA Stanbridge E.J., Lerman M.I.;
RT "Down-regulation of transmembrane carbonic anhydrases in renal cell
RT carcinoma cell lines by wild-type von Hippel-Lindau transgenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12596-12601(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Eye, and Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 30-292.
RX MEDLINE=21396545; PubMed=11493685; DOI=10.1073/pnas.161301298;
RA Whittington D.A., Waheed A., Ulmasov B., Shah G.N., Grubb J.H.,
RA Sly W.S., Christianson D.W.;
RT "Crystal structure of the dimeric extracellular domain of human
RT carbonic anhydrase XII, a bitopic membrane protein overexpressed in
RT certain cancer tumor cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9545-9550(2001).
CC -!- FUNCTION: Reversible hydration of carbon dioxide.
CC -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC -!- COFACTOR: Zinc (By similarity).
CC -!- ENZYME REGULATION: Inhibited by acetazolamide.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43570-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O43570-2; Sequence=VSP_000772;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in colon, kidney, prostate,
CC intestine and activated lymphocytes. Expressed at much higher
CC levels in the renal cell cancers than in surrounding normal kidney
CC tissue. Moderately expressed in pancreas, ovary and testis.
CC -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC family.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; AF051882; AAC39789.1; -.
DR EMBL; AF037335; AAC63952.1; -.
DR EMBL; BC000278; AAH00278.1; -.
DR EMBL; BC011691; AAH11691.1; -.
DR EMBL; BC023981; AAH23981.1; -.
DR PDB; 1JCZ; X-ray; A/B=29-291.
DR PDB; 1JD0; X-ray; A/B=29-291.
DR Genew; HGNC:1371; CA12.
DR H-InvDB; HIX0012325; -.
DR MIM; 603263; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004089; F:carbonate dehydratase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR InterPro; IPR001148; Euk_COanhd.
DR Pfam; PF00194; Carb_anhydrase; 1.
DR ProDom; PD000865; Euk_COanhd; 1.
DR PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW 3D-structure; Alternative splicing; Lyase; Signal; Transmembrane;
KW Zinc.

FT	SIGNAL	1	24	Potential.
FT	CHAIN	25	354	Carbonic anhydrase XII.
FT	DOMAIN	25	301	Extracellular (Potential).
FT	TRANSMEM	302	322	Potential.
FT	DOMAIN	323	354	Cytoplasmic (Potential).
FT	METAL	119	119	Zinc (catalytic).
FT	METAL	121	121	Zinc (catalytic).
FT	METAL	145	145	Zinc (catalytic).
FT	DISULFID	50	230	
FT	CARBOHYD	28	28	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	80	80	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	162	162	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	292	302	Missing (in isoform 2).
FT				/FTId=VSP_000772.
FT	TURN	37	38	
FT	HELIX	40	42	

```
FT   HELIX        43     46
FT   HELIX        48     51
FT   STRAND       59     60
FT   HELIX        62     64
FT   STRAND       65     67
FT   TURN         69     70
FT   STRAND       75     77
FT   STRAND       80     80
FT   TURN         83     84
FT   STRAND       86     91
FT   STRAND       96     99
FT   TURN        102    103
FT   STRAND      105    107
FT   STRAND      113    122
FT   STRAND      124    124
FT   TURN        125    126
FT   STRAND      127    127
FT   STRAND      134    135
FT   TURN        136    137
FT   STRAND      138    138
FT   STRAND      142    150
FT   TURN        151    153
FT   HELIX       157    160
FT   TURN        161    162
FT   TURN        164    165
FT   STRAND      167    176
FT   TURN        181    183
FT   HELIX       184    187
FT   TURN        188    189
FT   HELIX       190    192
FT   TURN        196    197
FT   STRAND      199    203
FT   STRAND      206    206
FT   HELIX       207    210
FT   TURN        215    216
FT   STRAND      218    223
FT   TURN        228    229
FT   STRAND      234    239
FT   STRAND      243    245
FT   HELIX       247    255
FT   STRAND      258    258
FT   TURN        262    263
FT   STRAND      269    269
FT   STRAND      285    287
SQ   SEQUENCE   354 AA;  39451 MW;  9016216BF2CA6C0C CRC64;

  Query Match           39.2%;  Score 696.5;  DB 1;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 7.5e-50;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352
```

```
RESULT 5
CAHC_MOUSE
ID   CAHC_MOUSE     STANDARD;      PRT;   354 AA.
AC   Q8CI85; Q8BKG6;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   XII) (CA-XII).
GN   Name=Ca12; Synonyms=Car12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
CC   -!- FUNCTION: Reversible hydration of carbon dioxide.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK052639; BAC35074.1; -.
DR   EMBL; BC035941; AAH35941.1; -.
DR   HSSP; O43570; 1JD0.
DR   MGD; MGI:1923709; Car12.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    354       Carbonic anhydrase XII.
FT   DOMAIN       25    301       Extracellular (Potential).
FT   TRANSMEM    302    322       Potential.
FT   DOMAIN      323    354       Cytoplasmic (Potential).
FT   METAL       120    120       Zinc (catalytic).
FT   METAL       122    122       Zinc (catalytic).
FT   METAL       146    146       Zinc (catalytic).
FT   DISULFID     50    231       By similarity.
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     42     42       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     80     80       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    297    297       D -> N (in Ref. 1).
SQ   SEQUENCE   354 AA;  39695 MW;  98ED581BF2A16111 CRC64;

  Query Match             38.8%;  Score 690;  DB 1;  Length 354;
  Best Local Similarity   44.3%;  Pred. No. 2.6e-49;
  Matches  143;  Conservative   62;  Mismatches  102;  Indels   16;  Gaps    8;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |: :|   || ||   |||||: :| : :|  |  ||  ||:    : |:
Db         29 GSKWTYVGPAGEKNWSKKYPSCGGLLQSPIDLHSDILQYDASLAPLQFQGYNVSVEKLLN 88

Qy         79 LHNNGHTVQLSLPSTLYLGGL-PRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIV 137
              | |:||:|:|:|  | :|: || |  | | |||||||  :  | |||| :: :   ||||||
Db         89 LTNDGHSVRLNLNSDMYIQGLQPHHYRAEQLHLHWGNRNDPHGSEHTVSGKHFAAELHIV 148

Qy        138 HYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197
              ||:|| |    | |::: :||||| :|||:| : | :|: | |||  |::| |:  :| ||
Db        149 HYNSDLYPDFSTASDKSEGLAVLAVLIEIG-SANPSYDKIFSHLQHVKYKGQQVLIPGFN 207

Qy        198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS 256
              : ||||:  |:|:|| ||||||||| :||||||    ||| |||  |:  |: |  ::|:
Db        208 IEELLPESPGEYYRYEGSLTTPPCYPTVLWTVFRNPVQISQEQLLALETALYFTHMDDPT 267

Qy        257 -KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAV 308
               : :: |:| :|  ::|:|: || | |     ||  ||||:       |:|   : | :::
Db        268 PREMINNFRQVQKFDERLVYISFRQ-GLLTDTG--LSLGIILSVALAGVLGISIVLAVSI 324

Qy        309 YFIARKIRKKRLENRKSVVFTSA 331
              :   ||  ||   : | |::  |
Db        325 WLFKRKKSKK--GDNKGVIYKPA 345


RESULT 6
Q8K2J1
ID   Q8K2J1      PRELIMINARY;      PRT;   344 AA.
AC   Q8K2J1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Car12 protein.
GN   Name=Car12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
DR   EMBL; BC031385; AAH31385.1; -.
DR   HSSP; O43570; 1JD0.
DR   MGD; MGI:1923709; Car12.
DR   GO; GO:0004089; F:carbonate dehydratase activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Zinc.
SQ   SEQUENCE   344 AA;  38724 MW;  12DCBD6C3E45D75A CRC64;

  Query Match             38.4%;  Score 684;  DB 2;  Length 344;
  Best Local Similarity   43.7%;  Pred. No. 8.1e-49;
  Matches  138;  Conservative   65;  Mismatches  101;  Indels   12;  Gaps    6;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |: :|   || ||   |||||: :| : :|  |  ||  ||:    : |:
Db         29 GSKWTYVGPAGEKNWSKKYPSCGGLLQSPIDLHSDILQYDASLAPLQFQGYNVSVEKLLN 88

Qy         79 LHNNGHTVQLSLPSTLYLGGL-PRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIV 137
              | |:||:|:|:|  | :|: || |  | | |||||||  :  | |||| :: :   ||||||
Db         89 LTNDGHSVRLNLNSDMYIQGLQPHHYRAEQLHLHWGNRNDPHGSEHTVSGKHFAAELHIV 148

Qy        138 HYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197
              ||:|| |    | |::: :||||| :|||:| : | :|: | |||  |::| |:  :| ||
Db        149 HYNSDLYPDFSTASDKSEGLAVLAVLIEIG-SANPSYDKIFSHLQHVKYKGQQVLIPGFN 207
```

```
Qy        198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS 256
              : ||||:  |:|:|| ||||||||| :|||||    ||| |||  |:  |: |  ::|:
Db        208 IEELLPESPGEYYRYEGSLTTPPCYPTVLWTVFRNPVQISQEQLLALETALYFTHMDDPT 267

Qy        257 -KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKI 315
               : :: |:| :|  ::|:|: || |       | :||: :  ::| : ::|||     |
Db        268 PREMINNFRQVQKFDERLVYISFRQ-------GIILSVALAGVLG-ISIVLAVSIWLFKR 319

Qy        316 RKKRLENRKSVVFTSA 331
              :| :  : | |::  |
Db        320 KKSKKGDNKGVIYKPA 335


RESULT 7
CAH9_HUMAN
ID   CAH9_HUMAN     STANDARD;      PRT;   459 AA.
AC   Q16790;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Carbonic anhydrase IX precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   IX) (CA-IX) (CAIX) (Membrane antigen MN) (P54/58N) (Renal cell
DE   carcinoma-associated antigen G250) (RCC-associated antigen G250)
DE   (pMW1).
GN   Name=CA9; Synonyms=G250, MN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Carcinoma;
RX   MEDLINE=94366734; PubMed=8084592;
RA   Pastorek J., Pastorekova S., Callebaut I., Mornon J.-P., Zelnik V.,
RA   Opavsky R., Zat'Ovicova M., Liao S., Portetelle D., Stanbridge E.J.,
RA   Zavada J., Burny A., Kettmann R.;
RT   "Cloning and characterization of MN, a human tumor-associated protein
RT   with a domain homologous to carbonic anhydrase and a putative helix-
RT   loop-helix DNA binding segment.";
RL   Oncogene 9:2877-2888(1994).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT VAL-33.
RC   TISSUE=Renal cell carcinoma;
RX   MEDLINE=20175484; PubMed=10709109;
RA   Grabmaier K., Vissers J.L.M., De Weijert M.C.A.,
RA   Oosterwijk-Wakka J.C., Van Bokhoven A., Brakenhoff R.H., Noessner E.,
RA   Mulders P.A., Merkx G., Figdor C.G., Adema G.J., Oosterwijk E.;
RT   "Molecular cloning and immunogenicity of renal cell carcinoma-
RT   associated antigen G250.";
RL   Int. J. Cancer 85:865-870(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 38-52.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=92188536; PubMed=1312272;
RA   Pastorekova S., Zavadova Z., Kostal M., Babusikova O., Zavada J.;
RT   "A novel quasi-viral agent, MaTu, is a two-component system.";
RL   Virology 187:620-626(1992).
RN   [6]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=93252505; PubMed=8486430;
RA   Zavada J., Zavadova Z., Pastorekova S., Ciampor F., Pastorek J.,
RA   Zelnik V.;
RT   "Expression of MaTu-MN protein in human tumor cultures and in clinical
RT   specimens.";
RL   Int. J. Cancer 54:268-274(1993).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide. May be involved
CC       in the control of cell proliferation and transformation. Appears
CC       to be a novel specific biomarker for a cervical neoplasia.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBUNIT: Forms oligomers linked by disulfide bonds.
CC   -!- SUBCELLULAR LOCATION: Found on the surface microvilli and in the
CC       nucleus, particularly in nucleolus.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in carcinoma cells lines.
CC       Expression is restricted to very few normal tissues and the most
CC       abundant expression is found in the epithelial cells of gastric
CC       mucosa.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X66839; CAA47315.1; -.
DR   EMBL; AJ010588; CAB82444.1; -.
DR   EMBL; BC014950; AAH14950.1; -.
DR   PIR; I38013; I38013.
DR   HSSP; P00918; 1BV3.
DR   Genew; HGNC:1383; CA9.
DR   H-InvDB; HIX0008019; -.
DR   MIM; 603179; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004089; F:carbonate dehydratase activity; TAS.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Antigen; Direct protein sequencing; Glycoprotein; Lyase;
KW   Nuclear protein; Polymorphism; Signal; Transmembrane; Zinc.
FT   SIGNAL        1     37
FT   CHAIN        38    459       Carbonic anhydrase IX.
FT   METAL       226    226       Zinc (catalytic) (By similarity).
FT   METAL       228    228       Zinc (catalytic) (By similarity).
FT   METAL       251    251       Zinc (catalytic) (By similarity).
FT   TRANSMEM    415    435       Potential.
FT   CARBOHYD    346    346       N-linked (GlcNAc. . .).
FT   VARIANT      33     33       M -> V.
FT                                /FTId=VAR_010787.
SQ   SEQUENCE   459 AA;  49729 MW;  5E3C1E2936050B3F CRC64;
```

```
  Query Match             31.6%;  Score 562;  DB 1;  Length 459;
  Best Local Similarity   38.8%;  Pred. No. 2e-38;
  Matches  128;  Conservative   47;  Mismatches  129;  Indels   26;  Gaps    7;

Qy         17 DGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEP 76
              |   || |    |   ||   | |    |||:||:     | | |  |:  |:  |
Db        136 DDQSHWRY---GGDPPWPRVSPACAGRFQSPVDIRPQLAAFCPALRPLELLGFQLPPLPE 192

Qy         77 LDLHNNGHTVQLSLPSTLYLG-GLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELH 135
              | | ||||:|||:||  | :  |  |:| | |||||||  | | |||| :      ||:|
Db        193 LRLRNNGHSVQLTLPPGLEMALGPGREYRALQLHLHWGAAGRP-GSEHTVEGHRFPAEIH 251

Qy        136 IVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP 195
              :||  | ::  : ||  || |||||   :| |  :| ||| :|| | |:  :  :| ||
Db        252 VVHL-STAFARVDEALGRPGGLAVLAAFLEEGPEENSAYEQLLSRLEEIAEEGSETQVPG 310

Qy        196 FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEP 255
               ::  |||    :||:| |||||||| | |:|||| :   :| :||  |  ||:   :
Db        311 LDISALLPSDFSRYFQYEGSLTTPPCAQGVIWTVFNQTVMLSAKQLHTLSDTLWGPGDSR 370

Qy        256 SKLLVQNYRALQPLNQRMVFASF------------IQAGSSYTTGEMLSLGVGILVGCL 302
               :|   |:|| |||| |:: |||             :|  |    |::|:|  |:|
Db        371 LQL---NFRATQPLNGRVIEASFPAGVDSSPRAAEPVQLNSCLAAGDILALVFGLLFA-- 425

Qy        303 CLLLAVYFIARKIRKKRLENRKSVVFTSAQ 332
                : :| |: :  |: |   :  | :  |:
Db        426 --VTSVAFLVQMRRQHRRGTKGGVSYRPAE 453


RESULT 8
CAH9_MOUSE
ID   CAH9_MOUSE     STANDARD;      PRT;   437 AA.
AC   Q8VHB5; Q8K1G1; Q8VDE4;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase IX precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   IX) (CA-IX) (CAIX) (Membrane antigen MN homolog).
GN   Name=Ca9; Synonyms=Car9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=129/Ola;
RX   PubMed=14604546; DOI=10.1016/j.jim.2003.08.011;
RA   Zat'ovicova M., Tarabkova K., Svastova E., Gibadulinova A., Mucha V.,
RA   Jakubickova L., Biesova Z., Rafajova M., Ortova Gut M.O., Parkkila S.,
RA   Parkkila A.-K., Waheed A., Sly W.S., Horak I., Pastorek J.,
RA   Pastorekova S.;
RT   "Monoclonal antibodies generated in carbonic anhydrase IX-deficient
RT   mice recognize different domains of tumour-associated hypoxia-induced
RT   carbonic anhydrase IX.";
RL   J. Immunol. Methods 282:117-134(2003).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Ortova M.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=ICR; TISSUE=Small intestine;
RA   Wang Y.P., Yoshikawa K., Kozaki K., Miyaishi O., Nakagawa A.,
RA   Muramatsu H., Kawada Y., Uchida K., Nishikawa N., Saga S.;
RT   "Alternative spliced mRNA coding for MN/CA9.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBUNIT: Forms oligomers linked by disulfide bonds (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q8VHB5-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q8VHB5-2; Sequence=VSP_007409, VSP_007410;
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY049077; AAL14193.1; -.
DR   EMBL; AJ245857; CAC80975.1; -.
DR   EMBL; AB086322; BAC00816.1; -.
DR   HSSP; O43570; 1JD0.
DR   MGD; MGI:2447188; Car9.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Alternative splicing; Glycoprotein; Lyase; Signal; Transmembrane;
KW   Zinc.
FT   SIGNAL       1     31       Potential.
FT   CHAIN       32    437       Carbonic anhydrase IX.
FT   METAL      205    205       Zinc (catalytic) (By similarity).
FT   METAL      207    207       Zinc (catalytic) (By similarity).
FT   METAL      230    230       Zinc (catalytic) (By similarity).
FT   TRANSMEM   391    411       Potential.
FT   CARBOHYD   325    325       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC   282    282       G -> V (in isoform 2).
FT                               /FTId=VSP_007409.
FT   VARSPLIC   283    437       Missing (in isoform 2).
FT                               /FTId=VSP_007410.
SQ   SEQUENCE   437 AA;  47264 MW;  88F23380DCD35344 CRC64;

  Query Match             31.6%;  Score 561.5;  DB 1;  Length 437;
  Best Local Similarity   39.0%;  Pred. No. 2.1e-38;
  Matches  130;  Conservative   48;  Mismatches  124;  Indels   31;  Gaps    8;

Qy         18 GGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPL 77
              |  ||:| |      ||   | |    |||:||: :   |   |  |:  ||:       |
Db        116 GHSHWSYGGTL---LWPQVSPACAGRFQSPVDIRLERTAFCRTLQPLELLGYELQPLPEL 172

Qy         78 DLHNNGHTVQLSLPSTLYLG-GLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHI 136
              | ||||||||:||  | :  |  ::| | |||||||    | |||| :|     ||:|:
Db        173 SLSNNGHTVQLTLPPGLKMALGPGQEYRALQLHLHWGTSDHP-GSEHTVNGHRFPAEIHV 231

Qy        137 VHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPF 196
              ||  | ::  | ||  || |||||   ::    :| ||| :|||| |:  :  |  :|
Db        232 VHL-STAFSELHEALGRPGGLAVLAAFLQESPEENSAYEQLLSHLEEISEEGSKIEIPGL 290

Qy        197 NLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPS 256
              ::  |||  | :|:|| ||||||||| | |:||||    ::| :||  |  :|:   :
Db        291 DVSALLPSDLSRYYRYEGSLTTPPCSQGVIWTVFNETVKLSAKQLHTLSVSLWGPRDSRL 350

Qy        257 KLLVQNYRALQPLNQRMVFASF----------IQAGSSYTTGEMLSLGVGILVGCLCLLL 306
              :|   |:|| |||| | : |||          :   | :| |::|:|  |        ||
Db        351 QL---NFRATQPLNGRTIEASFPAAEDSSPEPVHVNSCFTAGDILALVFG-------LLF 400

Qy        307 AVYFIARKIRKKRLENRKS-----VVFTSAQAT 334
              ||  ||  :: :|    :|     | :: |: |
Db        401 AVTSIAFLLQLRRQHRHRSGTKDRVSYSPAEMT 433


RESULT 9
CAH6_SHEEP
ID   CAH6_SHEEP     STANDARD;      PRT;   307 AA.
AC   P08060;
```

```
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase VI (EC 4.2.1.1) (Carbonate dehydratase VI) (CA-VI)
DE   (Secreted carbonic anhydrase) (Salivary carbonic anhydrase).
GN   Name=CA6;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Saliva;
RX   MEDLINE=88294021; PubMed=3135834;
RA   Fernley R.T., Wright R.D., Coghlan J.P.;
RT   "Complete amino acid sequence of ovine salivary carbonic anhydrase.";
RL   Biochemistry 27:2815-2820(1988).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide. Its role in
CC       saliva is unknown.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Major consistuent of saliva.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
DR   PIR; A29993; A29993.
DR   HSSP; O43570; 1JD0.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Direct protein sequencing; Glycoprotein; Lyase; Zinc.
FT   METAL        94     94       Zinc (catalytic) (By similarity).
FT   METAL        96     96       Zinc (catalytic) (By similarity).
FT   METAL       121    121       Zinc (catalytic) (By similarity).
FT   DISULFID     25    207       Potential.
FT   CARBOHYD     50     50       N-linked (GlcNAc. . .).
FT   CARBOHYD    239    239       N-linked (GlcNAc. . .).
FT   VARIANT      63     63       V -> M.
FT   VARIANT     297    297       I -> M.
SQ   SEQUENCE   307 AA;  35555 MW;  338682C2D45E5D6C CRC64;

  Query Match             30.1%;  Score 535.5;  DB 1;  Length 307;
  Best Local Similarity   40.2%;  Pred. No. 1.9e-36;
  Matches  125;  Conservative   54;  Mismatches  117;  Indels   15;  Gaps   11;

Qy         19 GQHWTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYD-QPGTEP 76
              |  ||| ||    : |||  ||:||   |||||:|    | ::| | ||    ||    |  |
Db          3 GVEWTYSEGMLDEAHWPLEYPKCGGRRQSPIDLQMKKVQYNPSLRALNLTGYGLWHGEFP 62

Qy         77 LDLHNNGHTVQLSLPSTLYLGGLP-RKYVAAQLHLHWGQKGSP-GGSEHQINSEATFAEL 134
              :   |||||||:|||||: :      :|:| |:| |||    |    |||| ::      |:
Db         63 VT--NNGHTVQISLPSTMSMTTSDGTQYLAKQMHFHWGGASSEISGSEHTVDGMRYVIEI 120

Qy        135 HIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGE-TKNIAYEHILSHLHEVRHKDQKTSV 193
              |:|||:|  |:|  || : | |||||  |:|| : |:|  |   :||| ::|:  | | :
Db        121 HVVHYNS-KYNSYEEAQKEPDGLAVLAALVEVKDYTENAYYSKFISHLEDIRYAGQSTVL 179

Qy        194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
                 :: ::||  |  |: | |||||||| ::| | |     ::|  |:|||: :| : :
Db        180 RGLDIEDMLPGDLRYYYSYLGSLTTPPCTENVHWFVVADTVKLSKTQVEKLENSLLNHQ- 238

Qy        254 EPSKLLVQNYRALQPLNQRMVFASFI-QAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIA 312
              :| :  :||  |||| |:| |:|: :    ||    |   :  :   | |    ||
Db        239 --NKTIQNDYRRTQPLNHRVVEANFMSRPHQEYTLASKLHFYLNNIDQTLEYLRR--FIE 294

Qy        313 RKI-RKKRLEN 322
              :|| ::|: ||
Db        295 QKIPKRKKQEN 305


RESULT 10
```

```
Q6GQ30
ID   Q6GQ30      PRELIMINARY;      PRT;   525 AA.
AC   Q6GQ30;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80389 protein.
GN   Name=MGC80389;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
DR   EMBL; BC072918; AAH72918.1; -.
DR   GO; GO:0004089; F:carbonate dehydratase activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001148; Euk_COanhd.
DR   InterPro; IPR001759; Pentaxin.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   Pfam; PF00354; Pentaxin; 1.
DR   PRINTS; PR00895; PENTAXIN.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   ProDom; PD002153; Pentaxin; 1.
DR   SMART; SM00159; PTX; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
DR   PROSITE; PS00289; PENTAXIN; UNKNOWN_1.
KW   Lyase; Zinc.
SQ   SEQUENCE   525 AA;  59643 MW;  D1DC237D63735578 CRC64;
```

```
  Query Match             30.0%;  Score 533;  DB 2;  Length 525;
  Best Local Similarity   43.5%;  Pred. No. 6.5e-36;
  Matches  113;  Conservative   40;  Mismatches  101;  Indels    6;  Gaps    4;

Qy         22 WTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLH 80
              ||| ||   : :|   || |    |||||||   |  :|:|  |:  ||| | |    :
Db         27 WTYQEGELDEANWGKKYPTCAAKHQSPIDIQRKKVRHNPELTQLELIGYDGPLTGHFKVT 86

Qy         81 NNGHTVQLSLPSTLYL-GGLPRKYVAAQLHLHW-GQKGSPGGSEHQINSEATFAELHIVH 138
              ||||:||: |||| : :  ||   | | |:|||| | :    |||| |:     |||||||
Db         87 NNGHSVQIDLPSTMTIKKGLNSLYTAVQMHLHWGGLESETSGSEHTIDGMRYLAELHIVH 146

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:| :|  | || ::| |||||  |   |  :|  |   :| | ::|:  |:| :   ::
Db        147 YNSGAYKSFDEAKDKPNGLAVLAFLYTTGNYENTYYSDFISKLAKIRYAGQETEMHTLDV 206

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKL 258
                :||: |  ::||:|||||||| ::||||||     :|  |:: |: ||       :|
Db        207 MAMLPENLVNFYRYDGSLTTPPCTENVLWTVFDSPVFLSKTQIDLLENTLLDWH---NKT 263

Qy        259 LVQNYRALQPLNQRMVFASF 278
              |  :||  || : | | |||
Db        264 LRNDYRHAQPWHDRTVEASF 283


RESULT 11
CAH6_BOVIN
ID   CAH6_BOVIN     STANDARD;      PRT;   319 AA.
AC   P18915; Q95322;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase VI precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   VI) (CA-VI) (Secreted carbonic anhydrase) (Salivary carbonic
DE   anhydrase).
GN   Name=CA6;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Submaxillary gland;
RX   MEDLINE=96358528; PubMed=8761494;
RA   Jiang W., Woitach J.T., Gupta D.;
RT   "Sequence of bovine carbonic anhydrase VI: potential recognition sites
RT   for N-acetylgalactosaminyltransferase.";
RL   Biochem. J. 318:291-296(1996).
RN   [2]
RP   SEQUENCE OF 15-39.
RX   MEDLINE=89246331; PubMed=2497732;
RA   Fernley R.T., Darling P., Aldred P., Wright R.D., Coghlan J.P.;
RT   "Tissue and species distribution of the secreted carbonic anhydrase
RT   isoenzyme.";
RL   Biochem. J. 259:91-96(1989).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide. Its role in
CC       saliva is unknown.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Major consistuent of saliva.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X96503; CAA65357.1; -.
DR   PIR; S71877; S71877.
DR   HSSP; O43570; 1JD0.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Direct protein sequencing; Glycoprotein; Lyase; Signal; Zinc.
FT   SIGNAL       1     14
FT   CHAIN       15    319       Carbonic anhydrase VI.
FT   METAL      106    106       Zinc (catalytic) (By similarity).
FT   METAL      108    108       Zinc (catalytic) (By similarity).
FT   METAL      133    133       Zinc (catalytic) (By similarity).
FT   DISULFID    37    219       Potential.
FT   CARBOHYD    62     62       N-linked (GlcNAc. . .).
FT   CARBOHYD   251    251       N-linked (GlcNAc. . .).
FT   CONFLICT    16     16       H -> S (in Ref. 2).
SQ   SEQUENCE   319 AA;  37006 MW;  179884A7A9083AED CRC64;

  Query Match             29.8%;  Score 530;  DB 1;  Length 319;
  Best Local Similarity   37.8%;  Pred. No. 5.9e-36;
  Matches  123;  Conservative   57;  Mismatches  125;  Indels   20;  Gaps   11;

Qy          6 LLLEVIWILAADGGQHWTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPAL 64
              : |  : :: |     ||| ||   : ||   ||:||   |||||::   | ::| | ||
Db          2 ITLLFLLVVGAQAQHEWTYSEGVLDEKHWRLQYPDCGGTRQSPIDLKMKKVRYNPSLRAL 61

Qy         65 QPHGYD-QPGTEPLDLHNNGHTVQLSLPSTLYL----GGLPRKYVAAQLHLHWGQKGSP- 118
                 ||  : |  |:   |||||||:||||:: :    |    :|:| |:| |||   |
Db         62 NLTGYGLRQGEFPMT--NNGHTVQISLPSSMRMTTSDGS---QYLAKQMHFHWGGDSSEI 116

Qy        119 GGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGE-TKNIAYEHI 177
               |||| ::      |:|:||| |  | |  ||   | |||||  |:|| :  :|  | :
Db        117 SGSEHTVDGMRYIIEIHVVHYHS-KYGSYEEAQNEPDGLAVLAALVEVKDYAENTYYSNF 175

Qy        178 LSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQIS 237
              :||| ::|:  | | :   ::::::||  |  |: | |||||| | ::| | |     ::|
Db        176 ISHLEDIRYAGQSTVLRDLDIQDMLPGDLRYYYSYLGSLTTPSCTENVHWFVVADTVKLS 235

Qy        238 MEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFI-QAGSSYTTGEMLSLGVG 296
               :|||: :| : : |    :  |||: |||| |:| |:|:      || |  |   :
Db        236 KTQIEKLENSLLNHQNE---TIQNNYRSTQPLNHRVVEANFVSHPHQEYTLGSKLHFYLN 292

Qy        297 ILVGCLCLLLAVYFIARKIRKKRLE 321
               :  |  |    || :|| |:: |
Db        293 NIDQNLEYLRR--FIEQKITKRKKE 315


RESULT 12
Q865C0
ID   Q865C0      PRELIMINARY;      PRT;   320 AA.
AC   Q865C0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Carbonic anhydrase VI precursor.
GN   Name=CA6;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Parotid gland;
RA   Murakami M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
DR   EMBL; AB080972; BAC65098.1; -.
DR   HSSP; O43570; 1JD0.
```

```
DR   GO; GO:0004089; F:carbonate dehydratase activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Signal; Zinc.
FT   SIGNAL        1     17       Potential.
SQ   SEQUENCE   320 AA;  36704 MW;  6E00A8D08AA0D23F CRC64;

  Query Match             29.1%;  Score 518.5;  DB 2;  Length 320;
  Best Local Similarity   38.1%;  Pred. No. 5.5e-35;
  Matches  125;  Conservative   54;  Mismatches  128;  Indels   21;  Gaps   11;

Qy          5 ALLLEVIWILA-ADGGQHWTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLP 62
              |||| :  : | |  |  ||| ||   | |||  || ||   |||||:|   | ::| |
Db          5 ALLLALPLLGARAQHGSLWTYSEGALDQVHWPREYPTCGGTRQSPIDLQRRKVQYNPSLK 64

Qy         63 ALQPHGYD-QPGTEPLDLHNNGHTVQLSLPSTL-YLGGLPRKYVAAQLHLHWGQKGSP-G 119
              ||:  ||  | |  |  : |||||||:||| |:  :     :|:| |:| |||   |
Db         65 ALKLTGYRIQVGEFP--MINNGHTVQISLPPTMRMMASDGTEYIAQQMHFHWGGASSEIS 122

Qy        120 GSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGE-TKNIAYEHIL 178
              |||| |:     ||:|||||:|  | |   |   | |||||  |::| :  :|  | : :
Db        123 GSEHTIDGIRFVAEIHIVHYNS-KYKSYDIAQHEPDGLAVLAALVKVEDYGENTYYSNFI 181

Qy        179 SHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISM 238
              |||: :|:  | | :   :: ::||:    |: | |||||||| ::| | |     ::|
Db        182 SHLNNIRYPGQSTVLSGLDIEDMLPENTHHYYTYRGSLTTPPCTENVHWFVLVHHVRLSS 241

Qy        239 EQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGIL 298
              |  ||: ::    :  :| |  :|| :|||| |:| ::|:   |    |       |  |
Db        242 IQTWKLENSIL---DHQNKTLHSDYRRIQPLNGRVVESNFVNLPSQ---GSEFQFYVNKL 295

Qy        299 VGCLCLLLAVYFIARKIRKKRLENRKSV 326
                   |      :: | : | ::| :  :
Db        296 NNKL------EYLRRLLEKTKVEKKPHI 317


RESULT 13
CAH6_HUMAN
ID   CAH6_HUMAN     STANDARD;      PRT;   308 AA.
AC   P23280; Q96QX8; Q9UF03;
DT   01-NOV-1991 (Rel. 20, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase VI precursor (EC 4.2.1.1) (Carbonate dehydratase
DE   VI) (CA-VI) (Secreted carbonic anhydrase) (Salivary carbonic
DE   anhydrase).
GN   Name=CA6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91105141; PubMed=1899030;
RA   Aldred P., Fu P., Barrett G., Penschow J.D., Wright R., Coghlan J.P.,
RA   Fernley R.T.;
RT   "Human secreted carbonic anhydrase: cDNA cloning, nucleotide sequence,
RT   and hybridization histochemistry.";
RL   Biochemistry 30:569-575(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Grubb D.J.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Frankland J.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide. Its role in
CC       saliva is unknown.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Major consistuent of saliva.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57892; AAA51892.1; -.
DR   EMBL; AF128418; AAF22565.1; -.
DR   EMBL; AF128411; AAF22565.1; JOINED.
DR   EMBL; AF128412; AAF22565.1; JOINED.
DR   EMBL; AF128413; AAF22565.1; JOINED.
DR   EMBL; AF128414; AAF22565.1; JOINED.
DR   EMBL; AF128415; AAF22565.1; JOINED.
DR   EMBL; AF128416; AAF22565.1; JOINED.
DR   EMBL; AF128417; AAF22565.1; JOINED.
DR   EMBL; AL139415; CAC42429.1; -.
DR   HSSP; O43570; 1JD0.
DR   Genew; HGNC:1380; CA6.
DR   MIM; 114780; -.
DR   GO; GO:0004089; F:carbonate dehydratase activity; TAS.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Glycoprotein; Lyase; Signal; Zinc.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    308       Carbonic anhydrase VI.
FT   METAL       111    111       Zinc (catalytic) (By similarity).
FT   METAL       113    113       Zinc (catalytic) (By similarity).
FT   METAL       138    138       Zinc (catalytic) (By similarity).
FT   DISULFID     42    224       Potential.
FT   CARBOHYD     67     67       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     90     90       G -> S (in Ref. 3).
FT   CONFLICT    103    103       T -> I (in Ref. 1).
FT   CONFLICT    148    148       T -> S (in Ref. 3).
FT   CONFLICT    270    270       K -> N (in Ref. 3).
SQ   SEQUENCE   308 AA;  35365 MW;  5B6BBFF2DD239333 CRC64;

  Query Match             28.0%;  Score 498;  DB 1;  Length 308;
  Best Local Similarity   38.3%;  Pred. No. 2.7e-33;
  Matches  113;  Conservative   53;  Mismatches  107;  Indels   22;  Gaps   11;

Qy          5 ALLLEVIWILAADGGQH---WTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPD 60
              ||:| :   |      ||   ||| ||   : |||  || ||   ||||::|   | ::|
Db          3 ALVLLLSLFLLGGQAQHVSDWTYSEGALDEAHWPQHYPACGGQRQSPINLQRTKVRYNPS 62

Qy         61 LPALQPHGYD-QPGTEPLDLHNNGHTVQLSLPSTLYL----GGLPRKYVAAQLHLHWGQK 115
              |  |   ||: | |  |  : |||||||: |||| :    |  :   |:| |:| |||
Db         63 LKGLNMTGYETQAGEFP--MVNNGHTVQIGLPSTMRMTVADGTV---YIAQQMHFHWGGA 117

Qy        116 GSP-GGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEV-GETKNIA 173
              |   |||| ::       |:|||||:|  | :   | : | |||||   :||    :|
Db        118 SSEISGSEHTVDGIRHVIEIHIVHYNS-KYKTYDIAQDAPDGLAVLAAFVEVKNYPENTY 176

Qy        174 YEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRR 233
              | : :|||  :::  |:|::   :::::||: |  |:.|:|||||||| ::| | |
Db        177 YSNFISHLANIKYPGQRTTLTGLDVQDMLPRNLQHYYTYHGSLTTPPCTENVHWFVLADF 236

Qy        234 SQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTG 288
              ::|  |: ||: :|    :  :| :  :||  |||  |:| ::|      || |
Db        237 VKLSRTQVWKLENSLL---DHRNKTIHNDYRRTQPLKHRVVESNF--PNQEYTLG 286
```

```
RESULT 14
CAH2_TRIHK
ID   CAH2_TRIHK     STANDARD;      PRT;   259 AA.
AC   Q8UWA5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Carbonic anhydrase II (EC 4.2.1.1) (Carbonate dehydratase II) (CA-II).
GN   Name=CA2;
OS   Tribolodon hakonensis (Japanese dace).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Tribolodon.
OX   NCBI_TaxID=151740;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22562542; PubMed=12531781; DOI=10.1152/ajpregu.00267.2002;
RA   Hirata T., Kaneko T., Ono T., Nakazato T., Furukawa N., Hasegawa S.,
RA   Wakabayashi S., Shigekawa M., Chang M.H., Romero M.F., Hirose S.;
RT   "Mechanism of acid adaptation of a fish living in a pH 3.5 lake.";
RL   Am. J. Physiol. 284:R1199-R1212(2003).
CC   -!- FUNCTION: Reversible hydration of carbon dioxide.
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- COFACTOR: Zinc (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB055617; BAB83090.1; -.
DR   HSSP; P00918; 1BV3.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Zinc.
FT   INIT_MET      0      0       By similarity.
FT   METAL        93     93       Zinc (catalytic) (By similarity).
FT   METAL        95     95       Zinc (catalytic) (By similarity).
FT   METAL       118    118       Zinc (catalytic) (By similarity).
SQ   SEQUENCE   259 AA;  29002 MW;  622D13D1C237B8B6 CRC64;

  Query Match             26.1%;  Score 465;  DB 1;  Length 259;
  Best Local Similarity   41.1%;  Pred. No. 1.3e-30;
  Matches  108;  Conservative   42;  Mismatches   99;  Indels   14;  Gaps    8;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              | |   :|   |  ::|       |||||||   ::|  |  |:   ||   |  ||: |
Db          4 WGYADHNGPQKWCENFPIANGPRQSPIDIQTKGASYDDTLKPLKLK-YDP--TTSLDILN 60

Qy         82 NGHTVQLSL-----PSTLYLGGLPRKYVAAQLHLHWGQKGSPG-GSEHQINSEATFAELH 135
              |||: |::       | |  | :  ||   | | |||   | | |||| :: :   ||||
Db         61 NGHSFQVTFADDNDSSMLTEGPISGKYRLKQFHFHWG--ASDGKGSEHTVDGKCYPAELH 118

Qy        136 IVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP 195
              :||:::  | |  ||| :| ||||:|: :::||  |   : ||  :  :: | ::||
Db        119 LVHWNT-KYASFGEAANKPDGLAVVGVFLQIGE-DNPKLQKILDAMDAIKSKGKQTSFTN 176

Qy        196 FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEP 255
              |:   |||| | :|: | ||||||| |:|| | |  :   :| ||::| :  ||: |||
Db        177 FDPTCLLPKSL-EYWTYPGSLTTPPLYESVTWIVCKQPISVSSEQMKKFRSLLFTAEEEK 235

Qy        256 SKLLVQNYRALQPLNQRMVFASF 278
              :  :| |||  |||  | | |||
Db        236 ACCMVNNYRPPQPLKDRKVCASF 258
```

```
RESULT 15
Q6NWD3
ID   Q6NWD3      PRELIMINARY;      PRT;   309 AA.
AC   Q6NWD3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC407683 protein (Fragment).
GN   Name=LOC407683;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
CC   -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC   -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC       family.
DR   EMBL; BC067635; AAH67635.1; -.
DR   HSSP; P23589; 1KEQ.
DR   GO; GO:0004089; F:carbonate dehydratase activity; IEA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR   InterPro; IPR001148; Euk_COanhd.
DR   Pfam; PF00194; Carb_anhydrase; 1.
DR   ProDom; PD000865; Euk_COanhd; 1.
DR   PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
KW   Lyase; Zinc.
FT   NON_TER       1      1
SQ   SEQUENCE   309 AA;  34656 MW;  95533D008488CFE5 CRC64;

  Query Match             25.9%;  Score 460.5;  DB 2;  Length 309;
  Best Local Similarity   36.4%;  Pred. No. 3.8e-30;
  Matches  114;  Conservative   57;  Mismatches  111;  Indels   31;  Gaps   13;

Qy          7 LLEVIWILAADGGQHWTYEGP-------HGQDHWPASYPECGNNAQSPIDIQTDSVTFDP 59
              |  |:  |    |: | |:          |   |  :|  ||   ||||:| |  | :||
Db          7 LSSVLLALKLCSGE-WCYQSQLSCNHTCEGPSQWKINYTSCGGQKQSPINIITSKVKYDP 65

Qy         60 DLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKGS 117
                | :    |::      : : |:||:   :|| : :|  |||  || | | |||||: ||
```

```
Db         66 KLTSFIFDGHEDAFN--MSVENHGHSAHFTLPPSAHLSGGGLKGKYKAVQFHLHWGENGS 123

Qy        118 PGGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHI 177
              |||| :: |    |||||  |  : | :|::| :   |:|||    ||   :|  :| |
Db        124 Q-GSEHSVDGERYPMELHIV-YIGEEYINLTKALQNSTGVAVLAFFFEVTALQNQKFERI 181

Qy        178 LSHLHEVRHKDQKTSVPPFNLRELLPKQLGQ-YFRYNGSLTTPPCYQSVLWTVFYRR--- 233
              :  | :|||::  : |  | | :::|:   | |:||:|||||| | ::|||||| :
Db        182 IEALKKVRHENTTSKVENFKLSDIIPQVNSQKYYRYSGSLTTPSCEEAVLWTVFQQTIGI 241

Qy        234 SQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSL 293
              |:: || ::||   || |:    | :   :| :| ||:|:|: | : | |      :|:
Db        242 SKMQMESMDKL--LLFGTD----KPMAGIFRPVQNLNERVVYTS-VPAHSLCVLPNLLT- 293

Qy        294 GVGILVGCL-CLL 305
                 |: || |:|
Db        294 ----LILCLFCVL 302
```

Search completed: May 4, 2005, 15:14:04
Job time : 258 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: May 4, 2005, 14:31:25 ; Search time 164 Seconds
(without alignments)
794.745 Million cell updates/sec
Title: US-10-063-583-74
Perfect score: 1779
Sequence: 1 MLFSALLLEVIWILAADGGQ.....KRLENRKSVVFTSAQATTEA 337
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	1779	100.0	337	3	AAY99460 Human PRO1335 amino acid sequence SEQ ID NO:423.
2	1779	100.0	337	4	AAB66209 Protein of the invention #121.
3	1779	100.0	337	4	AAU29157 Human PRO polypeptide sequence #134.
4	1779	100.0	337	4	AAB87562 Human PRO1335.
5	1779	100.0	337	4	ABG95887 Human secreted/transmembrane protein PRO1335.
6	1779	100.0	337	5	ABU58533 Human PRO polypeptide #134.
7	1779	100.0	337	6	ABU88081 Novel human secreted and transmembrane protein PRO1335.
8	1779	100.0	337	6	ABU84396 Human secreted/transmembrane protein (PRO) #134.
9	1779	100.0	337	6	ABR66270 Human secreted polypeptide PRO1335, SEQ ID NO:268.
10	1779	100.0	337	6	ABR65660 Human secreted polypeptide PRO1335, SEQ ID NO:268.
11	1779	100.0	337	6	ABU99600 Human secreted/transmembrane protein (PRO) #134.
12	1779	100.0	337	6	ABU82839 Human PRO polypeptide #134.
13	1779	100.0	337	6	ABU89960 Novel human secreted and transmembrane protein PRO1335.
14	1779	100.0	337	6	ABR68209 Human secreted polypeptide PRO1335, SEQ ID NO:268.
15	1779	100.0	337	6	ABU96262 Novel human secreted and transmembrane protein PRO1335.
16	1779	100.0	337	6	ABU92693 Human secreted/transmembrane protein (PRO) #134.

RESULT 1
ID AAY99460 standard; protein; 337 AA.
DE Human PRO1335 amino acid sequence SEQ ID NO:423.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 3; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 2
ID AAB66209 standard; protein; 337 AA.
DE Protein of the invention #121.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 3
ID AAU29157 standard; protein; 337 AA.
DE Human PRO polypeptide sequence #134.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 4
ID AAB87562 standard; protein; 337 AA.
DE Human PRO1335.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 5
ID ABG95887 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 6
ID ABU58533 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 7
ID ABU88081 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 8
ID ABU84396 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 9
ID ABR66270 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 10
ID ABR65660 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 11
ID ABU99600 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 12
ID ABU82839 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 13
ID ABU89960 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 14
ID ABR68209 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 15
ID ABU96262 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 16
ID ABU92693 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036149-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 17
ID ABO08770 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 18
ID ABO02822 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 19
ID ABR74976 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 20
ID ABR94738 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 21
ID ABU85711 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 22
ID ABU98871 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 23
ID ABU98086 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 24
ID ABU91792 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 25
ID ABU89485 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 26
ID ABU86326 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 27
ID ABU67539 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 28
ID ABU80567 standard; protein; 337 AA.
DE Human PRO protein #134.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 29
ID ABU90912 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 30
ID ABO33970 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1287.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 31
ID ABO33971 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 32
ID ABR99485 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 33
ID ABR98875 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 34
ID ABO16398 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 35
ID ABR92298 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 36
ID ABO18939 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044925-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 37
ID ABR78360 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 38
ID ABU71988 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 39
ID ABU85096 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 40
ID ABO00235 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 41
ID ABO11567 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 42
ID ABO02212 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 43
ID ABU88786 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 44
ID ABU83481 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 45
ID ABO06282 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 46
ID ABR59318 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 47
ID ABO09380 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 48
ID ABO19244 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 49
ID ABO11262 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 50
ID ABR66880 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 51
ID ABO16093 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 52
ID ABO13799 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 53
ID ABU71542 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 54
ID ABU65702 standard; protein; 337 AA.
DE Human secreted/transmembrane protein, SEQ ID 268.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 55
ID ABO07550 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 56
ID ABO03737 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;

Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 57
ID ABR67185 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 58
ID ABO15788 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 59
ID ABU56069 standard; protein; 337 AA.
DE Human secreted/transmembrane protein, PRO1335.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 60
ID ABU72323 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 61
ID ABU65397 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 62
ID ABU95342 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 63
ID ABU71245 standard; protein; 337 AA.
DE Human PRO1335 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 64
ID ABO07855 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 65
ID ABR70096 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 66
ID ABR69429 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 67
ID ABO01570 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 68
ID ABU81372 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 69
ID ABR60169 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 70
ID ABU90996 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 71
ID ABR67904 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 72
ID ABR65292 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 73
ID ABR68514 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 74
ID ABR71926 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 75
ID ABU85406 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 76
ID ABU89096 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;

Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 77
ID ABU83176 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 78
ID ABU95032 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 79
ID ABU90580 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 80
ID ABU84091 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 81
ID ABU93742 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 82
ID ABR64987 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 83
ID ABO27317 standard; protein; 337 AA.
DE Human secreted/transmembrane polypeptide PRO1335.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 84
ID ABR68819 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 85
ID ABO06635 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 86
ID ABR99180 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 87
ID ABU57064 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 88
ID ABU86016 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 89
ID ABU82303 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 90
ID ABU87314 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 91
ID ABU83786 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 92
ID ABO08160 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 93
ID ABU92512 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 94
ID ABU81871 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 95
ID ABU66035 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 96
ID ABU81182 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 97

ID ABR59864 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 98
ID ABU94052 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 99
ID ABU99905 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 100
ID ABR66575 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 101
ID ABR90993 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 102
ID ABU94420 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 103
ID ABU79302 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 104
ID ABU86631 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 105
ID ABU86936 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 106
ID ABU94725 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 107
ID ABO04652 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 108
ID ABR70401 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 109
ID ABU98566 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 110
ID ABR65965 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 111
ID ABR64682 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 112
ID ABU79607 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 113
ID ABU92998 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 114
ID ABU95957 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 115
ID ABU91177 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 116
ID ABU90270 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 117
ID ABO09685 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044931-A1.
PD 06-MAR-2003.

Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 118
ID ABO10957 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 119
ID ABR71011 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 120
ID ABU98299 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 121
ID ABU87619 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 122
ID ABU91487 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 123
ID ABU89304 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 124
ID ABU84701 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 125
ID ABR69791 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 126
ID ABU80168 standard; protein; 337 AA.
DE Human PRO protein #134.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 127
ID ABU82511 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 128
ID ABU93437 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 129
ID ABO09990 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 130
ID ABO09075 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 131
ID ABU96475 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 132
ID ABU10643 standard; protein; 337 AA.
DE Human secreted/transmembrane protein #134.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 133
ID ABU72145 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 134
ID ABU95652 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 135
ID ABU96861 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 136
ID ABR70706 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 137
ID ABO05057 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003008352-A1.

PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 138
ID ABO08465 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 139
ID ABO05672 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 140
ID ABR74061 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 141
ID ABR95653 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 142
ID ABR80950 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 143
ID ABR81255 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 144
ID ABM00951 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 145
ID ABR88553 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 146
ID ABM77374 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 147
ID ABO28858 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 148
ID ABO31603 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 149
ID ABM08020 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 150
ID ABO40500 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 151
ID ABO35925 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 152
ID ABO44064 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 153
ID ADA78020 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 154
ID ABM24859 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 155
ID ABO03127 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 156
ID ABR90383 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.

PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 157
ID ABM17297 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 158
ID ABR95043 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 159
ID ABR95348 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 160
ID ADB17131 standard; protein; 337 AA.
DE Human transmembrane PRO polypeptide (SeqID 74).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 161
ID ABO21586 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 162
ID ABR97850 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 163
ID ABR87638 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 164
ID ABM77679 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 165
ID ABM27909 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 166
ID ABM06190 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 167
ID ABM03696 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 168
ID ABM35147 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 169
ID ABM26384 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 170
ID ABO48166 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 171
ID ABR92908 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 172
ID ABO24669 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 173
ID ABM11680 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 174
ID ABM02781 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;

RESULT 175
ID ABM16077 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 176
ID ABO27638 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 177
ID ABM29129 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 178
ID ABM07105 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 179
ID ABM21199 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 180
ID ABM09545 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 181
ID ABO41415 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 182
ID ABO36230 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 183
ID ABO43759 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 184
ID ABM76459 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 185
ID ABM76155 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 186
ID ABM25774 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 187
ID ABM26079 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 188
ID ABO03432 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 189
ID ABO02517 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 190
ID ABO44275 standard; protein; 337 AA.
DE Human secreted/transmembrane polypeptide PRO 1335.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 191
ID ABR90688 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 192
ID ABR73756 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 193
ID ABO17008 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;

RESULT 194
ID ABR94433 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 195
ID ABR75940 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 196
ID ABR71316 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 197
ID ABR93213 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 198
ID ABR93518 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 199
ID ABR87943 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 200
ID ABO33702 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 201
ID ABO27943 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 202
ID ABO30078 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 203
ID ABO33287 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 204
ID ABM04975 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 205
ID ABM08935 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 206
ID ABO36535 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 207
ID ABO35620 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 208
ID ABO39585 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 209
ID ABM10460 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 210
ID ABM11985 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 211
ID ABO52131 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 212
ID ABO52436 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049771-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 213
ID ADA19936 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 214
ID ABO23754 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 215
ID ADB17319 standard; protein; 337 AA.
DE Human transmembrane PRO polypeptide (SeqID 74).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 216
ID ABR97240 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 217
ID ABR87028 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 218
ID ABM11070 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 219
ID ABM28214 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 220
ID ABO32213 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 221
ID ABM15340 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 222
ID ABM06495 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 223
ID ABM04306 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 224
ID ABM22419 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 225
ID ABM07715 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 226
ID ABO40805 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 227
ID ABM35452 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 228
ID ABM33215 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 229
ID ABO52741 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 230
ID ABO50301 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;

RESULT 231
ID ABU99295 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 232
ID ABO04347 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 233
ID ABO05977 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 234
ID ABM18517 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 235
ID ABR97545 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 236
ID ABR80645 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 237
ID ABM01256 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 238
ID ABR88858 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 239
ID ABM13510 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 240
ID ABM20894 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 241
ID ABO42025 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 242
ID ABO42635 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 243
ID ABM10155 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 244
ID ABO38670 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 245
ID ABM32910 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 246
ID ABM22724 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 247
ID ABM74935 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 248
ID ADA79812 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 249
ID ABR96325 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 250
ID ABM02476 standard; protein; 337 AA.

DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 251
ID ABR86418 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 252
ID ABR86723 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 253
ID ABM16687 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 254
ID ABM29739 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 255
ID ABO29163 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 256
ID ABM23944 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 257
ID ABM23334 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 258
ID ABM22114 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 259
ID ABO37755 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 260
ID ABM28519 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 261
ID ABM28824 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 262
ID ABM66468 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 263
ID ABM75850 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 264
ID ABM34130 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 265
ID ABM34435 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 266
ID ABO20366 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 267
ID ABO21281 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 268
ID ABO22196 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;

RESULT 269
ID ADA20108 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 270
ID ABO34203 standard; protein; 337 AA.
DE Human secreted/transmembrane polypeptide PRO 1335.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 271
ID ABR96630 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 272
ID ABR85808 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 273
ID ABR99790 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 274
ID ABM00341 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 275
ID ABM00646 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 276
ID ABO29773 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 277
ID ABM23639 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 278
ID ABM29434 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 279
ID ABO38365 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 280
ID ABO45665 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 281
ID ABM20589 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 282
ID ADA81539 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 283
ID ABO16703 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 284
ID ABO18329 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 285
ID ABO22756 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 286
ID ABO23061 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 287
ID ABR92603 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;

Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 288
ID ABR81560 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 289
ID ABM77984 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 290
ID ABR89773 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 291
ID ABM26689 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 292
ID ABM13815 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 293
ID ABO28553 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 294
ID ABO30383 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 295
ID ABM07410 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 296
ID ABM04001 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 297
ID ABO37145 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 298
ID ABO41720 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 299
ID ABO35315 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 300
ID ABM25164 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 301
ID ABO47556 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 302
ID ABO47861 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 303
ID ABO48471 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 304
ID ABO51521 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 305
ID ABO51826 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 306
ID ABO50606 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049779-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 307
ID ABR79730 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 308
ID ABM16992 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 309
ID ABO18024 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 310
ID ABO20976 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 311
ID ABR96935 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 312
ID ABM12290 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 313
ID ABM16382 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 314
ID ABM24249 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 315
ID ABM14730 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 316
ID ABM04611 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 317
ID ABM06800 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 318
ID ABM09240 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 319
ID ABO39280 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 320
ID ABM75545 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 321
ID ABM25469 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 322
ID ABM19979 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 323
ID ABO46885 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 324
ID ABO47190 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 325
ID ADA83337 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049752-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 326
ID ABR71621 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 327
ID ABR72231 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 328
ID ABR98570 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 329
ID ABO06940 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 330
ID ABR84893 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 331
ID ABR73451 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 332
ID ABR76545 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 333
ID ABR73146 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 334
ID ABM18212 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 335
ID ABO20671 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 336
ID ABO25414 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 337
ID ABO25719 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 338
ID ABR94128 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 339
ID ABR80035 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 340
ID ABM11375 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 341
ID ABO32982 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 342
ID ABO30688 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 343
ID ABO30993 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 344
ID ABM27299 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;

Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 345
ID ABM30044 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 346
ID ABM05580 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 347
ID ABM15645 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 348
ID ABM08630 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 349
ID ABO42330 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 350
ID ABO38060 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 351
ID ABO45970 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 352
ID ABM66773 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 353
ID ADB20380 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 354
ID ABM19674 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 355
ID ABO49386 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 356
ID ABO49691 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 357
ID ADA78632 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 358
ID ABR88248 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 359
ID ADA00405 standard; protein; 337 AA.
DE Human secreted/transmembrane polypeptide PRO 1335.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 360
ID ABM26994 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 361
ID ABM03391 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 362
ID ABO39890 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 363
ID ABO49996 standard; protein; 337 AA.

DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 364
ID ABO50911 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 365
ID ABO05367 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 366
ID ABR74671 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 367
ID ABO44555 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 368
ID ABR77150 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 369
ID ABM17907 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 370
ID ABR95958 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 371
ID ABO21891 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 372
ID ABO20061 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 373
ID ABO24364 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 374
ID ABR86113 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 375
ID ABM10765 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 376
ID ABM76764 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 377
ID ABR89468 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 378
ID ABM12595 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 379
ID ABM05885 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 380
ID ABO35010 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 381
ID ABM03086 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 382
ID ABM19064 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.

PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 383
ID ABM19369 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 384
ID ABO46580 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 385
ID ABO49081 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 386
ID ABR69124 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 387
ID ABR89163 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 388
ID ABR72536 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 389
ID ABR74366 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 390
ID ABO18634 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 391
ID ABR80340 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 392
ID ABM01561 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 393
ID ABM02171 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 394
ID ABR87333 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 395
ID ABM12900 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 396
ID ABM30654 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 397
ID ABM24554 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 398
ID ABO29468 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 399
ID ABO31298 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 400
ID ABM14425 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 401

ID ABM09850 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 402
ID ABO38975 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 403
ID ABM34740 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 404
ID ABO51216 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 405
ID ABO04042 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 406
ID ABO10512 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 407
ID ABR77755 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 408
ID ABR78965 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 409
ID ABO24059 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 410
ID ABR93823 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 411
ID ABM01866 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 412
ID ABM78289 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 413
ID ABO33579 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 414
ID ABR90078 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 415
ID ABM27604 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 416
ID ABM13205 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 417
ID ABO31908 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 418
ID ABM14120 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 419
ID ABM08325 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 420

ID ABO40195 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 421
ID ABM74630 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 422
ID ABM33825 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 423
ID ABM20284 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 424
ID ABO48776 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 425
ID ABR72841 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 426
ID ABO15483 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 427
ID ABR85198 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 428
ID ABO15178 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 429
ID ABO17313 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 430
ID ABM17602 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 431
ID ABR85503 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 432
ID ABM77069 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 433
ID ABO28248 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 434
ID ABM23029 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 435
ID ABM30349 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 436
ID ABM21809 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 437
ID ABM21504 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 438
ID ABM15035 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 439

ID ABO41110 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 440
ID ABO36840 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 441
ID ABO37450 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 442
ID ABM75240 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 443
ID ABM33520 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 444
ID ABO46275 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 445
ID ADA82703 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 446
ID ADB85647 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 447
ID ABM31874 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 448
ID ABM31264 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 449
ID ADB86011 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 450
ID ABM32179 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 451
ID ABM32484 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 452
ID ADB68326 standard; protein; 337 AA.
DE Human PRO1335 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 453
ID ADB68133 standard; protein; 337 AA.
DE Human PRO1335 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 454
ID ABM31569 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 455
ID ABM30959 standard; protein; 337 AA.
DE Human secreted polypeptide PRO1335, SEQ ID NO:268.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 456
ID ADB90950 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 457
ID ADC07030 standard; protein; 337 AA.
DE Human PRO1335 protein.
PN US2003060602-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 458
ID ADC18292 standard; protein; 337 AA.
DE Human PRO polypeptide #121.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 459
ID ADC17209 standard; protein; 337 AA.
DE Mammalian PRO polypeptide (SeqID 74).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 460
ID ADC14907 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 461
ID ADC52402 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 462
ID ADD05741 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 463
ID ADD70938 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 464
ID ADD40015 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 465
ID ADD70461 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 466
ID ADD36078 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 467
ID ADD38582 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 468
ID ADD39538 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 469
ID ADD39061 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 470
ID ADD40492 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 471
ID ADE50713 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 472
ID ADE20325 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 473
ID ADE50236 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 474
ID ADE21794 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 475
ID ADF30219 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

```
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 476
ID   ADF56112 standard; protein; 337 AA.
DE   Human secreted/transmembrane protein PRO1335.
PN   US2003204054-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 477
ID   ADG01079 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 478
ID   ADG08632 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 479
ID   ADG02736 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 480
ID   ADG01443 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 481
ID   ADF95618 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 482
ID   ADF95253 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 483
ID   ADG12433 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003207392-A1.
PD   06-NOV-2003.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 484
ID   ADH24106 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 485
ID   ADH34132 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 486
ID   ADH29965 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 487
ID   ADH23936 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 488
ID   ADH09093 standard; protein; 337 AA.
DE   Human PRO polypeptide #134.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 489
ID   ADG85340 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 490
ID   ADH24616 standard; protein; 337 AA.
DE   Novel human secreted and transmembrane protein PRO1335.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 491
ID   ADH37472 standard; protein; 337 AA.
DE   Human secreted and transmembrane protein PRO1335.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 492
ID   ADH02061 standard; protein; 337 AA.
DE   Human PRO polypeptide #37.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 493
ID   ADH37642 standard; protein; 337 AA.
DE   Human secreted and transmembrane protein PRO1335.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1779;  DB 7;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-177;
RESULT 494
```

ID ADG85680 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 495
ID ADH24276 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 496
ID ADH38570 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 497
ID ADG83691 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 498
ID ADH29499 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 499
ID ADH27615 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 500
ID ADH37812 standard; protein; 337 AA.
DE Human secreted and transmembrane protein PRO1335.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 501
ID ADH37989 standard; protein; 337 AA.
DE Human secreted and transmembrane protein PRO1335.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 502
ID ADH57409 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 503
ID ADH53551 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 504
ID ADH53721 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 505
ID ADH52057 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 506
ID ADH49912 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 507
ID ADI25422 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 508
ID ADH90215 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 509
ID ADI25592 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 510
ID ADH97766 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 511
ID ADH99616 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 512
ID ADI03614 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.

PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 513
ID ADI11971 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 514
ID ADH90045 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 515
ID ADH98446 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 516
ID ADI11121 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 517
ID ADI11631 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 518
ID ADH98276 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 519
ID ADH98616 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 520
ID ADH98106 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 521
ID ADI05094 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 522
ID ADI03444 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 523
ID ADI04839 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 524
ID ADH78293 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 525
ID ADI19637 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 526
ID ADH90385 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 527
ID ADI03104 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 528
ID ADH77953 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 529
ID ADH97936 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 530
ID ADI01321 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003190669-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 531
ID ADI02016 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 532
ID ADI03274 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 533
ID ADI11461 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 534
ID ADI02363 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 535
ID ADI11801 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 536
ID ADI05438 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 537
ID ADH79510 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 538
ID ADI19467 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 539
ID ADI05268 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 540
ID ADH79680 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 541
ID ADI01506 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 542
ID ADI01676 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 543
ID ADI01846 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 544
ID ADH79850 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 545
ID ADI04668 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 546
ID ADI02804 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 547
ID ADH78123 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 548
ID ADI25762 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;

Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 549
ID ADI25932 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 550
ID ADK65444 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 551
ID ADH98786 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 552
ID ADH80027 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 553
ID ADL32874 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 554
ID ADM30408 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 555
ID ADL93854 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 7; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 556
ID ADC52212 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 557
ID ADE74405 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 558
ID ADE75017 standard; protein; 337 AA.
DE Human secreted/transmembrane protein (PRO) #134.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 559
ID ADE96796 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 560
ID ADF26107 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 561
ID ADF25006 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 562
ID ADF29742 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 563
ID ADE97273 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 564
ID ADF96230 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 565
ID ADG04501 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 566
ID ADG00661 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 567
ID ADH06644 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180852-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 568
ID ADH06474 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 569
ID ADG68895 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 570
ID ADH27785 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 571
ID ADH25126 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 572
ID ADH33758 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 573
ID ADG82917 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 574
ID ADH03311 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 575
ID ADH02401 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 576
ID ADH08008 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 577
ID ADG69405 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 578
ID ADH39226 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 579
ID ADH04265 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 580
ID ADH03788 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 581
ID ADH26198 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 582
ID ADG83966 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 583
ID ADG85510 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 584
ID ADH06304 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 585
ID ADH30134 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 586
ID ADH24446 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 587
ID ADH33167 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 588
ID ADG69575 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 589
ID ADH07838 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 590
ID ADG85850 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 591
ID ADH39396 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 592
ID ADH33588 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 593
ID ADH33928 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 594
ID ADH01138 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 595
ID ADG69745 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 596
ID ADH02231 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 597
ID ADG69235 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 598
ID ADG86020 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 599
ID ADH24956 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 600
ID ADH39573 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 601
ID ADH02571 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 602
ID ADG69065 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 603
ID ADH07668 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;

RESULT 604
ID ADG86190 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 605
ID ADH24786 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 606
ID ADH25834 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 607
ID ADH38400 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 608
ID ADH57239 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 609
ID ADH52226 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 610
ID ADH04742 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 611
ID ADH49593 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 612
ID ADH90555 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 613
ID ADI11291 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 614
ID ADH98956 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 615
ID ADI02186 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 616
ID ADH61743 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 617
ID ADH90725 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 618
ID ADJ54906 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 619
ID ADJ98600 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 620
ID ADJ98770 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 621
ID ADH78929 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 622
ID ADJ99163 standard; protein; 337 AA.

DE Novel human secreted and transmembrane protein PRO1335.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 623
ID ADJ99333 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 624
ID ADJ98951 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 625
ID ADH79099 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 626
ID ADK00959 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 627
ID ADK14480 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 628
ID ADJ64677 standard; protein; 337 AA.
DE Human PRO polypeptide #134.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 629
ID ADM31573 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 630
ID ADM36620 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 631
ID ADM40425 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 632
ID ADM80929 standard; protein; 337 AA.
DE Human PRO polypeptide #37.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 633
ID ADL94942 standard; protein; 337 AA.
DE Human secreted/transmembrane protein PRO1335.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 634
ID ADN38033 standard; protein; 337 AA.
DE Novel human secreted and transmembrane protein PRO1335.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1779; DB 8; Length 337;
Best Local Similarity 100.0%; Pred. No. 7.9e-177;
RESULT 635
ID AAM93321 standard; protein; 337 AA.
DE Human polypeptide, SEQ ID NO: 2841.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.8%; Score 1775; DB 4; Length 337;
Best Local Similarity 99.7%; Pred. No. 2.1e-176;
RESULT 636
ID ADL30808 standard; protein; 337 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2841.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 99.8%; Score 1775; DB 8; Length 337;
Best Local Similarity 99.7%; Pred. No. 2.1e-176;
RESULT 637
ID ADD12549 standard; protein; 323 AA.
DE Human ENZM-9 protein SEQ ID NO:9.
PN WO2003072729-A2.
PD 04-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 86.4%; Score 1537; DB 7; Length 323;
Best Local Similarity 86.2%; Pred. No. 1.6e-151;
RESULT 638
ID ADL90207 standard; protein; 310 AA.
DE Human enzyme, ENZM-17, SEQ ID 17.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 85.9%; Score 1528; DB 8; Length 310;
Best Local Similarity 99.3%; Pred. No. 1.3e-150;
RESULT 639
ID ABG32378 standard; protein; 318 AA.
DE Novel human enzyme, NZMS-8, Incyte 2706884CD1.
PN WO200264795-A2.
PD 22-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 85.6%; Score 1522.5; DB 5; Length 318;
Best Local Similarity 99.3%; Pred. No. 5e-150;
RESULT 640
ID ABM83251 standard; protein; 322 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3500.
PN WO2004023973-A2.

PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 85.6%; Score 1522.5; DB 8; Length 322;
Best Local Similarity 86.0%; Pred. No. 5.1e-150;
RESULT 641
ID ADB85168 standard; protein; 337 AA.
DE Mouse carbonic anhydrase XIV SEQ ID NO:49.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 84.3%; Score 1500; DB 7; Length 337;
Best Local Similarity 84.0%; Pred. No. 1.2e-147;
RESULT 642
ID ABB89682 standard; protein; 262 AA.
DE Human polypeptide SEQ ID NO 2058.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 1327.5; DB 5; Length 262;
Best Local Similarity 77.7%; Pred. No. 9.3e-130;
RESULT 643
ID ADA57182 standard; protein; 262 AA.
DE Human secreted protein #465.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 1327.5; DB 6; Length 262;
Best Local Similarity 77.7%; Pred. No. 9.3e-130;
RESULT 644
ID ADA41051 standard; protein; 262 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 1327.5; DB 6; Length 262;
Best Local Similarity 77.7%; Pred. No. 9.3e-130;
RESULT 645
ID ADC74297 standard; protein; 262 AA.
DE Human secreted protein - SEQ ID 930.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 1327.5; DB 7; Length 262;
Best Local Similarity 77.7%; Pred. No. 9.3e-130;
RESULT 646
ID ADE11754 standard; protein; 262 AA.
DE Human secreted polypeptide #9.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 74.6%; Score 1327.5; DB 7; Length 262;
Best Local Similarity 77.7%; Pred. No. 9.3e-130;
RESULT 647
ID AAY76132 standard; protein; 263 AA.
DE Human secreted protein encoded by gene 9.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 1327.5; DB 3; Length 263;
Best Local Similarity 77.7%; Pred. No. 9.4e-130;
RESULT 648
ID ADR21584 standard; protein; 244 AA.
DE Human enzyme ENZM-5 protein SEQ ID NO:5.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 61.3%; Score 1090.5; DB 8; Length 244;
Best Local Similarity 74.0%; Pred. No. 5.2e-105;
RESULT 649
ID ADR21604 standard; protein; 248 AA.
DE Human enzyme ENZM-25 protein SEQ ID NO:25.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 61.0%; Score 1085.5; DB 8; Length 248;
Best Local Similarity 64.8%; Pred. No. 1.8e-104;
RESULT 650
ID AAU18647 standard; protein; 194 AA.
DE Renal and cardiovascular-associated protein, Seq ID 86.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 52.9%; Score 940.5; DB 4; Length 194;
Best Local Similarity 98.9%; Pred. No. 1.8e-89;
RESULT 651
ID ABU97262 standard; protein; 194 AA.
DE Human polypeptide #4.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 52.9%; Score 940.5; DB 6; Length 194;
Best Local Similarity 98.9%; Pred. No. 1.8e-89;
RESULT 652
ID ADL90205 standard; protein; 175 AA.
DE Human enzyme, ENZM-15, SEQ ID 15.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 50.8%; Score 903; DB 8; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.3e-85;
RESULT 653
ID AAR91950 standard; protein; 354 AA.
DE Lung cancer specific antigen HCAVIII pre-protein.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 39.2%; Score 696.5; DB 2; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 654
ID AAY96200 standard; protein; 354 AA.
DE Non-small cell lung carcinoma cell antigen LCGA.
PN US6117981-A.
PD 12-SEP-2000.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 39.2%; Score 696.5; DB 3; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 655
ID AAE02637 standard; protein; 354 AA.
DE Human cell surface glycoprotein antigen LCGA protein.
PN US6242204-B1.
PD 05-JUN-2001.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 39.2%; Score 696.5; DB 4; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 656
ID ABR58588 standard; protein; 354 AA.
DE Human cancer related protein SEQ ID NO:245.
PN WO2003025138-A2.
PD 27-MAR-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 39.2%; Score 696.5; DB 6; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 657
ID ADN38978 standard; protein; 354 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:296.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 39.2%; Score 696.5; DB 7; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 658
ID ADJ75534 standard; protein; 354 AA.
DE Marker gene related amino acid sequence SEQ ID NO:786.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 39.2%; Score 696.5; DB 8; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 659
ID ADL61292 standard; protein; 354 AA.
DE Human protein tyrosine kinase biomarker carbonic anhydrase XII protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 39.2%; Score 696.5; DB 8; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 660
ID ADQ20405 standard; protein; 354 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3225.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 39.2%; Score 696.5; DB 8; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 661
ID ABM81627 standard; protein; 354 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO54594, SEQ:4204.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 39.2%; Score 696.5; DB 8; Length 354;
Best Local Similarity 43.5%; Pred. No. 1.6e-63;
RESULT 662
ID ABR58589 standard; protein; 343 AA.
DE Human cancer related protein SEQ ID NO:246.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 39.0%; Score 694; DB 6; Length 343;
Best Local Similarity 44.0%; Pred. No. 2.8e-63;
RESULT 663
ID AAR91951 standard; protein; 325 AA.
DE Lung cancer specific antigen HCAVIII mature protein.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 38.9%; Score 691.5; DB 2; Length 325;
Best Local Similarity 43.6%; Pred. No. 4.6e-63;
RESULT 664
ID AAR91955 standard; protein; 325 AA.
DE HCAVIII phosphorylation-modified (S302G) protein.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 38.8%; Score 689.5; DB 2; Length 325;
Best Local Similarity 43.6%; Pred. No. 7.5e-63;
RESULT 665
ID AAR91953 standard; protein; 274 AA.
DE Lung cancer specific antigen HCAVIII truncated protein.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 36.8%; Score 654.5; DB 2; Length 274;
Best Local Similarity 46.5%; Pred. No. 2.6e-59;
RESULT 666
ID AAR91952 standard; protein; 270 AA.
DE Lung cancer specific antigen HCAVIII truncated protein.
PN WO9602552-A1.
PD 01-FEB-1996.
PA (CYTO-) CYTOCLONAL PHARM INC.
Query Match 36.5%; Score 648.5; DB 2; Length 270;
Best Local Similarity 47.1%; Pred. No. 1.1e-58;
RESULT 667
ID ADL70160 standard; protein; 362 AA.
DE Human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 31.9%; Score 568; DB 8; Length 362;
Best Local Similarity 38.4%; Pred. No. 4.6e-50;
RESULT 668
ID AAR88058 standard; protein; 459 AA.
DE Protein encdoed by MuTu putative oncogene MN.
PN WO9534650-A2.
PD 21-DEC-1995.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 31.6%; Score 562; DB 2; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 669
ID AAY53228 standard; protein; 459 AA.
DE Human MN protein SEQ ID NO:2.
PN US6027887-A.
PD 22-FEB-2000.
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
Query Match 31.6%; Score 562; DB 3; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 670
ID AAB03005 standard; protein; 459 AA.
DE Human MN protein.
PN WO200024913-A2.
PD 04-MAY-2000.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 31.6%; Score 562; DB 3; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 671
ID AAE17175 standard; protein; 459 AA.
DE Human RCC-associated antigen, G250 protein.
PN WO200198363-A2.
PD 27-DEC-2001.
PA (UYNI-) UNIV NIJMEGEN.
Query Match 31.6%; Score 562; DB 5; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 672
ID ABR58596 standard; protein; 459 AA.
DE Human cancer related protein SEQ ID NO:253.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 31.6%; Score 562; DB 6; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 673
ID ABP97744 standard; protein; 459 AA.
DE Amino acid sequence of human CA9 polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 31.6%; Score 562; DB 6; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 674
ID ABU56656 standard; protein; 459 AA.
DE Lung cancer-associated polypeptide #249.
PN WO200286443-A2.
PD 31-OCT-2002.

PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 31.6%; Score 562; DB 6; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 675
ID ABU56408 standard; protein; 459 AA.
DE Lung cancer-associated polypeptide #1.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 31.6%; Score 562; DB 6; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 676
ID ADN38988 standard; protein; 459 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:306.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 31.6%; Score 562; DB 7; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 677
ID ADN39921 standard; protein; 459 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C291.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 31.6%; Score 562; DB 7; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 678
ID ADG31414 standard; protein; 459 AA.
DE Human MN protein SeqID 2.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 679
ID ADK41804 standard; protein; 459 AA.
DE Human MN protein sequence SeqID2.
PN WO2004005348-A1.
PD 15-JAN-2004.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 680
ID ADL70156 standard; protein; 459 AA.
DE Human carbonic anhydrase isozyme CA IX.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 681
ID ADK15606 standard; protein; 459 AA.
DE Human G250 tumour antigen protein.
PN US2004053391-A1.
PD 18-MAR-2004.
PA (UYNI-) UNIV NIJMEGEN.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 682
ID ADQ17644 standard; protein; 459 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 461.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 683
ID ADP53999 standard; protein; 459 AA.
DE Human carbonic anhydrase IX protein sequence.
PN WO2004048544-A2.
PD 10-JUN-2004.
PA (FARB) BAYER HEALTHCARE.
PA (VIRO-) INST VIROLOGY.
PA (SUPU/) SUPURAN C.
PA (SCOZ/) SCOZZAFAVA A.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 684
ID ADQ29712 standard; protein; 459 AA.
DE Human colorectal cancer-associated protein #67.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 685
ID ADS88409 standard; protein; 459 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 264.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 686
ID ADT36534 standard; peptide; 459 AA.
DE Renal cell carcinoma (RCC)-associated antigen G250, SEQ:16.
PN AU2002300986-A1.
PD 01-APR-2004.
PA (UYNI-) UNIV NIJMEGEN.
Query Match 31.6%; Score 562; DB 8; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.8e-49;
RESULT 687
ID AAB82848 standard; protein; 610 AA.
DE Kidney cancer specific antigen G250-GM-CSF fusion protein.
PN WO200160317-A2.
PD 23-AUG-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 31.6%; Score 562; DB 4; Length 610;
Best Local Similarity 38.8%; Pred. No. 4.4e-49;
RESULT 688
ID ADG31476 standard; protein; 437 AA.
DE Murine carbonic anhydrase (MN/CA9) protein SeqID 90.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 31.6%; Score 561.5; DB 8; Length 437;
Best Local Similarity 39.0%; Pred. No. 3e-49;
RESULT 689
ID ADM05289 standard; protein; 283 AA.
DE Human protein of the invention SEQ ID NO:3974.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 30.2%; Score 536.5; DB 7; Length 283;
Best Local Similarity 43.1%; Pred. No. 6.1e-47;
RESULT 690
ID AAY53245 standard; protein; 377 AA.
DE MN protein extracellular domain SEQ ID NO:87.
PN US6027887-A.
PD 22-FEB-2000.
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
Query Match 30.1%; Score 535; DB 3; Length 377;
Best Local Similarity 42.5%; Pred. No. 1.4e-46;
RESULT 691
ID AAB03021 standard; protein; 377 AA.
DE Mature human MN protein N-terminal extracellular domain.
PN WO200024913-A2.
PD 04-MAY-2000.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 30.1%; Score 535; DB 3; Length 377;

Best Local Similarity 42.5%; Pred. No. 1.4e-46;
RESULT 692
ID ADG31451 standard; protein; 377 AA.
DE Extracellular domain of human MN protein SeqID 5.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 30.1%; Score 535; DB 8; Length 377;
Best Local Similarity 42.5%; Pred. No. 1.4e-46;
RESULT 693
ID AAR97235 standard; protein; 256 AA.
DE MuTu putative oncogene MN protein carbonic anhydrase domain.
PN WO9534650-A2.
PD 21-DEC-1995.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 30.0%; Score 533.5; DB 2; Length 256;
Best Local Similarity 43.7%; Pred. No. 1.1e-46;
RESULT 694
ID AAY53241 standard; protein; 257 AA.
DE MN protein carbonic anhydrase domain SEQ ID NO:51.
PN US6027887-A.
PD 22-FEB-2000.
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
Query Match 30.0%; Score 533.5; DB 3; Length 257;
Best Local Similarity 43.7%; Pred. No. 1.1e-46;
RESULT 695
ID AAB03018 standard; protein; 257 AA.
DE Human MN protein carbonic anhydrase (CA) domain.
PN WO200024913-A2.
PD 04-MAY-2000.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 30.0%; Score 533.5; DB 3; Length 257;
Best Local Similarity 43.7%; Pred. No. 1.1e-46;
RESULT 696
ID ADG31456 standard; protein; 277 AA.
DE Carbonic anhydrase domain of human MN protein SeqID 101.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 30.0%; Score 533.5; DB 8; Length 277;
Best Local Similarity 43.7%; Pred. No. 1.2e-46;
RESULT 697
ID ADG31478 standard; protein; 358 AA.
DE N-terminal extracellular domain of murine MN/CA9 protein SeqID 92.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 29.9%; Score 531.5; DB 8; Length 358;
Best Local Similarity 41.1%; Pred. No. 3e-46;
RESULT 698
ID ADG31480 standard; protein; 258 AA.
DE Murine MN/CA9 protein carbonic anhydrase domain SeqID 94.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 29.6%; Score 526.5; DB 8; Length 258;
Best Local Similarity 43.1%; Pred. No. 5.9e-46;
RESULT 699
ID ADJ95128 standard; protein; 308 AA.
DE Novel NOVX protein sequence #178.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 28.5%; Score 507; DB 7; Length 308;
Best Local Similarity 39.0%; Pred. No. 8.5e-44;
RESULT 700
ID ADN04269 standard; protein; 308 AA.
DE Antipsoriatic protein sequence #329.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.0%; Score 499; DB 8; Length 308;
Best Local Similarity 38.4%; Pred. No. 5.9e-43;
RESULT 701
ID AAB59592 standard; protein; 262 AA.
DE Human carbonic anhydrase isoform #5.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 27.7%; Score 493; DB 4; Length 262;
Best Local Similarity 39.8%; Pred. No. 1.9e-42;
RESULT 702
ID ABM82941 standard; protein; 313 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3190.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 27.0%; Score 480; DB 8; Length 313;
Best Local Similarity 37.7%; Pred. No. 5.9e-41;
RESULT 703
ID ABM82940 standard; protein; 305 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3189.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 26.4%; Score 469.5; DB 8; Length 305;
Best Local Similarity 38.0%; Pred. No. 7.1e-40;
RESULT 704
ID ABM82942 standard; protein; 310 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3191.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 26.3%; Score 468.5; DB 8; Length 310;
Best Local Similarity 37.7%; Pred. No. 9.2e-40;
RESULT 705
ID ADG31469 standard; protein; 232 AA.
DE Antigenic component of the human MN protein CA domain SeqID69.
PN WO2003100029-A2.
PD 04-DEC-2003.
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 26.1%; Score 465; DB 8; Length 232;
Best Local Similarity 44.3%; Pred. No. 1.4e-39;
RESULT 706
ID ADQ18489 standard; protein; 1445 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1308.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 25.4%; Score 451.5; DB 8; Length 1445;
Best Local Similarity 32.1%; Pred. No. 6.4e-37;
RESULT 707
ID AAR58809 standard; protein; 1445 AA.
DE Human RPTP-gamma.
PN WO9418309-A1.
PD 18-AUG-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 25.3%; Score 450.5; DB 2; Length 1445;
Best Local Similarity 32.1%; Pred. No. 8.1e-37;
RESULT 708
ID AAB59587 standard; protein; 267 AA.
DE Human receptor-type protein tyrosine phosphatase-gamma CAH-like domain.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 24.7%; Score 439.5; DB 4; Length 267;
Best Local Similarity 35.4%; Pred. No. 7.9e-37;
RESULT 709
ID ABG72434 standard; protein; 267 AA.

DE Receptor protein tyrosine phosphatase (RPTP) gamma.
PN US2002127226-A1.
PD 12-SEP-2002.
PA (SCHL/) SCHLESSINGER J.
PA (BARN/) BARNEA G.
PA (GRUM/) GRUMET M H.
PA (MARG/) MARGOLIS R U.
Query Match 24.7%; Score 439.5; DB 6; Length 267;
Best Local Similarity 35.4%; Pred. No. 7.9e-37;
RESULT 710
ID ABM82947 standard; protein; 274 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3196.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 24.0%; Score 427; DB 8; Length 274;
Best Local Similarity 34.5%; Pred. No. 1.7e-35;
RESULT 711
ID ABM82944 standard; protein; 279 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3193.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 23.9%; Score 426; DB 8; Length 279;
Best Local Similarity 34.1%; Pred. No. 2.2e-35;
RESULT 712
ID ABM82946 standard; protein; 276 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3195.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 23.8%; Score 424; DB 8; Length 276;
Best Local Similarity 34.0%; Pred. No. 3.5e-35;
RESULT 713
ID ABJ37885 standard; protein; 262 AA.
DE NOVX protein sequence SEQ ID No 16.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 23.8%; Score 423.5; DB 6; Length 262;
Best Local Similarity 38.9%; Pred. No. 3.6e-35;
RESULT 714
ID ADH41591 standard; protein; 262 AA.
DE Novel human protein NOV13a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 23.8%; Score 423.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 3.6e-35;
RESULT 715
ID ABM82943 standard; protein; 281 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3192.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 23.8%; Score 423; DB 8; Length 281;
Best Local Similarity 33.7%; Pred. No. 4.5e-35;
RESULT 716
ID ABP56702 standard; protein; 309 AA.
DE Rat carbonic anhydrase IV protein SEQ ID NO:9.
PN WO2002100336-A2.
PD 19-DEC-2002.
PA (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Query Match 23.8%; Score 423; DB 6; Length 309;
Best Local Similarity 34.0%; Pred. No. 5.3e-35;
RESULT 717
ID ABJ37886 standard; protein; 262 AA.
DE NOVX protein sequence SEQ ID No 18.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 23.7%; Score 422.5; DB 6; Length 262;
Best Local Similarity 38.5%; Pred. No. 4.6e-35;
RESULT 718
ID ADM04397 standard; protein; 262 AA.
DE Human protein of the invention SEQ ID NO:3082.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 23.7%; Score 422.5; DB 7; Length 262;
Best Local Similarity 38.5%; Pred. No. 4.6e-35;
RESULT 719
ID ADH41595 standard; protein; 262 AA.
DE Novel human protein NOV13c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 23.7%; Score 422.5; DB 8; Length 262;
Best Local Similarity 38.5%; Pred. No. 4.6e-35;
RESULT 720
ID ADQ88166 standard; protein; 262 AA.
DE Human 85553 protein, a carbonic anhydrase protein.
PN WO2004063340-A2.
PD 29-JUL-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 23.7%; Score 422.5; DB 8; Length 262;
Best Local Similarity 38.5%; Pred. No. 4.6e-35;
RESULT 721
ID AAB53405 standard; protein; 294 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:945.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.7%; Score 421; DB 3; Length 294;
Best Local Similarity 36.1%; Pred. No. 7.9e-35;
RESULT 722
ID AAB59589 standard; protein; 259 AA.
DE Human carbonic anhydrase isoform #2.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 23.6%; Score 420; DB 4; Length 259;
Best Local Similarity 36.5%; Pred. No. 8.2e-35;
RESULT 723
ID ADE62800 standard; protein; 259 AA.
DE Human Protein P00918, SEQ ID NO 8733.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 23.6%; Score 420; DB 7; Length 259;
Best Local Similarity 36.5%; Pred. No. 8.2e-35;
RESULT 724
ID ADE63735 standard; protein; 259 AA.
DE Human Protein P00918, SEQ ID NO 9679.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 23.6%; Score 420; DB 7; Length 259;
Best Local Similarity 36.5%; Pred. No. 8.2e-35;
RESULT 725
ID ADA10999 standard; protein; 260 AA.
DE Human cDNA differentially expressed in colon cancer #78 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 23.6%; Score 420; DB 6; Length 260;
Best Local Similarity 36.5%; Pred. No. 8.3e-35;
RESULT 726
ID ADL12915 standard; protein; 260 AA.
DE Human steroid-induced C3A liver cell protein #104.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.

Query Match 23.6%; Score 420; DB 8; Length 260;
Best Local Similarity 36.5%; Pred. No. 8.3e-35;
RESULT 727
ID ADO55152 standard; protein; 260 AA.
DE Protein #54 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 23.6%; Score 420; DB 8; Length 260;
Best Local Similarity 36.5%; Pred. No. 8.3e-35;
RESULT 728
ID ADO24558 standard; protein; 260 AA.
DE Human PRO62628 protein SEQ ID NO:197.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 23.6%; Score 420; DB 8; Length 260;
Best Local Similarity 36.5%; Pred. No. 8.3e-35;
RESULT 729
ID ADP24252 standard; protein; 260 AA.
DE PRO polypeptide SEQ ID NO:1430.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 23.6%; Score 420; DB 8; Length 260;
Best Local Similarity 36.5%; Pred. No. 8.3e-35;
RESULT 730
ID AAW75702 standard; protein; 260 AA.
DE Carbonic anhydrase II protein.
PN WO9836084-A2.
PD 20-AUG-1998.
PA (AGRI-) AGRIC TECHNOLOGIES INC.
Query Match 23.6%; Score 419; DB 2; Length 260;
Best Local Similarity 36.5%; Pred. No. 1.1e-34;
RESULT 731
ID ADH41593 standard; protein; 261 AA.
DE Novel human protein NOV13b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 23.5%; Score 417.5; DB 8; Length 261;
Best Local Similarity 38.0%; Pred. No. 1.5e-34;
RESULT 732
ID AAR41746 standard; protein; 429 AA.
DE MN protein.
PN WO9318152-A1.
PD 16-SEP-1993.
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
Query Match 23.3%; Score 414; DB 2; Length 429;
Best Local Similarity 32.1%; Pred. No. 7.8e-34;
RESULT 733
ID AAU18695 standard; protein; 164 AA.
DE Renal and cardiovascular-associated protein, Seq ID 134.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.2%; Score 413.5; DB 4; Length 164;
Best Local Similarity 68.0%; Pred. No. 1.9e-34;
RESULT 734
ID AAU23071 standard; protein; 164 AA.
DE Novel human enzyme polypeptide #157.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.2%; Score 413.5; DB 4; Length 164;
Best Local Similarity 68.0%; Pred. No. 1.9e-34;
RESULT 735
ID ABU97310 standard; protein; 164 AA.
DE Human polypeptide #52.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 23.2%; Score 413.5; DB 6; Length 164;
Best Local Similarity 68.0%; Pred. No. 1.9e-34;
RESULT 736
ID ABM82948 standard; protein; 273 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3197.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 23.2%; Score 412.5; DB 8; Length 273;
Best Local Similarity 34.0%; Pred. No. 5.4e-34;
RESULT 737
ID ABM82945 standard; protein; 278 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3194.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 23.1%; Score 411.5; DB 8; Length 278;
Best Local Similarity 33.7%; Pred. No. 7.1e-34;
RESULT 738
ID AAE25377 standard; protein; 247 AA.
DE Human NZMS-1 protein.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 23.1%; Score 411; DB 5; Length 247;
Best Local Similarity 37.7%; Pred. No. 6.7e-34;
RESULT 739
ID AAW23378 standard; protein; 288 AA.
DE Fusion comprising human and eel calcitonin fragments.
PN WO9729127-A1.
PD 14-AUG-1997.
PA (BION-) BIONEBRASKA INC.
Query Match 23.0%; Score 410; DB 2; Length 288;
Best Local Similarity 36.0%; Pred. No. 1.1e-33;
RESULT 740
ID AAB59590 standard; protein; 259 AA.
DE Human carbonic anhydrase isoform #3.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 22.8%; Score 406; DB 4; Length 259;
Best Local Similarity 34.5%; Pred. No. 2.4e-33;
RESULT 741
ID ADE54978 standard; protein; 259 AA.
DE Human Protein AAH04897, SEQ ID NO 783.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 22.8%; Score 406; DB 7; Length 259;
Best Local Similarity 34.5%; Pred. No. 2.4e-33;
RESULT 742
ID ABP62813 standard; protein; 260 AA.
DE Human polypeptide SEQ ID NO 250.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 22.8%; Score 405; DB 5; Length 260;
Best Local Similarity 34.1%; Pred. No. 3.1e-33;
RESULT 743
ID ADQ18304 standard; protein; 260 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1122.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.8%; Score 405; DB 8; Length 260;
Best Local Similarity 34.1%; Pred. No. 3.1e-33;
RESULT 744
ID AAM51157 standard; protein; 421 AA.
DE Streptavidin-carbonic anhydrase III (SAV-CAIII) fusion protein.
PN WO200216943-A2.

PD 28-FEB-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 22.8%; Score 405; DB 5; Length 421;
Best Local Similarity 34.1%; Pred. No. 6.6e-33;
RESULT 745
ID ADE62798 standard; protein; 259 AA.
DE Rat Protein AAC53104, SEQ ID NO 8731.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 22.7%; Score 404; DB 7; Length 259;
Best Local Similarity 35.3%; Pred. No. 3.9e-33;
RESULT 746
ID ADE63733 standard; protein; 259 AA.
DE Rat Protein P27139, SEQ ID NO 9677.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 22.7%; Score 404; DB 7; Length 259;
Best Local Similarity 35.3%; Pred. No. 3.9e-33;
RESULT 747
ID ABB57256 standard; protein; 260 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:708.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 22.5%; Score 401; DB 5; Length 260;
Best Local Similarity 36.1%; Pred. No. 8.1e-33;
RESULT 748
ID AAO27604 standard; protein; 259 AA.
DE Bovine carbonic anhydrase (CA) II sequence.
PN WO2003078584-A2.
PD 25-SEP-2003.
PA (THER-) THERMO FINNIGAN LLC.
Query Match 22.4%; Score 399; DB 7; Length 259;
Best Local Similarity 35.1%; Pred. No. 1.3e-32;
RESULT 749
ID AAB59593 standard; protein; 261 AA.
DE Human carbonic anhydrase isoform #6.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 22.1%; Score 393; DB 4; Length 261;
Best Local Similarity 37.3%; Pred. No. 5.6e-32;
RESULT 750
ID ABU11700 standard; protein; 256 AA.
DE Human MDDT polypeptide SEQ ID 647.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.9%; Score 389.5; DB 6; Length 256;
Best Local Similarity 34.2%; Pred. No. 1.3e-31;
RESULT 751
ID ADE54976 standard; protein; 259 AA.
DE Rat Protein P14141, SEQ ID NO 781.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 21.9%; Score 389; DB 7; Length 259;
Best Local Similarity 35.0%; Pred. No. 1.4e-31;
RESULT 752
ID ABP69520 standard; protein; 242 AA.
DE Human polypeptide SEQ ID NO 1567.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 21.8%; Score 387; DB 5; Length 242;
Best Local Similarity 35.0%; Pred. No. 2.1e-31;
RESULT 753
ID ADB79879 standard; protein; 1616 AA.
DE Rat phosphacan, SEQ ID 119.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 21.7%; Score 386; DB 7; Length 1616;
Best Local Similarity 34.2%; Pred. No. 5.4e-30;
RESULT 754
ID ADO31208 standard; protein; 1616 AA.
DE Rat phosphacan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 21.7%; Score 386; DB 8; Length 1616;
Best Local Similarity 34.2%; Pred. No. 5.4e-30;
RESULT 755
ID ADE62109 standard; protein; 2316 AA.
DE Rat Protein Q62656, SEQ ID NO 8038.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 21.7%; Score 386; DB 7; Length 2316;
Best Local Similarity 34.2%; Pred. No. 9.6e-30;
RESULT 756
ID ADE62036 standard; protein; 2316 AA.
DE Rat Protein Q62656, SEQ ID NO 7965.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 21.7%; Score 386; DB 7; Length 2316;
Best Local Similarity 34.2%; Pred. No. 9.6e-30;
RESULT 757
ID ADE62040 standard; protein; 2316 AA.
DE Rat Protein Q62656, SEQ ID NO 7969.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 21.7%; Score 386; DB 7; Length 2316;
Best Local Similarity 34.2%; Pred. No. 9.6e-30;
RESULT 758
ID AAU19418 standard; protein; 274 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP) #4.
PN WO200162927-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.5%; Score 383; DB 4; Length 274;
Best Local Similarity 35.4%; Pred. No. 6.7e-31;
RESULT 759
ID AAB59588 standard; protein; 260 AA.
DE Human carbonic anhydrase isoform #1.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 21.4%; Score 380.5; DB 4; Length 260;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 760
ID AAO15236 standard; protein; 261 AA.
DE Human carbonic anhydrase I (Cln115) protein.
PN US2002042088-A1.
PD 11-APR-2002.
PA (MACI/) MACINA R A.
PA (PIDE/) PIDERIT A.
PA (SUNY/) SUN Y.
Query Match 21.4%; Score 380.5; DB 5; Length 261;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 761
ID ADA10962 standard; protein; 261 AA.
DE Human cDNA differentially expressed in colon cancer #54 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.

PA (JONE/) JONES D A.
Query Match 21.4%; Score 380.5; DB 6; Length 261;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 762
ID ADJ68583 standard; protein; 261 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID389.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 21.4%; Score 380.5; DB 7; Length 261;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 763
ID ADG47985 standard; protein; 261 AA.
DE Human carbonic anhydrase I (CAI) protein.
PN US2003101002-A1.
PD 29-MAY-2003.
PA (BART/) BARTHA G T.
PA (WALK/) WALKER M.
Query Match 21.4%; Score 380.5; DB 8; Length 261;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 764
ID AAG73863 standard; protein; 263 AA.
DE Human colon cancer antigen protein SEQ ID NO:4627.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.4%; Score 380.5; DB 4; Length 263;
Best Local Similarity 34.0%; Pred. No. 1.1e-30;
RESULT 765
ID ABG76946 standard; protein; 312 AA.
DE Human protein, designated SEC10.
PN WO200255705-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 21.4%; Score 380.5; DB 5; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 766
ID ABP56703 standard; protein; 312 AA.
DE Human carbonic anhydrase IV protein SEQ ID NO:11.
PN WO2002100336-A2.
PD 19-DEC-2002.
PA (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
Query Match 21.4%; Score 380.5; DB 6; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 767
ID ADA10950 standard; protein; 312 AA.
DE Human cDNA differentially expressed in colon cancer #45 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 21.4%; Score 380.5; DB 6; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 768
ID ADB75224 standard; protein; 312 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 21.4%; Score 380.5; DB 7; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 769
ID ADL56810 standard; protein; 312 AA.
DE Human SECX polypeptide #10.
PN US2003215449-A1.
PD 20-NOV-2003.
PA (MEZE/) MEZES P D.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGHS C.
PA (SPYT/) SPYTEK K A.
PA (DIPI/) DIPIPPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYM/) PEYMAN J A.
PA (ELLE/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
PA (VOSS/) VOSS E Z.
PA (MILL/) MILLER C E.
Query Match 21.4%; Score 380.5; DB 8; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 770
ID ADO39194 standard; protein; 312 AA.
DE Human novel secreted protein SEC10.
PN US2004018196-A1.
PD 29-JAN-2004.
PA (MEZE/) MEZES P D.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGHS C.
PA (SPYT/) SPYTEK K A.
PA (DIPI/) DIPIPPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYM/) PEYMAN J A.
PA (ELLE/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
Query Match 21.4%; Score 380.5; DB 8; Length 312;
Best Local Similarity 34.0%; Pred. No. 1.5e-30;
RESULT 771
ID ABG12955 standard; protein; 323 AA.
DE Novel human diagnostic protein #12946.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.3%; Score 379; DB 4; Length 323;
Best Local Similarity 35.5%; Pred. No. 2.3e-30;
RESULT 772
ID ABB08900 standard; protein; 242 AA.
DE Human lyase HLYA-1 protein.
PN WO200200840-A2.
PD 03-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.2%; Score 376.5; DB 5; Length 242;
Best Local Similarity 37.0%; Pred. No. 2.6e-30;
RESULT 773
ID ABM83053 standard; protein; 242 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3302.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 21.1%; Score 376; DB 8; Length 242;
Best Local Similarity 34.2%; Pred. No. 3e-30;
RESULT 774
ID AAB59594 standard; protein; 260 AA.
DE Rat 3F8 carbonic anhydrase domain.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 21.1%; Score 374.5; DB 4; Length 260;
Best Local Similarity 33.5%; Pred. No. 4.8e-30;
RESULT 775
ID AAB59591 standard; protein; 268 AA.
DE Human carbonic anhydrase isoform #4.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 21.0%; Score 373; DB 4; Length 268;
Best Local Similarity 35.2%; Pred. No. 7.2e-30;
RESULT 776
ID ADJ76317 standard; protein; 1612 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1569.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 20.9%; Score 371; DB 8; Length 1612;
Best Local Similarity 33.8%; Pred. No. 2e-28;
RESULT 777
ID ADO31210 standard; protein; 1612 AA.
DE Mouse phosphacan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 20.9%; Score 371; DB 8; Length 1612;
Best Local Similarity 33.8%; Pred. No. 2e-28;
RESULT 778
ID AAE30333 standard; protein; 374 AA.
DE Human protein tyrosine phosphatase zeta SM1 variant protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 20.5%; Score 365; DB 6; Length 374;
Best Local Similarity 33.1%; Pred. No. 8.4e-29;
RESULT 779
ID ADQ18134 standard; protein; 1005 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 951.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 20.5%; Score 365; DB 8; Length 1005;
Best Local Similarity 33.1%; Pred. No. 4e-28;
RESULT 780
ID ADN39946 standard; protein; 1113 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C316.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1113;
Best Local Similarity 33.1%; Pred. No. 4.7e-28;
RESULT 781
ID ADN39948 standard; protein; 1359 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C318.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1359;
Best Local Similarity 33.1%; Pred. No. 6.5e-28;
RESULT 782
ID ABU56689 standard; protein; 1448 AA.
DE Lung cancer-associated polypeptide #282.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1448;
Best Local Similarity 33.1%; Pred. No. 7.2e-28;
RESULT 783
ID ABU56495 standard; protein; 1448 AA.
DE Lung cancer-associated polypeptide #88.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1448;
Best Local Similarity 33.1%; Pred. No. 7.2e-28;
RESULT 784
ID ADN39058 standard; protein; 1448 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:376.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1448;
Best Local Similarity 33.1%; Pred. No. 7.2e-28;
RESULT 785
ID ADN39941 standard; protein; 1448 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C311.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1448;
Best Local Similarity 33.1%; Pred. No. 7.2e-28;
RESULT 786
ID ABU56688 standard; protein; 1456 AA.
DE Lung cancer-associated polypeptide #281.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1456;
Best Local Similarity 33.1%; Pred. No. 7.3e-28;
RESULT 787
ID ABU56494 standard; protein; 1456 AA.
DE Lung cancer-associated polypeptide #87.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1456;
Best Local Similarity 33.1%; Pred. No. 7.3e-28;
RESULT 788
ID ADN39943 standard; protein; 1456 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C313.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1456;
Best Local Similarity 33.1%; Pred. No. 7.3e-28;
RESULT 789
ID ADN39056 standard; protein; 1456 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:374.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1456;
Best Local Similarity 33.1%; Pred. No. 7.3e-28;
RESULT 790
ID ADN39947 standard; protein; 1493 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C317.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1493;
Best Local Similarity 33.1%; Pred. No. 7.6e-28;
RESULT 791
ID ABU56691 standard; protein; 1494 AA.
DE Lung cancer-associated polypeptide #284.
PN WO200286443-A2.

PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1494;
Best Local Similarity 33.1%; Pred. No. 7.6e-28;
RESULT 792
ID ABU56497 standard; protein; 1494 AA.
DE Lung cancer-associated polypeptide #90.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 1494;
Best Local Similarity 33.1%; Pred. No. 7.6e-28;
RESULT 793
ID ADN39062 standard; protein; 1494 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:380.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1494;
Best Local Similarity 33.1%; Pred. No. 7.6e-28;
RESULT 794
ID ADN39945 standard; protein; 1494 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C315.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 1494;
Best Local Similarity 33.1%; Pred. No. 7.6e-28;
RESULT 795
ID AAR57902 standard; protein; 2308 AA.
DE Human RPTP-beta.
PN WO9418308-A1.
PD 18-AUG-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 20.5%; Score 365; DB 2; Length 2308;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 796
ID AAB59586 standard; protein; 2308 AA.
DE Human receptor-type protein tyrosine phosphatase-beta.
PN US6160090-A.
PD 12-DEC-2000.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 20.5%; Score 365; DB 4; Length 2308;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 797
ID ABG72433 standard; protein; 2308 AA.
DE Receptor protein tyrosine phosphatase (RPTP) beta.
PN US2002127226-A1.
PD 12-SEP-2002.
PA (SCHL/) SCHLESSINGER J.
PA (BARN/) BARNEA G.
PA (GRUM/) GRUMET M H.
PA (MARG/) MARGOLIS R U.
Query Match 20.5%; Score 365; DB 6; Length 2308;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 798
ID ABR58521 standard; protein; 2314 AA.
DE Human protein tyrosine phosphatase receptor-type z polypeptide 1.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 799
ID ABU56692 standard; protein; 2314 AA.
DE Lung cancer-associated polypeptide #285.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 800
ID AAE30332 standard; protein; 2314 AA.
DE Human PTPRZ1 protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 20.5%; Score 365; DB 6; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 801
ID ADE62111 standard; protein; 2314 AA.
DE Human Protein P23471, SEQ ID NO 8040.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 20.5%; Score 365; DB 7; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 802
ID ADE62042 standard; protein; 2314 AA.
DE Human Protein P23471, SEQ ID NO 7971.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 20.5%; Score 365; DB 7; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 803
ID ADE62038 standard; protein; 2314 AA.
DE Human Protein P23471, SEQ ID NO 7967.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 20.5%; Score 365; DB 7; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 804
ID ADN39064 standard; protein; 2314 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:382.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 805
ID ADJ75597 standard; protein; 2314 AA.
DE Marker gene related amino acid sequence SEQ ID NO:849.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 20.5%; Score 365; DB 8; Length 2314;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 806
ID ABU56687 standard; protein; 2315 AA.
DE Lung cancer-associated polypeptide #280.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 2315;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 807
ID ABU56493 standard; protein; 2315 AA.
DE Lung cancer-associated polypeptide #86.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 6; Length 2315;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 808
ID ADN39942 standard; protein; 2315 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C312.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 2315;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;

RESULT 809
ID ADN39054 standard; protein; 2315 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:372.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 365; DB 7; Length 2315;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
RESULT 810
ID AAE30334 standard; protein; 2353 AA.
DE Human protein tyrosine phosphatase zeta SM2 variant protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 20.5%; Score 365; DB 6; Length 2353;
Best Local Similarity 33.1%; Pred. No. 1.6e-27;
RESULT 811
ID ABP53572 standard; protein; 336 AA.
DE Human NOV4 protein SEQ ID NO:8.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 20.5%; Score 364.5; DB 5; Length 336;
Best Local Similarity 31.5%; Pred. No. 8e-29;
RESULT 812
ID AAR52580 standard; protein; 2308 AA.
DE RPTP-beta amino acid sequence.
PN WO9409037-A1.
PD 28-APR-1994.
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
Query Match 20.4%; Score 363.5; DB 2; Length 2308;
Best Local Similarity 32.5%; Pred. No. 2.2e-27;
RESULT 813
ID ABJ05479 standard; protein; 289 AA.
DE Human breast cancer associated polypeptide SEQ ID NO: 239.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 20.4%; Score 363; DB 5; Length 289;
Best Local Similarity 30.5%; Pred. No. 9e-29;
RESULT 814
ID ABB62722 standard; protein; 335 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14958.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 20.3%; Score 362; DB 4; Length 335;
Best Local Similarity 31.7%; Pred. No. 1.5e-28;
RESULT 815
ID AAW06484 standard; peptide; 270 AA.
DE Carbonic anhydrase domain of RPTPbeta.
PN WO9637776-A1.
PD 28-NOV-1996.
PA (SUGE-) SUGEN INC.
Query Match 20.3%; Score 360.5; DB 2; Length 270;
Best Local Similarity 32.8%; Pred. No. 1.5e-28;
RESULT 816
ID ADO28597 standard; protein; 306 AA.
DE Human CAH4 protein SEQ ID NO:26.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 360; DB 8; Length 306;
Best Local Similarity 34.0%; Pred. No. 2e-28;
RESULT 817
ID ADL70162 standard; protein; 325 AA.
DE Glu-tagged human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 20.2%; Score 358.5; DB 8; Length 325;
Best Local Similarity 30.5%; Pred. No. 3.2e-28;
RESULT 818
ID ABB62051 standard; protein; 304 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12945.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 20.0%; Score 356; DB 4; Length 304;
Best Local Similarity 34.5%; Pred. No. 5.3e-28;
RESULT 819
ID ADN39944 standard; protein; 1456 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C314.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 19.8%; Score 351.5; DB 7; Length 1456;
Best Local Similarity 32.1%; Pred. No. 1.9e-26;
RESULT 820
ID ADJ95126 standard; protein; 248 AA.
DE Novel NOVX protein sequence #177.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 19.5%; Score 347.5; DB 7; Length 248;
Best Local Similarity 37.0%; Pred. No. 3e-27;
RESULT 821
ID ABM83054 standard; protein; 224 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3303.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 19.3%; Score 343; DB 8; Length 224;
Best Local Similarity 32.7%; Pred. No. 7.4e-27;
RESULT 822
ID AAB63110 standard; protein; 184 AA.
DE Human secreted protein sequence encoded by gene 27 SEQ ID NO:120.
PN WO200061748-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.9%; Score 335.5; DB 3; Length 184;
Best Local Similarity 41.8%; Pred. No. 3.3e-26;
RESULT 823
ID ADL70164 standard; protein; 325 AA.
DE Glu-tagged human carbonic anhydrase IX CA domain construct.
PN WO2004017923-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
Query Match 18.8%; Score 334.5; DB 8; Length 325;
Best Local Similarity 29.6%; Pred. No. 1e-25;
RESULT 824
ID ABB63491 standard; protein; 270 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.6%; Score 330.5; DB 4; Length 270;
Best Local Similarity 32.7%; Pred. No. 2e-25;
RESULT 825
ID AAU30162 standard; protein; 329 AA.
DE Novel human secreted protein #653.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 18.6%; Score 330.5; DB 4; Length 329;
Best Local Similarity 32.6%; Pred. No. 2.8e-25;
RESULT 826
ID ADL90198 standard; protein; 232 AA.
DE Human enzyme, ENZM-8, SEQ ID 8.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 18.4%; Score 326.5; DB 8; Length 232;
Best Local Similarity 28.1%; Pred. No. 4.2e-25;
RESULT 827
ID AAB63109 standard; protein; 183 AA.

DE Gene 27 human secreted protein homologous amino acid sequence #119.
PN WO200061748-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.0%; Score 321; DB 3; Length 183;
Best Local Similarity 39.6%; Pred. No. 1.1e-24;
RESULT 828
ID ABB61476 standard; protein; 322 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11220.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 17.9%; Score 318; DB 4; Length 322;
Best Local Similarity 32.4%; Pred. No. 5.5e-24;
RESULT 829
ID AAU27777 standard; protein; 328 AA.
DE Human full-length polypeptide sequence #102.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.5%; Score 312; DB 4; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 830
ID AAU12188 standard; protein; 328 AA.
DE Human PRO1076 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 4; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 831
ID ABB05677 standard; protein; 328 AA.
DE Human amygdala derived protein clone amy2_16e14.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 17.5%; Score 312; DB 5; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 832
ID ABB08902 standard; protein; 328 AA.
DE Human lyase HLYA-3 protein.
PN WO200200840-A2.
PD 03-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 17.5%; Score 312; DB 5; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 833
ID ABO17632 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 834
ID ABU80886 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 835
ID ABU66586 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 836
ID ABU59667 standard; protein; 328 AA.
DE Novel secreted and transmembrane protein PRO1076.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 837
ID ABO24857 standard; protein; 328 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 838
ID ABU66862 standard; protein; 328 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 34.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 839
ID ADA45553 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 840
ID ADA75984 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 841
ID ADA18634 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 842
ID ADA61257 standard; protein; 328 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 843
ID ADB19042 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 844
ID ADB27583 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 845
ID ADA86062 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082711-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 846
ID ADB15626 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 847
ID ADA47412 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 848
ID ADA67207 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 849
ID ADB30214 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 850
ID ADA85510 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 851
ID ADA96722 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 852
ID ADA79026 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 853
ID ADA87165 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 854
ID ADB16367 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 855
ID ADA91459 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 856
ID ADB14522 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 857
ID ADB18483 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 858
ID ADA93698 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 859
ID ADB19594 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 860
ID ADB12906 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 861
ID ABO43165 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 862
ID ADA74160 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 863
ID ADB24393 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 864
ID ADA81917 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 865
ID ADA74880 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 866
ID ADA84958 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 867
ID ADA84406 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 868
ID ADB29662 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 869
ID ADA80190 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 870
ID ADA75432 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 871
ID ADA46657 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 872
ID ADB24953 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 873
ID ADA93129 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 874
ID ADB26479 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 875
ID ADB30766 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 876
ID ADA60694 standard; protein; 328 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 877
ID ADB23841 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 878
ID ADA96170 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 879
ID ADA80742 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 880
ID ADA95618 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 881
ID ADB25927 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;

RESULT 882
ID ADB21412 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 6; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 883
ID ADA77191 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 884
ID ADB17931 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 885
ID ADA86614 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 886
ID ADA87717 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 887
ID ADA46105 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 888
ID ADB28135 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 889
ID ADB28687 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 890
ID ADA76639 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 891
ID ADA88269 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 892
ID ADA97274 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 893
ID ADB27031 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 894
ID ADB21964 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 895
ID ADA66655 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 896
ID ADB22516 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 897
ID ADB23289 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 898
ID ADA92011 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 899
ID ADB15074 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 900
ID ADB38326 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082766-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 901
ID ADB37774 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 902
ID ADB66246 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 903
ID ADB89326 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 904
ID ADB90058 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 905
ID ADB39159 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 906
ID ADB46782 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 907
ID ADB86389 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 908
ID ADB76994 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 909
ID ADB34151 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 910
ID ADB35255 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 911
ID ADB33599 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 912
ID ADB34703 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 913
ID ADB35807 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 34.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 914
ID ADB46202 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 915
ID ADC50075 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 916
ID ADC71622 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 917
ID ADC59601 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 918
ID ADC52608 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 919
ID ADC56962 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 920
ID ADC60153 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 921
ID ADC50628 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 922
ID ADC65155 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 923
ID ADC54253 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 924
ID ADC53214 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 925
ID ADC58737 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 926
ID ADC55615 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 927
ID ADC58185 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID34.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 928
ID ADD02859 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 929
ID ADC89851 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 930
ID ADC69270 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 931
ID ADC48159 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 932
ID ADD09688 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 933
ID ADD04263 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 934
ID ADC80219 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 935
ID ADD10726 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 936
ID ADC47607 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;

RESULT 937
ID ADC79667 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 938
ID ADD09136 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 939
ID ADD40849 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 940
ID ADD51988 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 941
ID ADD52728 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 942
ID ADD53280 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 943
ID ADD51436 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 944
ID ADD02235 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 945
ID ADD01669 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 946
ID ADD53851 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 947
ID ADD92168 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 948
ID ADD91064 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 949
ID ADE03678 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 950
ID ADE31975 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 951
ID ADE21907 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 952
ID ADD79131 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 953
ID ADE41667 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 954
ID ADE17484 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 955
ID ADD91616 standard; protein; 328 AA.

DE Human PRO polypeptide #17.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 956
ID ADE33079 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 957
ID ADE33631 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 958
ID ADD79683 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 959
ID ADD92720 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 960
ID ADE19140 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 961
ID ADE18588 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 962
ID ADE42784 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 963
ID ADD95573 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 964
ID ADE22459 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 965
ID ADD78577 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 966
ID ADE32527 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 967
ID ADE42219 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 968
ID ADD80235 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 969
ID ADD89263 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 970
ID ADE40547 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 971
ID ADE04346 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 972
ID ADE92475 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 973
ID ADG21184 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207355-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 974
ID ADG22825 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 975
ID ADF97160 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 976
ID ADG80224 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 977
ID ADG79672 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 978
ID ADH54964 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 979
ID ADH55516 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 980
ID ADI63735 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 981
ID ADI64684 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 982
ID ADI63183 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 983
ID ADH81597 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 984
ID ADH81045 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 985
ID ADM82214 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 986
ID ADN15613 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 987
ID ADN16242 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 988
ID ADN15061 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 989
ID ADN14509 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 7; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 990
ID ADC80771 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 991
ID ADD76219 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 992
ID ADD87583 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 993
ID ADD85987 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 994
ID ADE75435 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 995
ID ADE23011 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 996
ID ADE23563 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 997
ID ADE24206 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 998
ID ADD87031 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 999
ID ADE88897 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1000
ID ADE18036 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1001
ID ADE88345 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1002
ID ADE94365 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1003
ID ADE90776 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1004
ID ADE94917 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1005
ID ADE93027 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1006
ID ADF34608 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1007
ID ADE91923 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1008
ID ADE90224 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1009
ID ADE91371 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;

RESULT 1010
ID ADG01950 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1011
ID ADG21736 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1012
ID ADG19806 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1013
ID ADF97712 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1014
ID ADG23929 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1015
ID ADF98283 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1016
ID ADG03114 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1017
ID ADF98835 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1018
ID ADG16420 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1019
ID ADG04879 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1020
ID ADG19146 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1021
ID ADG12983 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1022
ID ADG08040 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1023
ID ADG15210 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1024
ID ADF96608 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1025
ID ADG05793 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1026
ID ADG23377 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1027
ID ADG03666 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1028
ID ADG24567 standard; protein; 328 AA.

DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1029
ID ADG06864 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1030
ID ADG07416 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1031
ID ADG54911 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1032
ID ADG60575 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1033
ID ADG61679 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1034
ID ADG81880 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1035
ID ADG57119 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1036
ID ADG56567 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1037
ID ADG55463 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1038
ID ADG58223 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1039
ID ADG70589 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1040
ID ADG57671 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1041
ID ADG53255 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1042
ID ADG71141 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1043
ID ADG81328 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1044
ID ADH30290 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1045
ID ADH11657 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1046
ID ADG52079 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207414-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1047
ID ADG53807 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1048
ID ADG80776 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1049
ID ADG56015 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1050
ID ADH12281 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1051
ID ADG61127 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1052
ID ADH28214 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1053
ID ADG54359 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1054
ID ADG59399 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1055
ID ADI80823 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1056
ID ADG09566 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1057
ID ADI15037 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1058
ID ADG08914 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1059
ID ADI14369 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1060
ID ADI17964 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1061
ID ADJ63245 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1062
ID ADJ77140 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1063
ID ADJ65262 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1064
ID ADM27398 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;

Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1065
ID ADM42122 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1066
ID ADM27984 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1067
ID ADI95466 standard; protein; 328 AA.
DE Human PRO polypeptide #17.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1068
ID ADI96018 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO1076.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.5%; Score 312; DB 8; Length 328;
Best Local Similarity 30.3%; Pred. No. 2.4e-23;
RESULT 1069
ID ABB08213 standard; protein; 328 AA.
DE Human carbonic anhydrase (CAH).
PN WO200190321-A2.
PD 29-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.3%; Score 307; DB 5; Length 328;
Best Local Similarity 29.9%; Pred. No. 8e-23;
RESULT 1070
ID ADA09126 standard; protein; 328 AA.
DE Novel human carbonic anhydrase CAH.
PN US2003059919-A1.
PD 27-MAR-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.3%; Score 307; DB 7; Length 328;
Best Local Similarity 29.9%; Pred. No. 8e-23;
RESULT 1071
ID ABB58854 standard; protein; 235 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3354.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 17.0%; Score 302.5; DB 4; Length 235;
Best Local Similarity 33.1%; Pred. No. 1.4e-22;
RESULT 1072
ID ABB60294 standard; protein; 302 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7674.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 16.2%; Score 288.5; DB 4; Length 302;
Best Local Similarity 29.4%; Pred. No. 6e-21;
RESULT 1073
ID AAY41737 standard; protein; 328 AA.
DE Human PRO237 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 2; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1074
ID AAY39999 standard; protein; 328 AA.
DE Human carbonic anhydrase VIII protein sequence.
PN US5972684-A.
PD 26-OCT-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 16.2%; Score 288.5; DB 2; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1075
ID AAB19525 standard; protein; 328 AA.
DE Antitumour PRO237 protein.
PN WO200053751-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 3; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1076
ID AAB44293 standard; protein; 328 AA.
DE Human PRO237 (UNQ211) protein sequence SEQ ID NO:358.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 3; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1077
ID AAB24041 standard; protein; 328 AA.
DE Human PRO237 protein sequence SEQ ID NO:2.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 3; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1078
ID AAU12334 standard; protein; 328 AA.
DE Human PRO237 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 4; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1079
ID ABO17778 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1080
ID ABO25239 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1081
ID ABU81032 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1082
ID ABU72245 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1083

ID ABU66732 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1084
ID ABU84925 standard; protein; 328 AA.
DE Human secreted and transmembrane PRO polypeptide #1.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1085
ID ABU59813 standard; protein; 328 AA.
DE Novel secreted and transmembrane protein PRO237.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1086
ID ABU61123 standard; protein; 328 AA.
DE Human PRO237 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1087
ID ABO25003 standard; protein; 328 AA.
DE Human secreted/transmembrane protein (PRO) #163.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1088
ID ABU80392 standard; protein; 328 AA.
DE Human secreted/transmembrane protein PRO237.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1089
ID ABU67008 standard; protein; 328 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 326.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1090
ID ADA45845 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1091
ID ADA76276 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1092
ID ADA18926 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1093
ID ADA61549 standard; protein; 328 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1094
ID ADB19334 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1095
ID ADB27875 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1096
ID ADA86354 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1097
ID ADB15918 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1098
ID ADA47704 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1099
ID ADA67499 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1100
ID ADB30506 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1101
ID ADA85802 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.

PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1102
ID ADA97014 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1103
ID ADA79318 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1104
ID ADA87457 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1105
ID ADB16659 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1106
ID ADA91751 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1107
ID ADB14814 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1108
ID ADA24897 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1109
ID ADB18775 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1110
ID ADA93990 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1111
ID ADB19886 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1112
ID ADB13198 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1113
ID ABO43311 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1114
ID ABO19694 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1115
ID ADA12558 standard; protein; 328 AA.
DE Human secreted/transmembrane polypeptide PRO237.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1116
ID ADA74452 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1117
ID ADB24685 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1118
ID ADA82209 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1119
ID ADA75172 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003073216-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1120
ID ADA85250 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1121
ID ADA84698 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1122
ID ADB29954 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1123
ID ADA80482 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1124
ID ADA75724 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1125
ID ADA46949 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1126
ID ADB25245 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1127
ID ADA93421 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1128
ID ADB26771 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1129
ID ADB31058 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1130
ID ADA60986 standard; protein; 328 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1131
ID ADB24133 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1132
ID ADA96462 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1133
ID ADA81034 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1134
ID ADA95910 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1135
ID ADB26219 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1136
ID ADB21704 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1137
ID ABO19585 standard; protein; 328 AA.
DE Novel human secreted and transmembrane polypeptide #53.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 16.2%; Score 288.5; DB 6; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;

RESULT 1138
ID ADA77483 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1139
ID ADB18223 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1140
ID ADA86906 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1141
ID ADA88009 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1142
ID ADA46397 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1143
ID ADB28427 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1144
ID ADB28979 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1145
ID ADA76931 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1146
ID ADA88561 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1147
ID ADA97566 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1148
ID ADB27323 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1149
ID ADB22256 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1150
ID ADA66947 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1151
ID ADB22808 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1152
ID ADB23581 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1153
ID ADA92303 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1154
ID ADB15366 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1155
ID ADB38618 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1156
ID ADB38066 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087347-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1157
ID ADB66538 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1158
ID ADB89618 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1159
ID ADB90350 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1160
ID ADB39451 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1161
ID ADB73864 standard; protein; 328 AA.
DE Human PRO polypeptide #53.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1162
ID ADB47074 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1163
ID ADB86681 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1164
ID ADB76580 standard; protein; 328 AA.
DE Human PRO polypeptide #53.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1165
ID ADB77286 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1166
ID ADB34443 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1167
ID ADB35547 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1168
ID ADB33891 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1169
ID ADB34995 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1170
ID ADB36099 standard; protein; 328 AA.
DE Human PRO polypeptide SEQ ID NO 326.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1171
ID ADB46494 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1172
ID ADC44006 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1173
ID ADC61766 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1174
ID ADC63730 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1175
ID ADC66830 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1176
ID ADC68954 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1177
ID ADC63014 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1178
ID ADC68079 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1179
ID ADC41399 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1180
ID ADC67454 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1181
ID ADC62390 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1182
ID ADC42023 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1183
ID ADC50367 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1184
ID ADC71914 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1185
ID ADC59893 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1186
ID ADC52900 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1187
ID ADC57254 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1188
ID ADC60445 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1189
ID ADC50920 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1190
ID ADC65447 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1191
ID ADC54545 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1192
ID ADC53506 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;

RESULT 1193
ID ADC59029 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1194
ID ADC55907 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1195
ID ADC58477 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein Seq ID326.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1196
ID ADD03151 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1197
ID ADC90143 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1198
ID ADC69562 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1199
ID ADC48451 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1200
ID ADD09980 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1201
ID ADD04555 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1202
ID ADC80511 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1203
ID ADD11018 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1204
ID ADC47899 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1205
ID ADC79959 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1206
ID ADD09428 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1207
ID ADD41141 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1208
ID ADD52280 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1209
ID ADD53020 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1210
ID ADD53572 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1211
ID ADD51728 standard; protein; 328 AA.

DE Human PRO polypeptide #163.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1212
ID ADD02527 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1213
ID ADD01961 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1214
ID ADD54143 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1215
ID ADE49392 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1216
ID ADD92460 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1217
ID ADD91356 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1218
ID ADE03970 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1219
ID ADE32267 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1220
ID ADE22199 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1221
ID ADD79423 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1222
ID ADE35446 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1223
ID ADE16560 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1224
ID ADD73175 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1225
ID ADE41959 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1226
ID ADE17776 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1227
ID ADD91908 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1228
ID ADE33371 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1229
ID ADE33923 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003194791-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1230
ID ADD79975 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1231
ID ADD93012 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1232
ID ADD72533 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1233
ID ADE19432 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1234
ID ADE18880 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1235
ID ADE43076 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1236
ID ADD95865 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1237
ID ADE22751 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1238
ID ADD78869 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1239
ID ADE32819 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1240
ID ADE42511 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1241
ID ADE17184 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1242
ID ADD80527 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1243
ID ADD89555 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1244
ID ADE40839 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1245
ID ADE04638 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1246
ID ADE92767 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1247
ID ADF47198 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1248
ID ADG21476 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1249
ID ADG23117 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1250
ID ADF97452 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1251
ID ADG80516 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1252
ID ADG52955 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1253
ID ADG60275 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1254
ID ADG79964 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1255
ID ADH55256 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1256
ID ADH55808 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1257
ID ADI61035 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1258
ID ADI64027 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1259
ID ADI64976 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1260
ID ADH81889 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1261
ID ADH81337 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1262
ID ADM82506 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1263
ID ADN15905 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1264
ID ADN16534 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1265
ID ADN15353 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;

RESULT 1266
ID ADN14801 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1267
ID ADI63475 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 7; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1268
ID ADC81063 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1269
ID ADD76511 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1270
ID ADD87875 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1271
ID ADD86279 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1272
ID ADE75727 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1273
ID ADE48692 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1274
ID ADE23303 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1275
ID ADE23855 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1276
ID ADE24498 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1277
ID ADD87323 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1278
ID ADE89189 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1279
ID ADE18328 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1280
ID ADE88637 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1281
ID ADE89793 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.

PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1282
ID ADF61433 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1283
ID ADF40125 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1284
ID ADF45921 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1285
ID ADE94657 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1286
ID ADE91068 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1287
ID ADE95209 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1288
ID ADE93319 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1289
ID ADF24317 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1290
ID ADF40749 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1291
ID ADF23693 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1292
ID ADF33676 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1293
ID ADF34900 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1294
ID ADF27143 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1295
ID ADF27779 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1296
ID ADE92215 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1297
ID ADE90516 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1298
ID ADF41373 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1299
ID ADF33052 standard; protein; 328 AA.

DE Human secreted/transmembrane protein, PRO237.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1300
ID ADF25418 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1301
ID ADF26519 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1302
ID ADF34308 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1303
ID ADF46545 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1304
ID ADE91663 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1305
ID ADG02242 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1306
ID ADG22028 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1307
ID ADG20098 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1308
ID ADF98004 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1309
ID ADG24221 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1310
ID ADF98575 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1311
ID ADG03406 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1312
ID ADF99127 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1313
ID ADG16712 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1314
ID ADG05171 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1315
ID ADG19438 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1316
ID ADG13275 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1317
ID ADG08332 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207424-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1318
ID ADG15502 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1319
ID ADF96900 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1320
ID ADG06085 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1321
ID ADG23669 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1322
ID ADG03958 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1323
ID ADG24859 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1324
ID ADG07156 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1325
ID ADG07708 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1326
ID ADG55203 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1327
ID ADG60867 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1328
ID ADG61971 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1329
ID ADG82172 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1330
ID ADG57411 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1331
ID ADG56859 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1332
ID ADG55755 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1333
ID ADG58515 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1334
ID ADG70881 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1335
ID ADG57963 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1336
ID ADG53547 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1337
ID ADG71433 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1338
ID ADG50531 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1339
ID ADG81620 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1340
ID ADH30582 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1341
ID ADH11949 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1342
ID ADG49907 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1343
ID ADG51779 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1344
ID ADG52371 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1345
ID ADG54099 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1346
ID ADG49283 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1347
ID ADG81068 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1348
ID ADG56307 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1349
ID ADH12573 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1350
ID ADG48659 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1351
ID ADG61419 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1352
ID ADH28506 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1353
ID ADG54651 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1354

ID ADG59691 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1355
ID ADG51155 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1356
ID ADG59099 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1357
ID ADG62555 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1358
ID ADI81115 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1359
ID ADH25580 standard; protein; 328 AA.
DE Human neurotrimin homologue related protein sequence SEQ ID NO:358.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1360
ID ADG09858 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1361
ID ADI15329 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1362
ID ADG09206 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1363
ID ADI14661 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1364
ID ADI18256 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1365
ID ADJ63537 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1366
ID ADJ77432 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1367
ID ADJ65554 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1368
ID ADM27690 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1369
ID ADM17357 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1370
ID ADL07191 standard; protein; 328 AA.
DE Human secreted/transmembrane protein, PRO237.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1371
ID ADM42414 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1372
ID ADM28276 standard; protein; 328 AA.
DE Human PRO polypeptide #163.

PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1373
ID ADI95758 standard; protein; 328 AA.
DE Human PRO polypeptide #163.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1374
ID ADI96310 standard; protein; 328 AA.
DE Novel human secreted and transmembrane protein PRO237.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 288.5; DB 8; Length 328;
Best Local Similarity 29.3%; Pred. No. 6.9e-21;
RESULT 1375
ID AAE38242 standard; protein; 346 AA.
DE Human enzyme (ENZM) protein #34.
PN WO2003052075-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 16.2%; Score 288.5; DB 6; Length 346;
Best Local Similarity 29.3%; Pred. No. 7.5e-21;
RESULT 1376
ID AAW06552 standard; protein; 201 AA.
DE Human colon specific gene CSG10 polypeptide fragment.
PN WO9639419-A1.
PD 12-DEC-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 280.5; DB 2; Length 201;
Best Local Similarity 33.0%; Pred. No. 2.2e-20;
RESULT 1377
ID AAW46884 standard; protein; 201 AA.
DE Protein sequence encoded by a colon-specific gene.
PN US5733748-A.
PD 31-MAR-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 280.5; DB 2; Length 201;
Best Local Similarity 33.0%; Pred. No. 2.2e-20;
RESULT 1378
ID AAU76212 standard; protein; 201 AA.
DE Human colon specific gene 10 (CSG10) protein.
PN US6337195-B1.
PD 08-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 280.5; DB 5; Length 201;
Best Local Similarity 33.0%; Pred. No. 2.2e-20;
RESULT 1379
ID ABG32041 standard; protein; 201 AA.
DE Human colon specific gene (CSG) 11 protein.
PN US2002086314-A1.
PD 04-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 280.5; DB 5; Length 201;
Best Local Similarity 33.0%; Pred. No. 2.2e-20;
RESULT 1380
ID ADQ58736 standard; protein; 201 AA.
DE Human colon specific gene protein #8.
PN US2004132976-A1.
PD 08-JUL-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 280.5; DB 8; Length 201;
Best Local Similarity 33.0%; Pred. No. 2.2e-20;
RESULT 1381
ID ABP76873 standard; protein; 252 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 276.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 15.3%; Score 272.5; DB 6; Length 252;
Best Local Similarity 32.2%; Pred. No. 2.1e-19;
RESULT 1382
ID ABP78739 standard; protein; 252 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 4008.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 15.3%; Score 272.5; DB 6; Length 252;
Best Local Similarity 32.2%; Pred. No. 2.1e-19;
RESULT 1383
ID ADM48233 standard; protein; 264 AA.
DE Polypeptide sequence #283 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 15.0%; Score 267; DB 8; Length 264;
Best Local Similarity 30.6%; Pred. No. 8.7e-19;
RESULT 1384
ID ABB67177 standard; protein; 199 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28323.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.0%; Score 266.5; DB 4; Length 199;
Best Local Similarity 33.9%; Pred. No. 6.2e-19;
RESULT 1385
ID ABJ04662 standard; protein; 258 AA.
DE Protein of NOVX 19a SEQ ID No 46.
PN WO200246409-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 265; DB 5; Length 258;
Best Local Similarity 26.8%; Pred. No. 1.4e-18;
RESULT 1386
ID ABJ04663 standard; protein; 258 AA.
DE Protein of NOVX 19b SEQ ID No 48.
PN WO200246409-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 265; DB 5; Length 258;
Best Local Similarity 26.8%; Pred. No. 1.4e-18;
RESULT 1387
ID ABB64324 standard; protein; 332 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19764.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 259.5; DB 4; Length 332;
Best Local Similarity 27.1%; Pred. No. 7.6e-18;
RESULT 1388
ID ADL90209 standard; protein; 205 AA.
DE Human enzyme, ENZM-19, SEQ ID 19.
PN WO2004027022-A2.
PD 01-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.2%; Score 252.5; DB 8; Length 205;
Best Local Similarity 33.0%; Pred. No. 1.9e-17;
RESULT 1389
ID ABB67176 standard; protein; 235 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28320.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.0%; Score 249.5; DB 4; Length 235;
Best Local Similarity 31.1%; Pred. No. 4.9e-17;
RESULT 1390
ID ABU56496 standard; protein; 1337 AA.
DE Lung cancer-associated polypeptide #89.

PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.7%; Score 244; DB 6; Length 1337;
Best Local Similarity 33.3%; Pred. No. 2.9e-15;
RESULT 1391
ID ABU56690 standard; protein; 1337 AA.
DE Lung cancer-associated polypeptide #283.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.7%; Score 244; DB 6; Length 1337;
Best Local Similarity 33.3%; Pred. No. 2.9e-15;
RESULT 1392
ID ADN39060 standard; protein; 1337 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:378.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.7%; Score 244; DB 7; Length 1337;
Best Local Similarity 33.3%; Pred. No. 2.9e-15;
RESULT 1393
ID AAG00292 standard; protein; 132 AA.
DE Human secreted protein, SEQ ID NO: 4373.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 13.7%; Score 243.5; DB 3; Length 132;
Best Local Similarity 43.5%; Pred. No. 8.3e-17;
RESULT 1394
ID ABB65606 standard; protein; 250 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23610.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.2%; Score 235; DB 4; Length 250;
Best Local Similarity 29.4%; Pred. No. 1.8e-15;
RESULT 1395
ID AAO12529 standard; protein; 143 AA.
DE Human polypeptide SEQ ID NO 26421.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 233.5; DB 4; Length 143;
Best Local Similarity 37.9%; Pred. No. 1e-15;
RESULT 1396
ID ABG22003 standard; protein; 345 AA.
DE Novel human diagnostic protein #21994.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.2%; Score 217.5; DB 4; Length 345;
Best Local Similarity 27.5%; Pred. No. 2e-13;
RESULT 1397
ID ABB92636 standard; protein; 284 AA.
DE Herbicidally active polypeptide SEQ ID NO 1847.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 12.2%; Score 217; DB 5; Length 284;
Best Local Similarity 26.8%; Pred. No. 1.7e-13;
RESULT 1398
ID ABB91907 standard; protein; 248 AA.
DE Herbicidally active polypeptide SEQ ID NO 1118.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 12.1%; Score 215.5; DB 5; Length 248;
Best Local Similarity 28.1%; Pred. No. 1.9e-13;
RESULT 1399
ID AAG14078 standard; protein; 277 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13806.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 215; DB 3; Length 277;
Best Local Similarity 26.7%; Pred. No. 2.6e-13;
RESULT 1400
ID AAG22949 standard; protein; 358 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26072.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.8%; Score 209.5; DB 3; Length 358;
Best Local Similarity 27.2%; Pred. No. 1.5e-12;
RESULT 1401
ID ABB64583 standard; protein; 182 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20541.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.3%; Score 200.5; DB 4; Length 182;
Best Local Similarity 30.8%; Pred. No. 4.4e-12;
RESULT 1402
ID ADD15285 standard; protein; 182 AA.
DE Fruitfly odourant receptor protein (SeqId 37).
PN WO2003020913-A2.
PD 13-MAR-2003.
PA (SENT-) SENTIGEN CORP.
Query Match 11.3%; Score 200.5; DB 7; Length 182;
Best Local Similarity 30.8%; Pred. No. 4.4e-12;
RESULT 1403
ID ABB62614 standard; protein; 689 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14634.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.1%; Score 198; DB 4; Length 689;
Best Local Similarity 25.2%; Pred. No. 6.6e-11;
RESULT 1404
ID AAG04193 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 127.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 197.5; DB 3; Length 185;
Best Local Similarity 29.9%; Pred. No. 9.2e-12;
RESULT 1405
ID AAG12732 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11960.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 197.5; DB 3; Length 185;
Best Local Similarity 29.9%; Pred. No. 9.2e-12;
RESULT 1406
ID AAG12731 standard; protein; 277 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11959.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 197.5; DB 3; Length 277;
Best Local Similarity 29.9%; Pred. No. 1.7e-11;
RESULT 1407
ID AAG04192 standard; protein; 277 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 126.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.1%; Score 197.5; DB 3; Length 277;
Best Local Similarity 29.9%; Pred. No. 1.7e-11;
RESULT 1408
ID ABB93346 standard; protein; 277 AA.
DE Herbicidally active polypeptide SEQ ID NO 2557.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 11.1%; Score 197.5; DB 5; Length 277;
Best Local Similarity 29.9%; Pred. No. 1.7e-11;
RESULT 1409
ID AAG14079 standard; protein; 221 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13807.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.0%; Score 196.5; DB 3; Length 221;
Best Local Similarity 26.4%; Pred. No. 1.6e-11;
RESULT 1410
ID AAG22950 standard; protein; 228 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26073.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.0%; Score 195.5; DB 3; Length 228;
Best Local Similarity 27.3%; Pred. No. 2.1e-11;
RESULT 1411
ID AAG22951 standard; protein; 222 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26074.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.8%; Score 192; DB 3; Length 222;
Best Local Similarity 27.2%; Pred. No. 4.6e-11;
RESULT 1412
ID ADM48236 standard; protein; 310 AA.
DE Polypeptide sequence #286 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 10.5%; Score 187.5; DB 8; Length 310;
Best Local Similarity 29.3%; Pred. No. 2.3e-10;
RESULT 1413
ID AAG14080 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13808.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.5%; Score 187; DB 3; Length 215;
Best Local Similarity 25.8%; Pred. No. 1.5e-10;
RESULT 1414
ID ADC51426 standard; protein; 87 AA.
DE Ovine carbonate dehydratase SEQ ID NO:2.
PN JP2002306172-A.
PD 22-OCT-2002.
PA (KANF) KANEKA CORP.
Query Match 10.4%; Score 184.5; DB 7; Length 87;
Best Local Similarity 41.9%; Pred. No. 6.4e-11;
RESULT 1415
ID ABG12956 standard; protein; 411 AA.
DE Novel human diagnostic protein #12947.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 184.5; DB 4; Length 411;
Best Local Similarity 20.5%; Pred. No. 7.5e-10;
RESULT 1416
ID ADO58298 standard; protein; 379 AA.
DE S. domuncula silicase.
PN DE10246186-A1.
PD 15-APR-2004.
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
Query Match 10.3%; Score 183; DB 8; Length 379;
Best Local Similarity 26.7%; Pred. No. 9.5e-10;
RESULT 1417
ID AAW20248 standard; protein; 247 AA.
DE H. pylori cytoplasmic protein 23475342.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 10.2%; Score 181; DB 2; Length 247;
Best Local Similarity 25.7%; Pred. No. 7.8e-10;
RESULT 1418
ID ADK36805 standard; protein; 151 AA.
DE Novel human polypeptide SeqID8887.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 179.5; DB 5; Length 151;
Best Local Similarity 29.0%; Pred. No. 5.1e-10;
RESULT 1419
ID AAG04194 standard; protein; 145 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 128.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.0%; Score 178; DB 3; Length 145;
Best Local Similarity 31.2%; Pred. No. 6.9e-10;
RESULT 1420
ID AAG12733 standard; protein; 145 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11961.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.0%; Score 178; DB 3; Length 145;
Best Local Similarity 31.2%; Pred. No. 6.9e-10;
RESULT 1421
ID ABG12954 standard; protein; 115 AA.
DE Novel human diagnostic protein #12945.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 172.5; DB 4; Length 115;
Best Local Similarity 41.1%; Pred. No. 1.8e-09;
RESULT 1422
ID AAB54035 standard; protein; 198 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:487.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 170; DB 3; Length 198;
Best Local Similarity 37.1%; Pred. No. 7.7e-09;
RESULT 1423
ID ABB93025 standard; protein; 150 AA.
DE Herbicidally active polypeptide SEQ ID NO 2236.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 9.5%; Score 169.5; DB 5; Length 150;
Best Local Similarity 35.3%; Pred. No. 5.6e-09;
RESULT 1424
ID AAR21416 standard; protein; 376 AA.
DE Carbonic anhydrase.
PN JP04016192-A.
PD 21-JAN-1992.
PA (YAWA) NIPPON STEEL CORP.
Query Match 9.3%; Score 165; DB 2; Length 376;
Best Local Similarity 26.1%; Pred. No. 7.1e-08;
RESULT 1425
ID ADR21595 standard; protein; 102 AA.
DE Human enzyme ENZM-16 protein SEQ ID NO:16.
PN WO2004072267-A2.
PD 26-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.2%; Score 164; DB 8; Length 102;
Best Local Similarity 42.6%; Pred. No. 1.1e-08;
RESULT 1426
ID ABB93026 standard; protein; 260 AA.
DE Herbicidally active polypeptide SEQ ID NO 2237.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 9.2%; Score 164; DB 5; Length 260;
Best Local Similarity 28.4%; Pred. No. 5.1e-08;
RESULT 1427
ID AAW01622 standard; protein; 447 AA.
DE Oyster pearl protein, nacrein.
PN WO9635786-A1.
PD 14-NOV-1996.
PA (FUJI/) FUJIKAWA Y.
Query Match 9.2%; Score 163.5; DB 2; Length 447;
Best Local Similarity 20.5%; Pred. No. 1.3e-07;
RESULT 1428

ID ADA07854 standard; protein; 447 AA.
DE Pinctada fucata nacrein.
PN US2003027258-A1.
PD 06-FEB-2003.
PA (CHAN/) CHANG F F.
PA (LIHH/) LI H.
PA (HSIE/) HSIEH-LI H M.
Query Match 9.2%; Score 163.5; DB 6; Length 447;
Best Local Similarity 20.5%; Pred. No. 1.3e-07;
RESULT 1429
ID AAR21417 standard; protein; 377 AA.
DE Chlamydomonas carbonic anhydrase.
PN JP04016191-A.
PD 21-JAN-1992.
PA (YAWA) NIPPON STEEL CORP.
Query Match 9.0%; Score 160.5; DB 2; Length 377;
Best Local Similarity 26.0%; Pred. No. 2.1e-07;
RESULT 1430
ID ADC95656 standard; protein; 234 AA.
DE E. faecium protein sequence SEQ ID 5283.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 8.9%; Score 158.5; DB 7; Length 234;
Best Local Similarity 23.7%; Pred. No. 1.6e-07;
RESULT 1431
ID AAG01269 standard; protein; 105 AA.
DE Human secreted protein, SEQ ID NO: 5350.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 8.8%; Score 156; DB 3; Length 105;
Best Local Similarity 32.4%; Pred. No. 8.2e-08;
RESULT 1432
ID ABP01842 standard; protein; 88 AA.
DE Human ORFX protein sequence SEQ ID NO:3666.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 150; DB 5; Length 88;
Best Local Similarity 37.8%; Pred. No. 2.6e-07;
RESULT 1433
ID ADJ70941 standard; protein; 1329 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2747.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 150; DB 7; Length 1329;
Best Local Similarity 30.0%; Pred. No. 2e-05;
RESULT 1434
ID ABB49036 standard; protein; 233 AA.
DE Listeria monocytogenes protein #1740.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 8.1%; Score 143.5; DB 5; Length 233;
Best Local Similarity 20.7%; Pred. No. 5.9e-06;
RESULT 1435
ID ABB58069 standard; protein; 103 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 999.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 139.5; DB 4; Length 103;
Best Local Similarity 29.5%; Pred. No. 4.3e-06;
RESULT 1436
ID ADA07853 standard; protein; 568 AA.
DE Pinctada maxima nacrein.
PN US2003027258-A1.
PD 06-FEB-2003.
PA (CHAN/) CHANG F F.
PA (LIHH/) LI H.
PA (HSIE/) HSIEH-LI H M.
Query Match 7.2%; Score 128; DB 6; Length 568;
Best Local Similarity 27.5%; Pred. No. 0.001;
RESULT 1437
ID ABG08488 standard; protein; 822 AA.
DE Novel human diagnostic protein #8479.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 127; DB 4; Length 822;
Best Local Similarity 25.2%; Pred. No. 0.0023;
RESULT 1438
ID ABG08487 standard; protein; 831 AA.
DE Novel human diagnostic protein #8478.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 127; DB 4; Length 831;
Best Local Similarity 25.2%; Pred. No. 0.0024;
RESULT 1439
ID ADG76334 standard; protein; 97 AA.
DE Human Incyte enzymatic protein (SeqID 26).
PN WO2003083082-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 125.5; DB 7; Length 97;
Best Local Similarity 33.0%; Pred. No. 0.00011;
RESULT 1440
ID ABB64577 standard; protein; 142 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20523.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 125; DB 4; Length 142;
Best Local Similarity 28.3%; Pred. No. 0.00023;
RESULT 1441
ID ABB70312 standard; protein; 291 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37728.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 124.5; DB 4; Length 291;
Best Local Similarity 22.0%; Pred. No. 0.00082;
RESULT 1442
ID ADA07852 standard; protein; 611 AA.
DE Pinctada margaritifera nacrein.
PN US2003027258-A1.
PD 06-FEB-2003.
PA (CHAN/) CHANG F F.
PA (LIHH/) LI H.
PA (HSIE/) HSIEH-LI H M.
Query Match 6.5%; Score 115; DB 6; Length 611;
Best Local Similarity 31.4%; Pred. No. 0.026;
RESULT 1443
ID ABB93838 standard; protein; 350 AA.
DE Herbicidally active polypeptide SEQ ID NO 3049.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 112; DB 5; Length 350;
Best Local Similarity 22.6%; Pred. No. 0.022;
RESULT 1444
ID AAY76261 standard; protein; 16 AA.
DE Fragment of human secreted protein encoded by gene 9.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.2%; Score 111; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00021;
RESULT 1445
ID ADE11891 standard; protein; 16 AA.
DE Human secreted polypeptide #146.
PN US2003100051-A1.

PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 6.2%; Score 111; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00021;

RESULT 1446
ID AAW20911 standard; protein; 88 AA.
DE H. pylori cytoplasmic protein 14gp11820orf20.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.2%; Score 109.5; DB 2; Length 88;
Best Local Similarity 32.5%; Pred. No. 0.0046;

RESULT 1447
ID AAU18700 standard; protein; 106 AA.
DE Renal and cardiovascular-associated protein, Seq ID 139.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 108; DB 4; Length 106;
Best Local Similarity 23.1%; Pred. No. 0.0088;

RESULT 1448
ID AAU23070 standard; protein; 106 AA.
DE Novel human enzyme polypeptide #156.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 108; DB 4; Length 106;
Best Local Similarity 23.1%; Pred. No. 0.0088;

RESULT 1449
ID ABB17090 standard; protein; 106 AA.
DE Human nervous system related polypeptide SEQ ID NO 5747.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 108; DB 4; Length 106;
Best Local Similarity 23.1%; Pred. No. 0.0088;

RESULT 1450
ID ABU97315 standard; protein; 106 AA.
DE Human polypeptide #57.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.1%; Score 108; DB 6; Length 106;
Best Local Similarity 23.1%; Pred. No. 0.0088;

RESULT 1451
ID AAR63632 standard; protein; 1439 AA.
DE Human receptor-type protein tyrosine phosphatase (RPTP) kappa.
PN WO9424161-A1.
PD 27-OCT-1994.
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.9%; Score 105.5; DB 2; Length 1439;
Best Local Similarity 22.9%; Pred. No. 1;

RESULT 1452
ID ADJ68478 standard; protein; 1439 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID284.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.9%; Score 105.5; DB 7; Length 1439;
Best Local Similarity 22.9%; Pred. No. 1;

RESULT 1453
ID AAY29591 standard; protein; 1440 AA.
DE Human protein phosphatase k.
PN KR98026246-A.
PD 15-JUL-1998.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 5.9%; Score 105; DB 2; Length 1440;
Best Local Similarity 22.8%; Pred. No. 1.1;

RESULT 1454
ID ADI23886 standard; protein; 1440 AA.
DE Human PTPRK protein SEQ ID NO:4.
PN WO2004005312-A1.
PD 15-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 5.9%; Score 105; DB 8; Length 1440;
Best Local Similarity 22.8%; Pred. No. 1.1;

RESULT 1455
ID ABB09503 standard; protein; 3597 AA.
DE Human laminin alpha-5-like NOV1c protein, SEQ ID NO:6.
PN WO200253742-A2.
PD 11-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 104; DB 5; Length 3597;
Best Local Similarity 20.4%; Pred. No. 6.2;

RESULT 1456
ID ABB09501 standard; protein; 3600 AA.
DE Human laminin alpha-5-like NOV1a protein, SEQ ID NO:2.
PN WO200253742-A2.
PD 11-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 104; DB 5; Length 3600;
Best Local Similarity 20.4%; Pred. No. 6.2;

RESULT 1457
ID AAR63633 standard; protein; 1457 AA.
DE Murine receptor-type protein tyrosine phosphatase precursor protein.
PN WO9424161-A1.
PD 27-OCT-1994.
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.8%; Score 103.5; DB 2; Length 1457;
Best Local Similarity 22.5%; Pred. No. 1.7;

RESULT 1458
ID ABB57308 standard; protein; 1457 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:862.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 5.8%; Score 103.5; DB 5; Length 1457;
Best Local Similarity 22.5%; Pred. No. 1.7;

RESULT 1459
ID AAB95216 standard; protein; 838 AA.
DE Human protein sequence SEQ ID NO:17331.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.8%; Score 103; DB 4; Length 838;
Best Local Similarity 21.9%; Pred. No. 0.78;

RESULT 1460
ID ADK35477 standard; protein; 83 AA.
DE Novel human polypeptide SeqID7559.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 102.5; DB 5; Length 83;
Best Local Similarity 35.8%; Pred. No. 0.022;

RESULT 1461
ID ABB64008 standard; protein; 1775 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 18816.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 100.5; DB 4; Length 1775;
Best Local Similarity 17.0%; Pred. No. 4.7;
RESULT 1462
ID ABB66938 standard; protein; 2061 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27606.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 100.5; DB 4; Length 2061;
Best Local Similarity 17.0%; Pred. No. 6;
RESULT 1463
ID ABB59814 standard; protein; 1423 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6234.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 100; DB 4; Length 1423;
Best Local Similarity 25.6%; Pred. No. 3.7;
RESULT 1464
ID AAU18654 standard; protein; 124 AA.
DE Renal and cardiovascular-associated protein, Seq ID 93.
PN WO200155328-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 98.5; DB 4; Length 124;
Best Local Similarity 23.3%; Pred. No. 0.11;
RESULT 1465
ID ABU97269 standard; protein; 124 AA.
DE Human polypeptide #11.
PN US2003013649-A1.
PD 16-JAN-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.5%; Score 98.5; DB 6; Length 124;
Best Local Similarity 23.3%; Pred. No. 0.11;
RESULT 1466
ID AAR63631 standard; protein; 1407 AA.
DE Murine receptor-type protein tyrosine phosphatase protein (RPTP- kappa).
PN WO9424161-A1.
PD 27-OCT-1994.
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.5%; Score 98.5; DB 2; Length 1407;
Best Local Similarity 21.2%; Pred. No. 5.3;
RESULT 1467
ID AAR50972 standard; protein; 530 AA.
DE Norwalk virus strain 8FIIa protein (encoded by ORF2).
PN WO9405700-A2.
PD 17-MAR-1994.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.5%; Score 98; DB 2; Length 530;
Best Local Similarity 20.2%; Pred. No. 1.3;
RESULT 1468
ID AAB49701 standard; protein; 530 AA.
DE Small round structured virus protein SEQ ID 2.
PN WO200079280-A1.
PD 28-DEC-2000.
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (DENK-) DENKA SEIKEN KK.
Query Match 5.5%; Score 98; DB 4; Length 530;
Best Local Similarity 20.2%; Pred. No. 1.3;
RESULT 1469
ID ADC72176 standard; protein; 530 AA.
DE Norwalk virus protein 2 amino acid sequence.
PN US6572862-B1.
PD 03-JUN-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.5%; Score 98; DB 7; Length 530;
Best Local Similarity 20.2%; Pred. No. 1.3;
RESULT 1470
ID ADE96372 standard; protein; 530 AA.
DE Norwalk virus protein 2.
PN US2003129588-A1.
PD 10-JUL-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.5%; Score 98; DB 7; Length 530;
Best Local Similarity 20.2%; Pred. No. 1.3;
RESULT 1471
ID AAM40419 standard; protein; 352 AA.
DE Human polypeptide SEQ ID NO 3564.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 97; DB 4; Length 352;
Best Local Similarity 20.8%; Pred. No. 0.84;
RESULT 1472
ID AAU79683 standard; protein; 518 AA.
DE Xenopus laevis protein relating to method for selective DNA isolation.
PN US6372434-B1.
PD 16-APR-2002.
PA (MOLE-) MOLECULAR STAGING INC.
Query Match 5.5%; Score 97; DB 5; Length 518;
Best Local Similarity 20.1%; Pred. No. 1.5;
RESULT 1473
ID AAM93393 standard; protein; 544 AA.
DE Human polypeptide, SEQ ID NO: 2986.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 97; DB 4; Length 544;
Best Local Similarity 20.8%; Pred. No. 1.7;
RESULT 1474
ID ADL30953 standard; protein; 544 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2986.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.5%; Score 97; DB 8; Length 544;
Best Local Similarity 20.8%; Pred. No. 1.7;
RESULT 1475
ID AAY21556 standard; protein; 545 AA.
DE Amino acid sequence of pGC6 protein.
PN WO9925878-A2.
PD 27-MAY-1999.
PA (GERO-) GERON CORP.
Query Match 5.5%; Score 97; DB 2; Length 545;
Best Local Similarity 20.8%; Pred. No. 1.7;
RESULT 1476
ID AAU12266 standard; protein; 613 AA.
DE Human PRO5780 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 4; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1477
ID AAE05187 standard; protein; 613 AA.
DE Human drug metabolising enzyme (DME-18) protein.
PN WO200151638-A2.
PD 19-JUL-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 97; DB 4; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1478
ID ABO17710 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;

RESULT 1479
ID ABU80964 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1480
ID ABU66664 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1481
ID ABU59745 standard; protein; 613 AA.
DE Novel secreted and transmembrane protein PRO5780.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1482
ID ABO24935 standard; protein; 613 AA.
DE Human secreted/transmembrane protein (PRO) #95.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1483
ID ABU66940 standard; protein; 613 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 190.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1484
ID ADA45709 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1485
ID ADA76140 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1486
ID ADA18790 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1487
ID ADA61413 standard; protein; 613 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1488
ID ADB19198 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1489
ID ADB27739 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1490
ID ADA86218 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1491
ID ADB15782 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1492
ID ADA47568 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1493
ID ADA67363 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1494
ID ADB30370 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1495
ID ADA85666 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1496
ID ADA96878 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1497
ID ADA79182 standard; protein; 613 AA.

DE Human PRO polypeptide #95.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1498
ID ADA87321 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1499
ID ADB16523 standard; protein; 613 AA.
DE Human PRO polypeptide #95.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;
RESULT 1500
ID ADA91615 standard; protein; 613 AA.
DE Novel human secreted and transmembrane protein PRO5780.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 97; DB 6; Length 613;
Best Local Similarity 20.8%; Pred. No. 2;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:31:01 ; Search time 43 Seconds
(without alignments)
754.071 Million cell updates/sec

Title: US-10-063-583-74
Perfect score: 1779
Sequence: 1 MLFSALLLEVIWILAADGGQ.....KRLENRKSVVFTSAQATTEA 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	31.6	459	2	I38013	p54/58N - human
2	532.5	29.9	307	2	A29993	carbonate dehydrat
3	530	29.8	319	2	S71877	carbonate dehydrat
4	505	28.4	308	1	CRHU6	carbonate dehydrat
5	458.5	25.8	1442	1	B48148	protein-tyrosine-p
6	452.5	25.4	1422	2	T42636	protein-tyrosine-p
7	449.5	25.3	1445	1	A48148	protein-tyrosine-p
8	425	23.9	259	1	CRRB2	carbonate dehydrat
9	423	23.8	309	2	I51900	carbonic anhydrase
10	420	23.6	260	1	CRHU2	carbonate dehydrat
11	415	23.3	260	2	JC2580	carbonate dehydrat
12	411	23.1	264	1	CRHU7	carbonate dehydrat
13	409.5	23.0	261	2	A26344	carbonate dehydrat
14	409	23.0	306	2	A48993	protein-tyrosine-p
15	406	22.8	259	1	CRSH2	carbonate dehydrat
16	405	22.8	260	1	CRHU3	carbonate dehydrat
17	404	22.7	260	2	T08463	carbonate dehydrat
18	404	22.7	260	2	JH0527	carbonate dehydrat
19	403	22.7	259	1	CRBO2	carbonate dehydrat
20	402.5	22.6	260	1	CRHO1D	carbonate dehydrat
21	401	22.5	260	2	A43641	carbonate dehydrat
22	398	22.4	260	1	CRMS2	carbonate dehydrat
23	390.5	22.0	304	2	I59261	carbonate dehydrat
24	387	21.8	259	2	A22612	carbonate dehydrat
25	386.5	21.7	260	1	CRMQ1R	carbonate dehydrat
26	384.5	21.6	261	2	JN0836	carbonate dehydrat
27	380.5	21.4	261	1	CRHU1	carbonate dehydrat
28	380.5	21.4	312	1	CRHU4	carbonate dehydrat
29	379	21.3	305	1	CRHU5	carbonate dehydrat
30	378.5	21.3	261	2	JN0835	carbonate dehydrat
31	378	21.2	260	2	I52551	carbonate dehydrat
32	374	21.0	334	2	T16772	hypothetical prote
33	365	20.5	2314	1	A46151	protein-tyrosine-p
34	363	20.4	290	2	JN0576	carbonate dehydrat
35	363	20.4	303	2	S12867	carbonate dehydrat
36	356	20.0	298	2	S12579	carbonate dehydrat
37	340	19.1	235	2	A22962	carbonate dehydrat
38	319.5	18.0	246	2	T16575	hypothetical prote
39	289.5	16.3	328	2	JE0375	carbonic anhydrase
40	280.5	15.8	275	2	H83694	carbonic anhydrase
41	278.5	15.7	285	2	A36819	C9 protein - rabbi
42	268	15.1	324	2	T34196	hypothetical prote
43	267.5	15.0	304	2	H72162	F8L protein - vari
44	267.5	15.0	304	2	T28536	hypothetical prote
45	267.5	15.0	304	2	E36847	cell surface-bindi
46	267	15.0	264	2	AB2172	carbonic anhydrase
47	266.5	15.0	304	1	CRVZ7P	cell surface-bindi
48	263.5	14.8	304	1	CRVZW	cell surface-bindi
49	259.5	14.6	304	2	T37381	carbonic anhydrase
50	257.5	14.5	239	2	F82479	carbonic anhydrase
51	247.5	13.9	200	2	A60519	carbonate dehydrat
52	247.5	13.9	259	2	T23849	hypothetical prote
53	245	13.8	365	2	F88449	protein F54D8.4 [i
54	233	13.1	589	2	T08466	carbonate dehydrat
55	230.5	13.0	249	2	E95264	probable carbonate
56	230	12.9	246	2	S57767	dioscorin class B
57	226.5	12.7	273	2	S57766	dioscorin class A
58	217	12.2	284	2	T49025	carbonate dehydrat
59	215.5	12.1	248	2	B84682	probable carbonic
60	199.5	11.2	263	2	E86215	protein T6D22.16 [
61	193	10.8	319	2	T15137	hypothetical prote
62	187.5	10.5	310	2	T08078	carbonate dehydrat
63	181	10.2	247	2	A71847	carbonic anhydrase
64	177.5	10.0	2254	2	D86215	protein T6D22.14 [
65	169.5	9.5	150	2	T10641	carbonic anhydrase
66	164	9.2	260	2	T10642	carbonic anhydrase
67	160.5	9.0	377	2	A35795	carbonate dehydrat
68	159.5	9.0	380	2	S14188	carbonate dehydrat
69	143.5	8.1	233	2	AC1176	carbonic anhydrase
70	139.5	7.8	233	2	AG1533	carbonic anhydrase
71	119	6.7	568	2	JC7210	molluscan shell ma
72	105	5.9	1440	2	JC6312	protein-tyrosine-p
73	103.5	5.8	1457	1	A48066	protein-tyrosine-p
74	100.5	5.6	2061	2	T13751	transcription fact
75	99	5.6	202	2	B64668	carbonic anhydrase
76	98	5.5	530	2	B37471	capsid protein - N
77	97	5.5	534	2	S71800	transcription fact
78	95.5	5.4	461	2	D89894	hypothetical prote
79	95.5	5.4	823	2	T16758	hypothetical prote
80	95.5	5.4	1288	2	T09908	hypothetical prote
81	95	5.3	335	2	T12460	hypothetical prote
82	94	5.3	430	2	S66671	neuron-derived rec
83	93	5.2	734	2	S46765	hypothetical prote
84	92.5	5.2	1197	2	T30581	neural cell adhesi
85	90.5	5.1	326	2	AB1431	AraC-type regulato
86	90.5	5.1	368	2	F64017	hypothetical prote
87	89.5	5.0	326	2	AH1804	AraC-type regulato
88	89.5	5.0	353	2	B72468	hypothetical prote
89	89	5.0	749	2	T48782	lanosterol synthas
90	89	5.0	1032	2	T30270	major tegumental a
91	88.5	5.0	401	2	B37416	bloodstream-specif
92	88.5	5.0	744	2	T13429	hypothetical prote
93	88	4.9	786	2	D75630	glycerophosphoryl
94	87	4.9	1220	2	S64916	probable membrane
95	86.5	4.9	301	2	AB0164	FecCD transport fa
96	86.5	4.9	306	2	A31106	mitochondrial unco
97	86.5	4.9	312	2	AE2215	hypothetical prote
98	86.5	4.9	531	2	S06016	intercellular adhe
99	86.5	4.9	537	2	I49769	intercellular adhe
100	86.5	4.9	537	2	A45815	intercellular adhe
101	86	4.8	235	2	T03755	hypothetical prote
102	86	4.8	529	2	T00677	hypothetical prote

103	86	4.8	628	2	JC2493	neuron derived orp
104	86	4.8	1117	2	T11667	probable RNA helic
105	85.5	4.8	3194	2	D71917	toxin-like outer m
106	85.5	4.8	5369	2	T44807	mycosubtilin synth
107	85	4.8	286	2	B70722	hypothetical prote
108	85	4.8	332	2	C83423	conserved hypothet
109	85	4.8	384	2	A86324	protein F14D16.19
110	85	4.8	2481	2	A43908	fibronectin - Afri
111	84.5	4.7	263	2	JC5283	proopiomelanocorti
112	84.5	4.7	269	2	T16487	hypothetical prote
113	84.5	4.7	318	2	T33874	hypothetical prote
114	84.5	4.7	326	2	C97231	D-lactate dehydrog
115	84.5	4.7	438	2	T45602	glucosyltransferas
116	84.5	4.7	594	2	F98150	probable gamma-glu
117	84.5	4.7	594	2	AF3137	gamma-glutamyltran
118	84.5	4.7	874	4	GNHUER	retrovirus-related
119	84.5	4.7	1299	1	S06119	membrane protein p
120	84.5	4.7	1756	2	S45867	TyB protein - yeas
121	84	4.7	322	2	T23758	hypothetical prote
122	84	4.7	2825	2	I54352	neurofibromin - mo
123	83.5	4.7	307	2	A26294	uncoupling protein
124	83.5	4.7	312	2	T36986	probable ribosylgl
125	83.5	4.7	389	2	B82479	D-alanyl-D-alanine
126	83.5	4.7	758	2	S62432	major facilitator
127	83.5	4.7	1011	2	T40851	hypothetical prote
128	83.5	4.7	1172	2	T00065	hypothetical prote
129	83.5	4.7	1187	1	TVHUY2	protein-tyrosine k
130	83	4.7	362	2	T08813	transcription fact
131	83	4.7	498	2	T37527	probable allantoat
132	83	4.7	791	2	A82291	c-di-GMP phosphodi
133	83	4.7	1471	2	B48218	neurexin III-alpha
134	83	4.7	1755	2	S69949	TyB protein - yeas
135	83	4.7	1755	2	S69839	TyB protein - yeas
136	82.5	4.6	291	1	JN0631	protein kinase (EC
137	82.5	4.6	307	2	S34268	uncoupling protein
138	82.5	4.6	661	2	S21221	hemocyanin chain c
139	82.5	4.6	838	2	F84100	preprotein translo
140	82.5	4.6	912	2	G96830	hypothetical prote
141	82.5	4.6	1749	2	S69972	TyB protein - yeas
142	82.5	4.6	1755	2	S69975	TyB protein - yeas
143	82.5	4.6	1755	2	S69866	TyB protein - yeas
144	82.5	4.6	1755	2	S69963	TyB protein - yeas
145	82.5	4.6	1755	2	S50663	TyB protein - yeas
146	82.5	4.6	1755	2	S50641	TyB protein YER138
147	82.5	4.6	1755	2	S57047	TyB protein - yeas
148	82.5	4.6	1755	2	S69845	TyB protein - yeas
149	82.5	4.6	1755	2	S69838	TyB protein - yeas
150	82.5	4.6	1755	2	S61763	TyB protein - yeas
151	82.5	4.6	1755	2	S57045	TyB protein - yeas
152	82.5	4.6	1755	2	S69980	TyB protein - yeas
153	82.5	4.6	1755	2	S70298	TyB protein - yeas
154	82.5	4.6	1755	2	S69982	TyB protein - yeas
155	82.5	4.6	1756	2	S69983	TyB protein - yeas
156	82.5	4.6	1793	2	S52601	TyB protein - yeas
157	82	4.6	344	2	E75259	N-acetylmuramoyl-L
158	82	4.6	429	2	F71896	hypothetical prote
159	82	4.6	667	2	S66017	formate dehydrogen
160	82	4.6	977	2	I52657	seizure-related pr
161	82	4.6	1239	1	A32579	neuroglian - fruit
162	82	4.6	1442	2	S72441	protein-tyrosine-p
163	82	4.6	2588	2	AI2136	peptide synthetase
164	81.5	4.6	358	2	G70026	conserved hypothet
165	81.5	4.6	519	2	T45038	hypothetical prote
166	81.5	4.6	606	2	T35378	probable peptide h
167	81.5	4.6	855	2	T17460	disease resistance
168	81.5	4.6	949	2	H97322	DNA/RNA helicase,
169	81.5	4.6	1076	2	T30842	serine-repeat anti
170	81	4.6	347	2	AD3167	hypothetical prote
171	81	4.6	359	2	T27200	hypothetical prote
172	81	4.6	401	2	B32433	VSG expression sit
173	81	4.6	449	2	C70846	probable metC prot
174	81	4.6	543	2	AG2096	hypothetical prote
175	81	4.6	791	2	T41573	hypothetical prote
176	81	4.6	984	1	A34076	protein-tyrosine k
177	81	4.6	1187	1	A53661	protein-tyrosine-p
178	81	4.6	1189	2	AH2154	WD-repeat protein
179	81	4.6	1604	2	S70227	TyB protein - yeas
180	81	4.6	1755	2	S69979	TyB protein - yeas
181	81	4.6	1755	2	S69957	TyB protein - yeas
182	81	4.6	1755	2	S69955	TyB protein - yeas
183	80.5	4.5	268	2	H70118	glucosamine-6-phos
184	80.5	4.5	306	2	D75562	N-acetyl-gamma-glu
185	80.5	4.5	509	2	JC6203	SP8 binding protei
186	80.5	4.5	694	2	T01134	probable protein k
187	80.5	4.5	775	2	I49759	hepatocyte growth
188	80.5	4.5	851	2	D86254	hypothetical prote
189	80.5	4.5	899	2	S24223	uridylyl transfera
190	80.5	4.5	1234	2	T31623	hypothetical prote
191	80	4.5	503	2	AD0293	conserved hypothet
192	80	4.5	545	2	JU0341	intercellular adhe
193	80	4.5	628	2	S35547	double-strand-brea
194	80	4.5	725	2	S13426	multidrug resistan
195	80	4.5	780	2	F84470	probable retroelem
196	80	4.5	814	2	S19658	microbial collagen
197	80	4.5	1235	2	S24109	phosphorylase kina
198	80	4.5	1516	2	T41235	probable myosin he
199	80	4.5	1755	2	S69951	TyB protein - yeas
200	79.5	4.5	512	2	F86193	hypothetical prote
201	79.5	4.5	528	2	B64760	propionate catabol
202	79.5	4.5	537	2	F70400	carbamoyl-phosphat
203	79.5	4.5	808	2	A41538	ATP-binding casset
204	79.5	4.5	855	2	T07015	Cf-4A protein - to
205	79.5	4.5	887	2	AG2806	alanyl-tRNA synthe
206	79.5	4.5	890	2	C96654	hypothetical prote
207	79.5	4.5	900	2	F97585	alanyl-tRNA synthe
208	79.5	4.5	905	2	B71562	probable oxoglutar
209	79.5	4.5	977	2	AC1963	DNA polymerase I [
210	79.5	4.5	1307	2	T30882	multidrug resistan
211	79.5	4.5	1357	2	T29265	hypothetical prote
212	79.5	4.5	1474	2	T20488	hypothetical prote
213	79	4.4	324	2	H83153	probable transcrip
214	79	4.4	368	2	A45831	MHC class I histoc
215	79	4.4	399	2	I78852	neurofibromatosis
216	79	4.4	431	2	T00698	methionyl aminopep
217	79	4.4	447	2	E82729	outer membrane pro
218	79	4.4	502	2	C98047	conserved hypothet
219	79	4.4	732	2	T19923	hypothetical prote
220	79	4.4	789	1	B4AGA6	virB4 protein prec
221	79	4.4	819	2	A47018	lectin-like adhesi
222	79	4.4	1195	2	C87691	hypothetical prote
223	79	4.4	1212	2	T00332	hypothetical prote
224	79	4.4	1281	2	T00346	hypothetical prote
225	79	4.4	1423	1	I37275	death-associated p
226	79	4.4	3119	2	I49729	HD protein - mouse
227	78.5	4.4	266	2	A87099	thymidylate syntha
228	78.5	4.4	379	2	F82963	hypothetical prote
229	78.5	4.4	398	2	AE1082	B. subtilis YukC p
230	78.5	4.4	398	2	AF1439	B. subtilis YukC p
231	78.5	4.4	436	2	A53568	methylcrotonoyl-Co
232	78.5	4.4	448	1	VHIHBC	nucleocapsid prote
233	78.5	4.4	448	2	JQ1173	nucleocapsid prote
234	78.5	4.4	479	2	S30057	dihydrolipoamide d
235	78.5	4.4	512	2	H81847	hypothetical prote
236	78.5	4.4	537	2	AH1277	probable transport
237	78.5	4.4	609	2	AB0500	glutamine-fructose
238	78.5	4.4	675	2	B64646	polyphosphate kina
239	78.5	4.4	772	2	A55004	transcription fact
240	78.5	4.4	772	2	I50463	protein kinase - c
241	78.5	4.4	773	2	F90537	lipoprotein [impor
242	78.5	4.4	1311	2	G86471	unknown protein [i
243	78.5	4.4	2397	1	A55535	versican precursor
244	78	4.4	333	2	F85804	integrase for prop
245	78	4.4	333	2	A90956	probable integrase
246	78	4.4	354	2	E97128	magnesium and coba
247	78	4.4	370	2	JC2204	MAPK-activated pro
248	78	4.4	386	2	AB1481	conserved hypothet

249	78	4.4	448	1	A60003	nucleocapsid prote
250	78	4.4	448	2	T17290	hypothetical prote
251	78	4.4	453	2	H87373	hypothetical prote
252	78	4.4	630	1	A46149	transcription fact
253	78	4.4	650	2	S59630	dystroglycan alpha
254	78	4.4	672	2	JC7676	hemocyanin A precu
255	78	4.4	807	2	F85647	probable outer mem
256	78	4.4	807	2	F64844	ycdS protein precu
257	78	4.4	807	2	F90787	probable outer mem
258	78	4.4	890	2	A98017	probable 2-compone
259	78	4.4	890	2	C85861	probable 2-compone
260	78	4.4	1044	2	H97186	glycosyltransferas
261	78	4.4	1075	2	G59434	KIAA0411 protein [
262	78	4.4	1176	2	S51408	hypothetical prote
263	77.5	4.4	171	2	T43946	transcription acti
264	77.5	4.4	280	2	E87652	conserved hypothet
265	77.5	4.4	394	1	S77216	hypothetical prote
266	77.5	4.4	509	2	S08059	alpha-globulin typ
267	77.5	4.4	516	2	E81092	hypothetical prote
268	77.5	4.4	566	2	F85889	hypothetical prote
269	77.5	4.4	566	2	C91045	nitrate/nitrite se
270	77.5	4.4	631	2	T07670	probable protein k
271	77.5	4.4	716	1	A40332	macrophage-stimula
272	77.5	4.4	788	2	AG0786	secreted effector
273	77.5	4.4	826	2	B36203	iron-responsive el
274	77.5	4.4	944	1	S48821	probable membrane
275	77.5	4.4	952	2	B57238	iron-responsive el
276	77.5	4.4	1428	1	ISBYT2	DNA topoisomerase
277	77	4.3	268	2	A83651	hypothetical prote
278	77	4.3	337	2	C75287	hypothetical prote
279	77	4.3	376	2	A84840	probable strictosi
280	77	4.3	403	1	H64463	hypothetical prote
281	77	4.3	412	2	H84202	starvation sensing
282	77	4.3	502	2	B84411	probable carboxype
283	77	4.3	529	2	T23181	hypothetical prote
284	77	4.3	657	1	BHLOA	hemocyanin chain a
285	77	4.3	677	2	S65573	phosphate-specific
286	77	4.3	717	2	H84057	pullulanase amyX [
287	77	4.3	747	2	F83527	GTP pyrophosphokin
288	77	4.3	773	2	T00502	probable receptor-
289	77	4.3	829	2	AG0869	probable outer mem
290	77	4.3	1191	2	S70963	pyruvate (flavodox
291	77	4.3	1475	2	A60026	cell communication
292	77	4.3	1755	2	S69960	TyB protein - yeas
293	77	4.3	3869	2	A48205	All-1 protein +GTE
294	77	4.3	4096	2	A57099	DNA-activated prot
295	76.5	4.3	245	2	H86151	hypothetical prote
296	76.5	4.3	255	2	T45772	hypothetical prote
297	76.5	4.3	335	2	T39425	hypothetical prote
298	76.5	4.3	361	2	H70368	conserved hypothet
299	76.5	4.3	366	2	E84265	hypothetical prote
300	76.5	4.3	390	2	G75591	oxidoreductase, sh
301	76.5	4.3	460	1	A34180	sulfite oxidase (E
302	76.5	4.3	486	2	S76523	serine-type D-Ala-
303	76.5	4.3	649	2	A57352	GPI-anchored prote
304	76.5	4.3	653	2	F70864	probable oxidoredu
305	76.5	4.3	662	2	T25802	hypothetical prote
306	76.5	4.3	701	2	C84972	hypothetical prote
307	76.5	4.3	826	2	T33796	hypothetical prote
308	76.5	4.3	830	2	T41509	serine/threonine-p
309	76.5	4.3	943	2	JC4081	sucrase/fructanase
310	76.5	4.3	1896	2	T08851	Down syndrome cell
311	76	4.3	223	2	AH0409	conserved hypothet
312	76	4.3	355	2	C83850	gamma-D-glutamyl-L
313	76	4.3	368	1	S58437	probable phosphata
314	76	4.3	401	2	S74767	hypothetical prote
315	76	4.3	527	2	AE2380	type I restriction
316	76	4.3	583	2	AI1510	C-terminal domain
317	76	4.3	588	2	C95252	L-fucose isomerase
318	76	4.3	590	2	A45772	nitrate-inducible
319	76	4.3	598	2	D95207	oligoendopeptidase
320	76	4.3	598	2	D98072	oligoendopeptidase
321	76	4.3	618	2	B87564	conserved hypothet
322	76	4.3	719	2	C88216	protein B0495.2 [i
323	76	4.3	930	2	T32017	hypothetical prote
324	76	4.3	1042	2	S76045	hypothetical prote
325	76	4.3	1073	1	S56822	SKI2 protein homol
326	76	4.3	2201	2	AH0095	probable sideropho
327	76	4.3	2649	2	A40937	bullous pemphigoid
328	75.5	4.2	246	2	C72578	probable flagellin
329	75.5	4.2	264	1	CTMKP	corticotropin / li
330	75.5	4.2	266	2	AG0320	probable glucosami
331	75.5	4.2	453	2	T42428	mitochondrial proc
332	75.5	4.2	492	2	S65238	probable membrane
333	75.5	4.2	499	2	A28997	triacylglycerol li
334	75.5	4.2	504	1	JH0659	cholesterol 7alpha
335	75.5	4.2	546	1	VGNZRL	cell fusion glycop
336	75.5	4.2	589	2	T49653	related to SLY41 p
337	75.5	4.2	611	2	T44909	nifS-like protein
338	75.5	4.2	675	2	F71935	polyphosphate kina
339	75.5	4.2	843	2	T46717	hypothetical prote
340	75.5	4.2	1132	2	T49403	related to protein
341	75.5	4.2	1188	2	E89896	chromosome segrega
342	75.5	4.2	1659	2	T15666	hypothetical prote
343	75	4.2	331	2	T44902	probable riboflavi
344	75	4.2	393	2	S51321	mitogen-activated
345	75	4.2	420	2	C82910	histidyl-tRNA synt
346	75	4.2	437	2	B70540	probable adenosylm
347	75	4.2	449	2	B69398	hypothetical prote
348	75	4.2	462	2	G70015	conserved hypothet
349	75	4.2	467	2	B81095	conserved hypothet
350	75	4.2	503	2	C71550	hypothetical prote
351	75	4.2	572	2	D85504	proline tRNA synth
352	75	4.2	572	2	D90653	proline tRNA synth
353	75	4.2	666	2	T24170	hypothetical prote
354	75	4.2	706	2	T49899	zinc finger transc
355	75	4.2	720	2	T52564	Mre11 protein homo
356	75	4.2	789	2	F82426	probable phosphogl
357	75	4.2	822	2	S26872	DNA-directed RNA p
358	75	4.2	889	2	H96606	hypothetical prote
359	75	4.2	890	2	F64991	yojN protein - Esc
360	75	4.2	895	2	S20582	dystrophin-associa
361	75	4.2	1060	2	S63252	hypothetical prote
362	75	4.2	1087	2	T30844	serine-repeat anti
363	75	4.2	1089	2	T21582	hypothetical prote
364	75	4.2	1123	2	AD2045	hypothetical prote
365	75	4.2	1283	2	T49804	hypothetical prote
366	75	4.2	2819	2	T09080	probable chloroqui
367	75	4.2	4717	2	T41581	hypothetical coile
368	74.5	4.2	249	2	G81218	bioH protein, prob
369	74.5	4.2	258	1	A64451	probable 3-isoprop
370	74.5	4.2	290	2	T05009	hypothetical prote
371	74.5	4.2	312	2	C81795	probable hydrolase
372	74.5	4.2	342	2	S61978	hypothetical prote
373	74.5	4.2	387	2	T09839	oleate 12-hydroxyl
374	74.5	4.2	391	2	A42973	serum protein MSE5
375	74.5	4.2	396	2	S39793	MAPK-activated pro
376	74.5	4.2	457	2	T50402	probable mitochond
377	74.5	4.2	472	2	H91056	probable periplasm
378	74.5	4.2	472	2	D85901	probable periplasm
379	74.5	4.2	481	2	S77135	hypothetical prote
380	74.5	4.2	522	2	G02522	sorting nexin 1 -
381	74.5	4.2	537	2	AH1640	probable transport
382	74.5	4.2	580	2	T28725	hypothetical prote
383	74.5	4.2	678	2	S54308	DNA binding protei
384	74.5	4.2	688	2	JC2248	polyprotein - swee
385	74.5	4.2	710	2	S60042	phenylalanine ammo
386	74.5	4.2	729	2	AH2857	anthranilate synth
387	74.5	4.2	729	2	F97634	anthranilate synth
388	74.5	4.2	733	2	T03117	glycoprotein H - a
389	74.5	4.2	736	1	S31809	translation elonga
390	74.5	4.2	747	2	A69591	asparagine synthet
391	74.5	4.2	816	2	T48123	hypothetical prote
392	74.5	4.2	860	1	C35905	endopeptidase Clp
393	74.5	4.2	909	2	H87729	protein Y23H5A.7 [
394	74.5	4.2	1200	2	S77524	chromosome segrega

395	74.5	4.2	1274	2	S55050	cardiac myosin-bin
396	74.5	4.2	2013	2	AD1129	probable peptidogl
397	74	4.2	146	2	C69131	ribosomal protein
398	74	4.2	182	2	S33990	finger protein ZNF
399	74	4.2	194	2	H71939	hypothetical prote
400	74	4.2	246	2	I53855	neurofibromatosis
401	74	4.2	277	2	C97073	transcription anti
402	74	4.2	296	2	S72444	DNA-binding protei
403	74	4.2	307	2	F87952	protein T26E3.4 [i
404	74	4.2	313	1	FOVDA	gag polyprotein -
405	74	4.2	357	2	S75954	hypothetical prote
406	74	4.2	362	1	KHRZOG	oryzain (EC 3.4.22
407	74	4.2	393	2	H81745	conserved hypothet
408	74	4.2	409	2	B71198	hypothetical prote
409	74	4.2	460	2	JL0145	interleukin-6 rece
410	74	4.2	521	2	S67210	probable membrane
411	74	4.2	548	2	S50557	hypothetical prote
412	74	4.2	588	2	T07085	probable lysine-tR
413	74	4.2	593	2	I51213	drebrin - chicken
414	74	4.2	638	2	I39196	amiloride sensitiv
415	74	4.2	675	2	AH0979	alpha-amylase (EC
416	74	4.2	717	2	T27066	hypothetical prote
417	74	4.2	717	2	T27067	hypothetical prote
418	74	4.2	757	2	A39283	gamma-glutamyl car
419	74	4.2	772	2	T26330	hypothetical prote
420	74	4.2	805	2	S73374	phenylalanine-tRNA
421	74	4.2	989	2	I56333	apolipoprotein B -
422	74	4.2	1108	2	I59385	guanylate cyclase
423	74	4.2	1232	2	T43027	neural cell adhesi
424	74	4.2	1388	2	E82533	RNA polymerase bet
425	74	4.2	1520	2	S46444	myosin MYA1, class
426	74	4.2	1822	2	S44849	K12H4.8 protein -
427	73.5	4.1	287	2	S73712	cytochrome-c oxida
428	73.5	4.1	318	2	AD0575	ferrienterobactin-
429	73.5	4.1	365	2	S46357	casein kinase-1 ho
430	73.5	4.1	379	2	E75460	conserved hypothet
431	73.5	4.1	387	2	H69971	spore coat protein
432	73.5	4.1	411	2	D87014	conserved hypothet
433	73.5	4.1	425	2	B96750	hypothetical prote
434	73.5	4.1	448	1	A56018	transcription fact
435	73.5	4.1	448	1	VHIHN1	nucleocapsid prote
436	73.5	4.1	449	1	S30205	transcription fact
437	73.5	4.1	451	1	A40168	transcription fact
438	73.5	4.1	461	2	I39160	dystonin isoform 1
439	73.5	4.1	462	2	T42679	hypothetical prote
440	73.5	4.1	468	2	G81180	sensor histidine k
441	73.5	4.1	511	1	XNDOU	UTP-glucose-1-phos
442	73.5	4.1	511	2	G96672	hypothetical prote
443	73.5	4.1	511	2	I49290	dystonin - mouse (
444	73.5	4.1	528	2	C85527	regulator for prp
445	73.5	4.1	528	2	H90676	regulator for prp
446	73.5	4.1	555	2	T30349	structural protein
447	73.5	4.1	566	2	D65022	nitrate/nitrite se
448	73.5	4.1	572	2	C96024	probable glycerone
449	73.5	4.1	590	2	AI0174	probable Lon prote
450	73.5	4.1	610	2	F95898	probable nodulatio
451	73.5	4.1	664	2	A56695	notch2 protein hom
452	73.5	4.1	673	2	T48701	hypothetical prote
453	73.5	4.1	686	2	I49298	dystonin isoform 2
454	73.5	4.1	872	2	E71852	valine-tRNA ligase
455	73.5	4.1	925	2	S27920	nuclear antigen EB
456	73.5	4.1	942	2	T38649	hypothetical homeo
457	73.5	4.1	1041	2	C83548	hypothetical prote
458	73.5	4.1	1129	2	T25635	hypothetical prote
459	73.5	4.1	1175	2	T25634	hypothetical prote
460	73.5	4.1	1755	2	S69969	TyB protein - yeas
461	73.5	4.1	1943	2	B64596	toxin-like outer m
462	73.5	4.1	2515	2	A41519	posterior-group pr
463	73.5	4.1	2541	2	T29340	hypothetical prote
464	73.5	4.1	2869	2	T18518	apolipoprotein(a)
465	73.5	4.1	3724	2	T18427	hypothetical prote
466	73	4.1	224	1	A33861	trans-activating t
467	73	4.1	265	2	C70963	hypothetical prote
468	73	4.1	268	2	H83760	hypothetical prote
469	73	4.1	297	2	AH3149	hypothetical prote
470	73	4.1	297	2	A98138	hypothetical prote
471	73	4.1	333	2	JC7139	endo-1,4-beta-xyla
472	73	4.1	334	2	S77413	hypothetical prote
473	73	4.1	383	2	T10480	Delta12 fatty acid
474	73	4.1	391	2	A75451	probable soluble h
475	73	4.1	462	1	S00552	mitochondrial proc
476	73	4.1	547	2	S44841	K06H7.1 protein -
477	73	4.1	552	1	G69652	endopeptidase La (
478	73	4.1	602	2	S36475	E1 protein - human
479	73	4.1	620	2	S56790	probable membrane
480	73	4.1	700	2	T43469	hypothetical prote
481	73	4.1	705	2	S51635	fibroblast growth
482	73	4.1	810	2	B71639	virb4 protein prec
483	73	4.1	884	1	IJMSCE	E-cadherin precurs
484	73	4.1	884	2	S34438	uvomorulin - mouse
485	73	4.1	913	2	T51923	related to heterok
486	73	4.1	943	2	G83448	2-oxoglutarate deh
487	73	4.1	992	2	E75093	translation initia
488	73	4.1	1034	2	S50917	aminomethyltransfe
489	73	4.1	1044	2	H71049	translation initia
490	73	4.1	1069	2	T00377	KIAA0642 protein -
491	73	4.1	1124	2	B84742	probable receptor-
492	73	4.1	1290	2	T00018	period protein hom
493	73	4.1	1311	2	T08986	hypothetical prote
494	73	4.1	1339	2	JC5508	DNA-directed DNA p
495	73	4.1	2529	2	A56923	transcription fact
496	73	4.1	4957	2	T03455	ALR protein - huma
497	73	4.1	5232	2	A45086	HC-toxin synthetas
498	73	4.1	5262	2	T03454	ALR protein - huma
499	72.5	4.1	112	2	S50515	hypothetical prote
500	72.5	4.1	210	2	I49294	CD7 antigen - mous
501	72.5	4.1	255	2	T06811	dehydrin 2 - garde
502	72.5	4.1	286	2	E89875	FolD bifunctional
503	72.5	4.1	301	2	E83865	hypothetical prote
504	72.5	4.1	327	2	AH0983	dipeptide transpor
505	72.5	4.1	354	2	S62086	hrpQ protein - Pse
506	72.5	4.1	366	2	B41565	env polyprotein -
507	72.5	4.1	366	2	F72062	hypothetical prote
508	72.5	4.1	366	2	A86561	CT449 hypothetical
509	72.5	4.1	372	2	AE1370	S. pyogenes RofA r
510	72.5	4.1	376	2	S55275	fibromodulin precu
511	72.5	4.1	399	2	AE2616	hypothetical prote
512	72.5	4.1	402	2	E97398	probable oxygen-in
513	72.5	4.1	490	2	T43184	DEAD box ATP-depen
514	72.5	4.1	492	1	CSSY	catalase (EC 1.11.
515	72.5	4.1	493	2	A83581	probable c-type cy
516	72.5	4.1	504	1	A30247	cytochrome P450 2D
517	72.5	4.1	565	2	T39863	zinc finger protei
518	72.5	4.1	683	2	D83481	probable oligopept
519	72.5	4.1	692	2	AE0218	flagellar biosynth
520	72.5	4.1	700	1	S01991	transforming prote
521	72.5	4.1	727	2	S54512	hypothetical prote
522	72.5	4.1	756	2	S67433	hypothetical prote
523	72.5	4.1	846	2	H70599	hypothetical prote
524	72.5	4.1	899	2	S17546	furin (EC 3.4.21.7
525	72.5	4.1	908	2	G72085	2-oxoglutarate deh
526	72.5	4.1	908	2	H86537	oxoglutarate dehyd
527	72.5	4.1	922	2	B82168	insulinase-type zi
528	72.5	4.1	1157	1	GNLJLK	pol polyprotein -
529	72.5	4.1	1269	2	S35366	furin (EC 3.4.21.7
530	72.5	4.1	1342	1	S32680	DNA-directed RNA p
531	72.5	4.1	1345	2	S46817	hypothetical prote
532	72.5	4.1	1378	2	AB2817	DNA-directed RNA p
533	72.5	4.1	1411	2	C97595	RNA polymerase bet
534	72.5	4.1	1434	2	T30172	transmembrane prot
535	72.5	4.1	1537	2	F86509	CT147 hypothetical
536	72.5	4.1	1537	2	C81558	conserved hypothet
537	72.5	4.1	1537	2	H72112	ct147 hypothetical
538	72.5	4.1	1916	2	S46157	RIF1 protein - yea
539	72.5	4.1	3135	2	A48584	transmission block
540	72.5	4.1	6831	2	A88852	protein unc-22 [im

541	72.5	4.1	6839	2	S57242	twitchin [similari
542	72.5	4.1	7160	2	T27935	hypothetical prote
543	72	4.0	131	2	T07768	profilin 1 - soybe
544	72	4.0	258	2	A48820	homeobox protein (
545	72	4.0	272	2	H87075	probable conserved
546	72	4.0	278	2	A42400	probable transcrip
547	72	4.0	294	2	H85785	hypothetical prote
548	72	4.0	301	2	T33702	hypothetical prote
549	72	4.0	326	2	E84812	hypothetical prote
550	72	4.0	329	2	T47448	sulfotransferase-1
551	72	4.0	346	2	D90937	hypothetical prote
552	72	4.0	361	2	T21977	hypothetical prote
553	72	4.0	392	2	A65086	probable hydrogena
554	72	4.0	397	2	T35289	probable multifunc
555	72	4.0	400	1	A48081	mitogen-activated
556	72	4.0	400	1	JS0349	exonuclease (EC 3.
557	72	4.0	400	2	H90684	ATP-dependent dsDN
558	72	4.0	400	2	D85535	ATP-dependent dsDN
559	72	4.0	401	1	I52829	mitogen-activated
560	72	4.0	402	2	S29757	nitrogenase cofact
561	72	4.0	408	2	AD2473	hypothetical prote
562	72	4.0	453	2	S00967	hypothetical prote
563	72	4.0	478	2	A86580	DNA gyrase subunit
564	72	4.0	478	2	D72043	DNA gyrase, chain
565	72	4.0	550	1	A40449	protein-tyrosine-p
566	72	4.0	551	2	T22121	hypothetical prote
567	72	4.0	556	2	B82882	conserved hypothet
568	72	4.0	561	1	HMIV49	hemagglutinin prec
569	72	4.0	576	2	T05843	peptide transport
570	72	4.0	578	2	E70645	hypothetical prote
571	72	4.0	583	2	AH1151	glycerophosphoryl
572	72	4.0	586	1	VGVNBF	nonstructural glyc
573	72	4.0	588	2	A99717	L-fucose isomerase
574	72	4.0	620	2	T32966	hypothetical prote
575	72	4.0	656	2	S61097	hypothetical prote
576	72	4.0	657	1	BHLOB	hemocyanin chain b
577	72	4.0	691	2	S78135	NADH2 dehydrogenas
578	72	4.0	702	2	H90757	probable oxidoredu
579	72	4.0	702	2	F85621	probable oxidoredu
580	72	4.0	702	2	C64835	hypothetical prote
581	72	4.0	724	2	T25700	mechanosensory pro
582	72	4.0	749	2	E86774	hypothetical prote
583	72	4.0	810	1	A33380	interleukin-4 rece
584	72	4.0	837	2	AD0159	outer membrane ush
585	72	4.0	845	2	T07039	Hcr9-0 protein - t
586	72	4.0	851	2	S12159	env protein - huma
587	72	4.0	912	2	C71004	probable ATP-depen
588	72	4.0	925	2	T19361	hypothetical prote
589	72	4.0	939	2	C81730	metalloproteinase,
590	72	4.0	1061	2	T18085	DNA topoisomerase
591	72	4.0	1083	2	S54293	regulator protein
592	72	4.0	1180	2	T20773	hypothetical prote
593	72	4.0	1240	1	VHWVEV	structural polypro
594	72	4.0	1241	2	S26373	genome polyprotein
595	72	4.0	1242	2	A56605	structural polypro
596	72	4.0	1242	2	S72350	structural polypro
597	72	4.0	1244	2	S76102	hypothetical prote
598	72	4.0	1281	2	G83405	hypothetical prote
599	72	4.0	1608	2	T13216	minor capsid prote
600	72	4.0	2108	2	H70819	probable polyketid
601	72	4.0	2199	2	T40008	Cdc20p - fission y
602	72	4.0	2279	2	T42531	acetyl-CoA carboxy
603	72	4.0	4549	2	T20771	hypothetical prote
604	72	4.0	4667	2	T20774	hypothetical prote
605	71.5	4.0	273	2	D71221	probable morphine
606	71.5	4.0	276	2	G83304	chloroperoxidase p
607	71.5	4.0	287	2	S69774	transcription init
608	71.5	4.0	300	2	JQ2220	hydroxyproline-ric
609	71.5	4.0	306	2	A32446	uncoupling protein
610	71.5	4.0	324	2	E83320	conserved hypothet
611	71.5	4.0	329	2	AF2369	hypothetical prote
612	71.5	4.0	357	2	D64013	hypothetical prote
613	71.5	4.0	388	2	F97331	alpha/beta superfa
614	71.5	4.0	393	2	D70539	probable citrate s
615	71.5	4.0	393	2	D90533	nitrogen fixation
616	71.5	4.0	394	2	F82491	ferrisiderophore r
617	71.5	4.0	402	2	AD2677	hypothetical prote
618	71.5	4.0	402	2	B97459	sulfate-binding pr
619	71.5	4.0	419	2	D45045	phycobiliprotein h
620	71.5	4.0	426	2	B53580	neurexin III beta
621	71.5	4.0	446	2	T09568	protein kinase p58
622	71.5	4.0	450	2	B97292	probable ATP-depen
623	71.5	4.0	463	2	C87306	cysteinyl-tRNA syn
624	71.5	4.0	468	2	E81924	probable two-compo
625	71.5	4.0	472	2	E65033	hypothetical 53.2
626	71.5	4.0	492	2	S17493	catalase (EC 1.11.
627	71.5	4.0	494	1	CSPM	catalase (EC 1.11.
628	71.5	4.0	514	2	D89775	hypothetical prote
629	71.5	4.0	519	2	S23796	modifier-3 protein
630	71.5	4.0	536	2	T41652	hypothetical prote
631	71.5	4.0	566	2	AD0816	nitrate/nitrite se
632	71.5	4.0	583	2	I50518	DNA binding protei
633	71.5	4.0	591	2	T25636	hypothetical prote
634	71.5	4.0	593	2	T04446	hypothetical prote
635	71.5	4.0	594	2	F82895	hypothetical prote
636	71.5	4.0	638	2	T05606	protein kinase hom
637	71.5	4.0	666	2	I52648	class A helix-loop
638	71.5	4.0	677	2	JC7202	glucan 1,4-alpha-m
639	71.5	4.0	679	2	S37842	hypothetical prote
640	71.5	4.0	708	2	T25725	hypothetical prote
641	71.5	4.0	712	1	VCLJS4	env polyprotein pr
642	71.5	4.0	735	2	T45059	hypothetical prote
643	71.5	4.0	746	2	S34656	amine oxidase (cop
644	71.5	4.0	758	2	JC2521	endothelin convert
645	71.5	4.0	770	2	JC4136	endothelin convert
646	71.5	4.0	770	2	T51024	related to C2H2 zi
647	71.5	4.0	859	1	VCLJCT	env polyprotein pr
648	71.5	4.0	874	2	D75307	leucyl-tRNA synthe
649	71.5	4.0	880	2	E69680	DNA polymerase I p
650	71.5	4.0	924	2	T06636	hypothetical prote
651	71.5	4.0	932	2	AB0003	DNA-directed DNA p
652	71.5	4.0	954	2	E86174	protein F19P19.26
653	71.5	4.0	1165	2	A46180	adenylyl cyclase t
654	71.5	4.0	1194	2	C59436	KIAA1391 protein [
655	71.5	4.0	1231	2	T30841	serine-repeat anti
656	71.5	4.0	1246	2	S56752	helicase SKI2W - h
657	71.5	4.0	1396	2	S36851	L-shaped tail fibe
658	71.5	4.0	1571	2	T14155	zinc finger protei
659	71.5	4.0	1616	2	T16600	vitellogenin vit-1
660	71.5	4.0	2021	2	A84771	similar to ch-TOG
661	71.5	4.0	3144	2	S64791	VPS13 protein - ye
662	71.5	4.0	26926	1	I38344	titin, cardiac mus
663	71	4.0	151	2	S30459	env protein - huma
664	71	4.0	198	2	D70509	hypothetical prote
665	71	4.0	198	2	S14456	XA-1 protein precu
666	71	4.0	205	2	S33693	lexA protein - Pro
667	71	4.0	250	2	D39534	MADS box protein A
668	71	4.0	268	2	T15693	hypothetical prote
669	71	4.0	282	2	S43577	C28A5.4 protein (c
670	71	4.0	296	2	E83292	conserved hypothet
671	71	4.0	329	2	T10444	peroxidase (EC 1.1
672	71	4.0	370	2	H84351	hypothetical prote
673	71	4.0	376	2	A36978	MAP kinase mpk-1 (
674	71	4.0	384	2	T38544	probable exopolyph
675	71	4.0	386	2	G81729	succinyl-CoA synth
676	71	4.0	391	2	E83840	hypothetical prote
677	71	4.0	392	2	H91113	hypothetical prote
678	71	4.0	392	2	H85958	hypothetical prote
679	71	4.0	394	2	S33635	mitogen-activated
680	71	4.0	397	2	AC3521	replication protei
681	71	4.0	414	2	PS0323	von Willebrand fac
682	71	4.0	428	1	AJRZQD	glutamate-ammonia
683	71	4.0	444	2	A36977	MAP kinase sur-1 (
684	71	4.0	468	2	E96673	similar to CGI-13
685	71	4.0	469	2	A55484	p52(Shc) protein -
686	71	4.0	530	2	T48627	hypothetical prote

687	71	4.0	538	2	S29521	casein kinase I ho
688	71	4.0	554	2	T48483	hypothetical prote
689	71	4.0	564	2	T12489	hypothetical prote
690	71	4.0	570	2	AC2886	hypothetical prote
691	71	4.0	570	2	H97661	probable hemin-bin
692	71	4.0	577	2	A37779	histocompatibility
693	71	4.0	604	1	D46113	glycoprotein E pre
694	71	4.0	635	2	S36718	phosphoprotein pho
695	71	4.0	643	2	H83635	conserved hypothet
696	71	4.0	660	2	S73597	lactococcin transp
697	71	4.0	680	2	T43077	probable relaxase
698	71	4.0	707	2	T40070	origin recognition
699	71	4.0	713	2	JC6012	glutamine-fructose
700	71	4.0	738	2	S59842	probable membrane
701	71	4.0	798	2	T19864	hypothetical prote
702	71	4.0	841	2	S69563	suppressor protein
703	71	4.0	867	2	T27136	hypothetical prote
704	71	4.0	877	2	C64809	ybgB protein - Esc
705	71	4.0	885	2	AG3350	alanine-tRNA ligas
706	71	4.0	895	2	I54343	dystroglycan - hum
707	71	4.0	980	2	G75523	probable cell divi
708	71	4.0	1015	2	A42915	type II cAMP-depen
709	71	4.0	1023	2	T30257	IgG Fc binding pro
710	71	4.0	1054	2	S77008	cation efflux syst
711	71	4.0	1086	2	T05407	hypothetical prote
712	71	4.0	1203	2	T51029	related to pathway
713	71	4.0	1217	2	D88996	protein C17B7.7 [i
714	71	4.0	1239	2	S74355	hypothetical prote
715	71	4.0	1291	2	T22382	hypothetical prote
716	71	4.0	1360	2	T12064	DNA binding protei
717	71	4.0	1378	1	I48751	protein-tyrosine k
718	71	4.0	1378	2	T30173	zinc finger protei
719	71	4.0	1400	1	I38185	protein-tyrosine k
720	71	4.0	1403	2	S24548	homeotic protein p
721	71	4.0	1573	2	T50113	3-dehydroquinate s
722	71	4.0	1874	1	JQ0533	genome polyprotein
723	71	4.0	2319	2	A47004	coagulation factor
724	71	4.0	3144	2	A46068	Huntington disease
725	71	4.0	3707	2	S18252	heparan sulfate pr
726	71	4.0	4574	2	G02520	plectin - human
727	70.5	4.0	193	1	H69398	probable phosphoes
728	70.5	4.0	214	2	T49381	hypothetical prote
729	70.5	4.0	227	2	E75499	GGDEF family prote
730	70.5	4.0	263	2	C70881	probable thyA prot
731	70.5	4.0	296	1	G71196	probable ribokinas
732	70.5	4.0	297	1	WJMS29	homeotic protein H
733	70.5	4.0	306	2	E64348	tyrosine-tRNA liga
734	70.5	4.0	326	2	T38706	hypothetical prote
735	70.5	4.0	346	2	E86715	transcription regu
736	70.5	4.0	349	2	S08278	macrophage scaveng
737	70.5	4.0	383	2	S24156	polygalacturonase
738	70.5	4.0	388	2	S49445	RING finger protei
739	70.5	4.0	402	1	BOHUS	sex steroid-bindin
740	70.5	4.0	418	2	T34606	probable fumarylac
741	70.5	4.0	421	2	T20827	hypothetical prote
742	70.5	4.0	442	2	B71083	hypothetical prote
743	70.5	4.0	444	2	AE3564	l-gulonolactone ox
744	70.5	4.0	449	2	F72681	probable cytosine-
745	70.5	4.0	453	2	S08276	macrophage scaveng
746	70.5	4.0	455	2	T04448	hypothetical prote
747	70.5	4.0	479	2	H83590	dihydropyrimidinas
748	70.5	4.0	490	2	T48608	hypothetical prote
749	70.5	4.0	499	2	F70418	conserved hypothet
750	70.5	4.0	499	2	S73810	transcription init
751	70.5	4.0	506	2	T41760	UDP-glucosyl trans
752	70.5	4.0	521	2	E82377	ABC transporter, p
753	70.5	4.0	603	2	B86215	protein T6D22.10 [
754	70.5	4.0	603	2	T39674	hypothetical dnaJ
755	70.5	4.0	615	2	D83558	transport protein
756	70.5	4.0	625	2	S71930	neuron-derived rec
757	70.5	4.0	658	2	D81099	membrane-bound lyt
758	70.5	4.0	658	2	D81842	probable membrane
759	70.5	4.0	667	2	A41311	transcription fact
760	70.5	4.0	679	2	T08430	GTP-binding membra
761	70.5	4.0	691	2	D71430	hypothetical prote
762	70.5	4.0	708	2	T48022	hypothetical prote
763	70.5	4.0	734	1	S09156	diacylglycerol kin
764	70.5	4.0	782	2	T43277	host cell factor 1
765	70.5	4.0	823	2	A36378	probable transcrip
766	70.5	4.0	849	2	S61631	probable membrane
767	70.5	4.0	950	2	S27473	URBS1 protein - sm
768	70.5	4.0	969	2	AB3388	soluble lytic mure
769	70.5	4.0	984	2	JN0658	restriction endonu
770	70.5	4.0	1091	2	C75585	carboxylase - Dein
771	70.5	4.0	1113	2	T14260	period protein Per
772	70.5	4.0	1212	2	T44236	hypothetical prote
773	70.5	4.0	1359	2	T10235	xanthine dehydroge
774	70.5	4.0	1784	2	C96615	hypothetical prote
775	70.5	4.0	2712	2	T05113	hypothetical prote
776	70.5	4.0	3844	2	T18402	asparagine/asparta
777	70.5	4.0	4848	2	T30289	pristinamycin I sy
778	70	3.9	151	2	S30458	env protein - huma
779	70	3.9	191	2	E86389	cauliflower [impor
780	70	3.9	204	2	S65795	superoxide dismuta
781	70	3.9	231	2	D72532	hypothetical prote
782	70	3.9	251	2	T45707	CHLOROPHYLL A-B BI
783	70	3.9	282	2	E96775	unknown protein F1
784	70	3.9	313	2	F64851	flagellar protein
785	70	3.9	313	2	C90811	flagellar basal bo
786	70	3.9	313	2	G85670	flagellar biosynth
787	70	3.9	316	2	D82857	hypothetical prote
788	70	3.9	345	2	AG0366	thiosulfate-bindin
789	70	3.9	360	2	S69063	probable membrane
790	70	3.9	372	2	F95870	conserved hypothet
791	70	3.9	373	2	A71690	hypothetical prote
792	70	3.9	385	2	C83871	hypothetical prote
793	70	3.9	385	2	C64708	conserved hypothet
794	70	3.9	385	2	F71046	probable ferredoxi
795	70	3.9	386	2	G71467	probable succinyl-
796	70	3.9	387	2	B64936	hypothetical prote
797	70	3.9	388	2	AC0137	succinate-CoA liga
798	70	3.9	388	2	E75163	hypothetical prote
799	70	3.9	395	2	A82283	vibriobactin-speci
800	70	3.9	399	2	H71810	hypothetical prote
801	70	3.9	403	2	S62979	hypothetical prote
802	70	3.9	410	2	T13531	hypothetical prote
803	70	3.9	427	2	T49122	hypothetical prote
804	70	3.9	477	2	H81845	hypothetical prote
805	70	3.9	479	1	YKBY	citrate (si)-synth
806	70	3.9	483	2	T03909	hypothetical prote
807	70	3.9	488	2	S74629	hypothetical prote
808	70	3.9	491	2	T38448	probable alpha-amy
809	70	3.9	491	2	JC1390	cyclin A - fruit f
810	70	3.9	501	2	S76581	hypothetical prote
811	70	3.9	508	2	T19350	hypothetical prote
812	70	3.9	522	1	I37037	involucrin - commo
813	70	3.9	543	2	A41211	early growth respo
814	70	3.9	547	2	T40314	hypothetical coile
815	70	3.9	566	1	HMIVT1	hemagglutinin prec
816	70	3.9	572	1	YPEC	proline-tRNA ligas
817	70	3.9	590	2	D69068	methyl coenzyme M
818	70	3.9	604	2	T41249	DEAD box ATP-depen
819	70	3.9	625	2	JC7362	Erc protein - rat
820	70	3.9	625	2	S48941	regulatory protein
821	70	3.9	628	2	C82039	conserved hypothet
822	70	3.9	644	2	S65302	hypothetical prote
823	70	3.9	645	2	C64979	molR_2 protein - E
824	70	3.9	648	2	S04832	glutenin high mole
825	70	3.9	660	2	S50383	gamma-glutamyltran
826	70	3.9	670	2	T49510	fibroin-3 related
827	70	3.9	770	2	S77523	hypothetical prote
828	70	3.9	776	2	A87330	sensory box histid
829	70	3.9	844	2	C91212	probable outer mem
830	70	3.9	844	2	C86058	probable fimbrial
831	70	3.9	885	2	S61189	probable membrane
832	70	3.9	888	2	D84824	probable DNA-direc

833	70	3.9	914	1	S07047	iodide peroxidase
834	70	3.9	994	1	MNWVM	nonstructural prot
835	70	3.9	1007	2	S48535	rho-type GTPase-ac
836	70	3.9	1012	2	T13603	probable N-methyl-
837	70	3.9	1015	2	B83627	probable RND efflu
838	70	3.9	1017	2	S64782	probable membrane
839	70	3.9	1044	2	T02615	probable glycine d
840	70	3.9	1072	2	T30846	serine-repeat anti
841	70	3.9	1102	2	C64477	glutamine-fructose
842	70	3.9	1172	2	D72482	probable antibioti
843	70	3.9	1208	2	T23467	hypothetical prote
844	70	3.9	1259	2	JC5523	transmembrane prot
845	70	3.9	1267	1	MWXR32	lambda 3 protein -
846	70	3.9	1375	2	F82336	DNA-directed RNA p
847	70	3.9	1398	2	T13741	hypothetical prote
848	70	3.9	1451	2	T33083	hypothetical prote
849	70	3.9	1633	2	JC5056	polybromo 1 - chic
850	70	3.9	1677	2	T14267	Xin protein, stage
851	70	3.9	2110	2	B44110	mycocerosate synth
852	70	3.9	2111	2	A70668	mycocerosate synth
853	70	3.9	2344	2	S64740	genome polyprotein
854	70	3.9	2971	2	T08026	hypothetical prote
855	69.5	3.9	131	2	T07773	profilin 2 - soybe
856	69.5	3.9	138	2	H72534	hypothetical prote
857	69.5	3.9	151	2	S30457	env protein - huma
858	69.5	3.9	189	2	T43766	hypothetical prote
859	69.5	3.9	213	2	T02697	hypothetical prote
860	69.5	3.9	259	2	AG2462	hypothetical prote
861	69.5	3.9	266	2	H82387	glucosamine-6-phos
862	69.5	3.9	272	2	S16325	homeotic protein A
863	69.5	3.9	273	2	C88429	protein ceh-43 [im
864	69.5	3.9	293	2	C83845	superoxide dismuta
865	69.5	3.9	312	2	JC5481	replication initia
866	69.5	3.9	333	2	T07009	omega-6 fatty acid
867	69.5	3.9	355	2	A45451	aryldialkylphospha
868	69.5	3.9	368	2	T41032	hypothetical wtf10
869	69.5	3.9	372	2	B72579	probable drug resi
870	69.5	3.9	379	2	A87632	epoxide hydrolase,
871	69.5	3.9	385	2	S78100	MAPK-activated pro
872	69.5	3.9	387	2	S48123	mitogen-activated
873	69.5	3.9	391	2	H84298	2',3'-cyclic-nucle
874	69.5	3.9	393	2	AD2219	hypothetical prote
875	69.5	3.9	395	2	B71483	probable ABC trans
876	69.5	3.9	418	2	E86871	proteinase [import
877	69.5	3.9	460	2	JQ1275	RAD57 protein - ye
878	69.5	3.9	462	2	B96560	hypothetical prote
879	69.5	3.9	463	2	S37962	probable purine nu
880	69.5	3.9	471	2	E86322	hypothetical prote
881	69.5	3.9	474	1	ERAD41	early E2A DNA-bind
882	69.5	3.9	478	2	T45661	hypothetical prote
883	69.5	3.9	487	2	G86272	hypothetical prote
884	69.5	3.9	512	2	T07788	probable serine/th
885	69.5	3.9	512	2	JH0098	anthranilate synth
886	69.5	3.9	529	2	T43156	probable nitrate a
887	69.5	3.9	557	2	AI2239	hypothetical prote
888	69.5	3.9	595	2	A35919	carotenoid biosynt
889	69.5	3.9	607	2	A43776	drebrin E2 - chick
890	69.5	3.9	617	2	S77077	hypothetical prote
891	69.5	3.9	640	2	C72351	hypothetical prote
892	69.5	3.9	650	2	E82937	DNA topoisomerase,
893	69.5	3.9	679	2	C71413	hypothetical prote
894	69.5	3.9	688	2	E64671	polynucleotide pho
895	69.5	3.9	699	2	A54767	transcription fact
896	69.5	3.9	702	2	AH0625	conserved hypothet
897	69.5	3.9	715	2	B83222	regulatory protein
898	69.5	3.9	729	2	AE0538	Rhs-family protein
899	69.5	3.9	729	2	T46270	hypothetical prote
900	69.5	3.9	745	2	T10924	3C3.15c protein -
901	69.5	3.9	747	2	T23882	hypothetical prote
902	69.5	3.9	748	2	D84595	pEARLI 4 protein [
903	69.5	3.9	749	2	H91170	hypothetical membr
904	69.5	3.9	753	2	AE0187	probable iron-side
905	69.5	3.9	758	2	A47439	gamma-glutamyl car
906	69.5	3.9	772	2	H86016	hypothetical prote
907	69.5	3.9	784	2	AH2560	hypothetical prote
908	69.5	3.9	826	2	T28858	hypothetical prote
909	69.5	3.9	854	1	VCLJSI	env polyprotein pr
910	69.5	3.9	866	1	S59872	replication licens
911	69.5	3.9	870	2	A96637	hypothetical prote
912	69.5	3.9	926	2	F88632	protein F56B3.4 [i
913	69.5	3.9	972	2	T09595	glucuronosyltransf
914	69.5	3.9	982	2	T13653	hypothetical prote
915	69.5	3.9	1020	2	JN0124	glycine dehydrogen
916	69.5	3.9	1032	2	F98043	SWF/SNF family ATP
917	69.5	3.9	1050	2	A89769	hypothetical prote
918	69.5	3.9	1052	2	JC4200	protein-tyrosine k
919	69.5	3.9	1068	2	I51670	focal adhesion kin
920	69.5	3.9	1115	2	F86280	protein T5E21.11 [
921	69.5	3.9	1115	2	T13955	period protein Per
922	69.5	3.9	1208	2	AE1947	chromosome segrega
923	69.5	3.9	1272	2	S60999	ubiquitin-specific
924	69.5	3.9	1278	1	E69615	enterobactin synth
925	69.5	3.9	1299	2	T47182	hypothetical prote
926	69.5	3.9	1324	2	T18265	endo-1,3(4)-beta-g
927	69.5	3.9	1389	2	T30824	RNA polymerase bet
928	69.5	3.9	1442	2	T18538	patched protein -
929	69.5	3.9	1449	2	AI2017	hypothetical prote
930	69.5	3.9	1550	2	AB2276	two-component hybr
931	69.5	3.9	1559	2	T07757	probable DNA (cyto
932	69.5	3.9	1755	2	S45736	TyB protein - yeas
933	69.5	3.9	1912	2	A56178	protein-tyrosine-p
934	69.5	3.9	2157	2	AI3009	peptide synthetase
935	69.5	3.9	2468	2	A83412	hypothetical prote
936	69.5	3.9	2566	2	E98274	hypothetical prote
937	69.5	3.9	3027	2	JQ1917	polyprotein - pars
938	69.5	3.9	3530	2	A59266	unconventional myo
939	69.5	3.9	3588	2	I40485	surfactin syntheta
940	69.5	3.9	3670	2	T36249	CDA peptide synthe
941	69	3.9	211	2	S60437	hypothetical prote
942	69	3.9	252	2	B64322	ribosomal protein
943	69	3.9	305	1	DGBE59	uracil-DNA glycosy
944	69	3.9	306	2	H83395	probable transcrip
945	69	3.9	329	2	S49490	MAPK-activated pro
946	69	3.9	331	2	F82742	ribosomal large su
947	69	3.9	331	2	T19311	hypothetical prote
948	69	3.9	338	2	AI0811	thiosulphate-bindi
949	69	3.9	340	2	T49770	hypothetical prote
950	69	3.9	350	2	B43670	sulfate-binding pr
951	69	3.9	366	2	T36689	probable transpept
952	69	3.9	400	1	A46723	MAP kinase kinase
953	69	3.9	411	2	D69459	conserved hypothet
954	69	3.9	437	2	AE0805	long-chain fatty a
955	69	3.9	439	1	FWSYCB	beta-conglycinin b
956	69	3.9	446	2	T46736	glutamate-ammonia
957	69	3.9	452	2	T12981	hypothetical prote
958	69	3.9	468	2	AE1942	two-component sens
959	69	3.9	500	1	D31579	cytochrome P450 2D
960	69	3.9	513	2	S50915	SIN3 protein-bindi
961	69	3.9	515	2	I50637	dynein light chain
962	69	3.9	523	2	T04332	glutamate-cysteine
963	69	3.9	537	2	AG2259	transposase all363
964	69	3.9	548	2	H95017	sensor histidine k
965	69	3.9	571	2	C70353	succinate dehydrog
966	69	3.9	588	2	H89885	succinate dehydrog
967	69	3.9	594	2	T39677	transcription regu
968	69	3.9	599	1	A54906	afamin precursor -
969	69	3.9	605	1	WZBE33	gene 33 protein -
970	69	3.9	618	2	A75015	phosphoenolpyruvat
971	69	3.9	618	2	S53384	hypothetical prote
972	69	3.9	642	2	G72265	hypothetical prote
973	69	3.9	701	2	T15235	hypothetical prote
974	69	3.9	720	2	H95221	alpha-galactosidas
975	69	3.9	738	2	T38767	probable RNA-bindi
976	69	3.9	757	1	I50667	transforming prote
977	69	3.9	760	2	T16726	hypothetical prote
978	69	3.9	763	1	S29548	transferrin recept

979	69	3.9	785	2	S73098	aminopeptidase (EC
980	69	3.9	860	2	I48839	tenascin-X - mouse
981	69	3.9	869	2	S53098	envelope polyprote
982	69	3.9	875	2	T30023	hypothetical prote
983	69	3.9	881	1	VCLJG3	env polyprotein -
984	69	3.9	887	2	AE0415	pyruvate dehydroge
985	69	3.9	900	2	T33482	hypothetical prote
986	69	3.9	935	2	T29390	hypothetical prote
987	69	3.9	936	2	H71728	2-oxoglutarate deh
988	69	3.9	963	2	T12087	H+-exporting ATPas
989	69	3.9	976	2	A36355	protein-tyrosine k
990	69	3.9	1040	2	T39936	probable helicase
991	69	3.9	1052	2	T37133	hypothetical prote
992	69	3.9	1081	2	B81303	probable membrane
993	69	3.9	1153	1	RWHU1B	cell surface glyco
994	69	3.9	1191	2	S76414	beta transducin-li
995	69	3.9	1206	2	A64207	hypothetical prote
996	69	3.9	1218	2	JS0069	hypothetical P1 op
997	69	3.9	1289	2	AB2217	hypothetical prote
998	69	3.9	1356	2	T16718	hypothetical prote
999	69	3.9	1358	2	T01698	aldehyde oxidase (
1000	69	3.9	1474	2	T18281	hypothetical prote
1001	69	3.9	1573	2	S01845	DNA (cytosine-5-)-
1002	69	3.9	1706	2	B75633	probable RNA helic
1003	69	3.9	1744	2	T32228	hypothetical prote
1004	69	3.9	1869	2	A59290	class V chitin syn
1005	69	3.9	2117	2	T36180	CDA peptide synthe
1006	69	3.9	2241	2	T02857	conserved hypothet
1007	69	3.9	2471	2	T42977	large tegument pro
1008	69	3.9	2485	1	H71621	serine/threonine-s
1009	69	3.9	2606	2	T03159	large tegument pro
1010	69	3.9	2783	2	T34416	hypothetical prote
1011	69	3.9	3165	2	S15010	hypothetical prote
1012	69	3.9	4006	2	T09070	probable tenascin
1013	69	3.9	4377	2	A55575	ankyrin 3, long sp
1014	69	3.9	4385	2	T29042	hypothetical prote
1015	68.5	3.9	130	2	E72651	hypothetical prote
1016	68.5	3.9	151	2	S30456	env protein - huma
1017	68.5	3.9	159	2	G75277	comA protein - Dei
1018	68.5	3.9	228	2	E69190	conserved hypothet
1019	68.5	3.9	243	2	G86524	lysophospholipase
1020	68.5	3.9	243	2	D72098	serine esterase, p
1021	68.5	3.9	248	2	AE0281	two-component regu
1022	68.5	3.9	252	2	A71001	hypothetical prote
1023	68.5	3.9	259	2	F95258	ribosomal protein
1024	68.5	3.9	259	2	A99524	30S ribosomal prot
1025	68.5	3.9	267	2	E82786	hypothetical prote
1026	68.5	3.9	269	2	E86807	beta-glucoside ope
1027	68.5	3.9	274	2	B64979	molybdate metaboli
1028	68.5	3.9	284	2	AH0442	probable glutathio
1029	68.5	3.9	302	2	G84005	hypothetical prote
1030	68.5	3.9	309	2	T24804	hypothetical prote
1031	68.5	3.9	339	1	TVRTM	protein kinase (EC
1032	68.5	3.9	348	2	T29663	hypothetical prote
1033	68.5	3.9	372	2	AF2000	permease protein o
1034	68.5	3.9	374	2	T06244	gibberellin 3 beta
1035	68.5	3.9	378	2	T14269	Delta12 fatty acid
1036	68.5	3.9	379	2	F69210	conserved hypothet
1037	68.5	3.9	389	2	H90083	polyadenylate-bind
1038	68.5	3.9	409	2	S72438	phosphatidylserine
1039	68.5	3.9	418	2	E85064	hypothetical prote
1040	68.5	3.9	427	2	T46955	dihydroorotase (EC
1041	68.5	3.9	447	2	F82341	acetyl-CoA carboxy
1042	68.5	3.9	462	2	D84858	hypothetical prote
1043	68.5	3.9	464	2	AG2769	cytochrome P450 cy
1044	68.5	3.9	464	2	H97549	cytochrome p450 hy
1045	68.5	3.9	468	1	VGBEEH	glycoprotein gp13
1046	68.5	3.9	476	2	C54415	transcription fact
1047	68.5	3.9	488	2	S71029	flaK protein - Vib
1048	68.5	3.9	502	2	T45422	glutamyl-tRNA synt
1049	68.5	3.9	505	1	S19169	cytochrome P450 2D
1050	68.5	3.9	516	2	T35542	probable large sec
1051	68.5	3.9	545	2	AF0442	probable carbohydr
1052	68.5	3.9	586	2	B70503	probable pyrG prot
1053	68.5	3.9	598	2	S65770	maltooligosyltreha
1054	68.5	3.9	604	2	A39369	homeotic protein B
1055	68.5	3.9	633	2	B85555	probable Vgr prote
1056	68.5	3.9	633	2	G90704	probable Vgr prote
1057	68.5	3.9	642	1	S34416	transcription fact
1058	68.5	3.9	642	2	T39607	fork head protein
1059	68.5	3.9	689	2	A31794	mdm-1 nuclear prot
1060	68.5	3.9	692	2	E90952	flagellar biosynth
1061	68.5	3.9	692	2	A85801	flagellar biosynth
1062	68.5	3.9	698	2	AC2501	hypothetical prote
1063	68.5	3.9	700	2	D70917	probable tkt prote
1064	68.5	3.9	707	2	S77094	glycogen operon pr
1065	68.5	3.9	710	2	S04128	phenylalanine ammo
1066	68.5	3.9	716	1	JC5061	macrophage-stimula
1067	68.5	3.9	725	2	T08989	hypothetical prote
1068	68.5	3.9	743	2	T00634	hypothetical prote
1069	68.5	3.9	769	2	C83710	transcription regu
1070	68.5	3.9	772	2	D91195	hypothetical prote
1071	68.5	3.9	772	2	E86042	hypothetical prote
1072	68.5	3.9	807	2	T18454	hypothetical prote
1073	68.5	3.9	813	2	S36018	gene tramtrack-p88
1074	68.5	3.9	814	2	G02878	cadherin-15 precur
1075	68.5	3.9	815	2	B82746	DNA topoisomerase
1076	68.5	3.9	855	2	T41336	probable nitrogen
1077	68.5	3.9	859	1	VCLJST	env polyprotein pr
1078	68.5	3.9	880	2	AF0397	probable acetyltra
1079	68.5	3.9	887	2	AG0521	pyruvate dehydroge
1080	68.5	3.9	893	2	AH2007	toxin secretion AB
1081	68.5	3.9	915	2	T23937	hypothetical prote
1082	68.5	3.9	921	2	AE0332	conserved hypothet
1083	68.5	3.9	995	2	T32466	hypothetical prote
1084	68.5	3.9	1025	2	B54718	dihydropyrimidine
1085	68.5	3.9	1065	2	A43421	SEC8 protein - yea
1086	68.5	3.9	1065	2	A57410	transcription fact
1087	68.5	3.9	1147	2	T42627	ADP-ribosylation f
1088	68.5	3.9	1216	2	T34101	hypothetical prote
1089	68.5	3.9	1246	2	S60954	probable membrane
1090	68.5	3.9	1326	2	H89134	protein F25G6.9 [i
1091	68.5	3.9	1529	2	T02730	RNA-directed DNA p
1092	68.5	3.9	1531	2	T42218	slit-1 protein hom
1093	68.5	3.9	1547	2	T13847	sno protein - frui
1094	68.5	3.9	1711	2	T06119	hypothetical prote
1095	68.5	3.9	2163	2	T15276	hypothetical prote
1096	68.5	3.9	2482	2	I48922	cation-independent
1097	68.5	3.9	2483	1	A49617	insulin-like growt
1098	68.5	3.9	2491	1	A28372	insulin-like growt
1099	68	3.8	21	2	S48632	carbonic anhydrase
1100	68	3.8	129	2	B48470	ubiquitin / riboso
1101	68	3.8	151	2	S30451	env protein - huma
1102	68	3.8	188	2	A64021	hypothetical prote
1103	68	3.8	211	2	S34616	superoxide dismuta
1104	68	3.8	222	1	DSHUN	superoxide dismuta
1105	68	3.8	247	2	S73076	hypothetical prote
1106	68	3.8	256	2	G69997	hypothetical prote
1107	68	3.8	256	2	C70687	hypothetical prote
1108	68	3.8	256	2	B83612	hypothetical prote
1109	68	3.8	282	2	E95956	hypothetical prote
1110	68	3.8	288	2	AD0884	probable transfera
1111	68	3.8	308	2	C89799	conserved hypothet
1112	68	3.8	334	2	F86831	hypothetical prote
1113	68	3.8	365	2	A75375	hypothetical prote
1114	68	3.8	392	2	G87106	conserved hypothet
1115	68	3.8	392	2	AD1485	ABC transporter, A
1116	68	3.8	393	2	H83747	two-component sens
1117	68	3.8	395	1	S36186	mitogen-activated
1118	68	3.8	397	1	S41054	mitogen-activated
1119	68	3.8	402	2	A86194	hypothetical prote
1120	68	3.8	406	2	D84898	probable mitogen-a
1121	68	3.8	410	2	S28485	lipopolysaccharide
1122	68	3.8	427	1	KGHUL1	kininogen, LMW pre
1123	68	3.8	429	2	B72109	GMP synthase CP059
1124	68	3.8	429	2	C86512	GMP synthase [impo

1125	68	3.8	437	2	S22889	vitellogenin 1 - M
1126	68	3.8	449	2	T45605	glucosyltransferas
1127	68	3.8	476	2	E82134	o-succinylbenzoic
1128	68	3.8	487	2	A82835	anthranilate synth
1129	68	3.8	495	2	T28722	hypothetical prote
1130	68	3.8	500	1	JC2231	prostaglandin-I sy
1131	68	3.8	518	2	F75460	hypothetical prote
1132	68	3.8	524	2	T06134	hypothetical prote
1133	68	3.8	529	2	S76831	hypothetical prote
1134	68	3.8	531	2	T08760	hypothetical prote
1135	68	3.8	536	2	A34596	transcription fact
1136	68	3.8	555	2	T43842	DNA-directed RNA p
1137	68	3.8	556	2	B83847	cytochrome c bioge
1138	68	3.8	560	2	AF0279	acetolactate synth
1139	68	3.8	565	1	HMIVGM	hemagglutinin prec
1140	68	3.8	568	2	AG3071	hypothetical prote
1141	68	3.8	574	2	A96612	hypothetical prote
1142	68	3.8	591	2	B98215	hypothetical prote
1143	68	3.8	594	1	E64622	excinuclease ABC c
1144	68	3.8	597	2	D64711	glutamine-fructose
1145	68	3.8	633	2	S69734	hypothetical prote
1146	68	3.8	666	2	H75295	transketolase - De
1147	68	3.8	667	2	G69723	transketolase (EC
1148	68	3.8	682	2	S50436	hypothetical prote
1149	68	3.8	777	2	E83748	hypothetical prote
1150	68	3.8	803	1	RGBYW6	regulatory protein
1151	68	3.8	803	2	T40475	bromeodomain prote
1152	68	3.8	822	2	S70012	methionine-S-oxide
1153	68	3.8	834	2	D57282	ankyrin-related pr
1154	68	3.8	834	2	S54563	hypothetical prote
1155	68	3.8	852	1	VCLJGG	env polyprotein pr
1156	68	3.8	855	2	A45713	Env transmembrane
1157	68	3.8	925	2	A72096	ct234 hypothetical
1158	68	3.8	925	2	E81573	conserved hypothet
1159	68	3.8	925	2	E86527	CT234 hypothetical
1160	68	3.8	936	2	E71405	probable ankyrin -
1161	68	3.8	973	2	T05894	probable oxoglutar
1162	68	3.8	1027	2	T50644	oxoglutarate dehyd
1163	68	3.8	1037	2	E65022	acriflavin resista
1164	68	3.8	1051	2	G84316	ribonucleoside red
1165	68	3.8	1098	2	JQ2209	helicase homolog g
1166	68	3.8	1099	2	A59311	myosin VIII, ZMM3
1167	68	3.8	1123	2	D96756	receptor-like prot
1168	68	3.8	1133	2	JT0665	helicase II-like p
1169	68	3.8	1193	2	B96943	2,3-cyclic-nucleot
1170	68	3.8	1193	2	A44018	laminin B2t chain
1171	68	3.8	1248	2	A53588	adenylate cyclase
1172	68	3.8	1291	2	T17242	hypothetical prote
1173	68	3.8	1324	2	S06187	RNA2 polyprotein -
1174	68	3.8	1366	2	B86292	F7H2.12 protein -
1175	68	3.8	1367	2	C72360	DNA polymerase III
1176	68	3.8	1403	2	T49093	hypothetical prote
1177	68	3.8	1417	2	H83132	probable sensor/re
1178	68	3.8	1447	2	T00530	hypothetical prote
1179	68	3.8	1558	2	T29253	hypothetical prote
1180	68	3.8	1785	2	A45546	major merozoite su
1181	68	3.8	1900	2	AG2391	serine/threonine k
1182	68	3.8	2578	2	A56922	transcription fact
1183	68	3.8	2649	2	T51023	hypothetical prote
1184	68	3.8	2708	2	T09079	probable chloroqui
1185	68	3.8	4391	2	A38096	perlecan precursor
1186	68	3.8	4613	2	T17409	polyketide synthas
1187	68	3.8	5170	2	T15348	hypothetical prote
1188	68	3.8	10797	2	T30192	probable peptide s
1189	67.5	3.8	154	2	A69267	transposase homolo
1190	67.5	3.8	166	2	G85057	hypothetical prote
1191	67.5	3.8	203	2	T02868	probable GTP-bindi
1192	67.5	3.8	223	2	H82482	transcription regu
1193	67.5	3.8	235	2	D89101	protein F25E5.8 [i
1194	67.5	3.8	265	2	S62363	D-2-chloropropioni
1195	67.5	3.8	270	2	AH2143	hypothetical prote
1196	67.5	3.8	284	2	D84057	hypothetical prote
1197	67.5	3.8	305	1	S29853	polyubiquitin 4 -
1198	67.5	3.8	314	2	B83536	probable transcrip
1199	67.5	3.8	330	2	A82538	pseudouridylate sy
1200	67.5	3.8	333	1	HLHUCC	T-cell surface gly
1201	67.5	3.8	336	2	T05538	hypothetical prote
1202	67.5	3.8	341	1	DEKWG4	glyceraldehyde-3-p
1203	67.5	3.8	381	1	A29277	aldose 1-epimerase
1204	67.5	3.8	383	1	SZBPSP	deoxyuridylate hyd
1205	67.5	3.8	386	2	B86595	amino acid (branch
1206	67.5	3.8	386	2	C72029	amino acid (branch
1207	67.5	3.8	391	2	G95085	conserved hypothet
1208	67.5	3.8	393	2	T41211	hypothetical wtf1
1209	67.5	3.8	396	2	C84797	hypothetical prote
1210	67.5	3.8	397	2	C97953	conserved hypothet
1211	67.5	3.8	399	2	T18853	probable transcrip
1212	67.5	3.8	412	2	C81511	branched-chain ami
1213	67.5	3.8	443	2	E64640	hypothetical prote
1214	67.5	3.8	449	2	F95055	potassium uptake p
1215	67.5	3.8	449	2	C97925	hypothetical prote
1216	67.5	3.8	464	2	T33249	hypothetical prote
1217	67.5	3.8	484	2	A38179	rpoN-1 protein - B
1218	67.5	3.8	500	2	B83910	hypothetical prote
1219	67.5	3.8	504	1	VCPV3A	coat protein - ade
1220	67.5	3.8	512	2	S50599	SHC1 protein - yea
1221	67.5	3.8	528	2	AG1937	glucose-6-phosphat
1222	67.5	3.8	534	2	T47836	beta-glucosidase-1
1223	67.5	3.8	541	2	T13162	cytosolic phosphol
1224	67.5	3.8	549	2	T38496	hypothetical prote
1225	67.5	3.8	571	2	A42138	conditioned medium
1226	67.5	3.8	571	2	S24482	conditioned medium
1227	67.5	3.8	584	2	S49594	capsid protein VP2
1228	67.5	3.8	589	2	F86549	CT365 hypothetical
1229	67.5	3.8	589	2	D72074	conserved hypothet
1230	67.5	3.8	594	2	H81954	probable periplasm
1231	67.5	3.8	595	2	JC6550	sex-determining re
1232	67.5	3.8	598	2	S39621	DNA-directed DNA p
1233	67.5	3.8	600	2	S58681	selenocysteine tRN
1234	67.5	3.8	611	2	A83926	hypothetical prote
1235	67.5	3.8	621	2	T48492	hypothetical prote
1236	67.5	3.8	623	2	G81346	heat shock protein
1237	67.5	3.8	640	2	G96733	auxin transport pr
1238	67.5	3.8	648	2	T34999	probable neuramida
1239	67.5	3.8	662	2	S55387	hemocyanin precurs
1240	67.5	3.8	666	2	B56639	1,4-alpha-glucan b
1241	67.5	3.8	682	2	A42121	transcription fact
1242	67.5	3.8	687	1	HYRTTH	thimet oligopeptid
1243	67.5	3.8	692	2	G64950	flagellar biosynth
1244	67.5	3.8	712	2	S71626	3',5'-cyclic-nucle
1245	67.5	3.8	715	2	G86239	protein F20B24.6 [
1246	67.5	3.8	719	2	S25237	homeotic protein H
1247	67.5	3.8	763	2	T48702	hypothetical prote
1248	67.5	3.8	781	1	S64576	hypothetical prote
1249	67.5	3.8	788	2	S70079	1,4-alpha-glucan b
1250	67.5	3.8	808	2	S73947	preprotein translo
1251	67.5	3.8	840	2	C75313	probable proteinas
1252	67.5	3.8	848	2	I55498	testicular dynamin
1253	67.5	3.8	850	2	S54553	SIN3 protein-bindi
1254	67.5	3.8	859	2	S24571	env protein - huma
1255	67.5	3.8	888	2	S23065	ufo protein - mous
1256	67.5	3.8	891	2	A82755	beta-mannosidase p
1257	67.5	3.8	892	2	T01899	disease resistance
1258	67.5	3.8	921	2	AC1327	isoleucyl-tRNA syn
1259	67.5	3.8	921	2	AE1698	isoleucyl-tRNA syn
1260	67.5	3.8	929	2	H84582	hypothetical prote
1261	67.5	3.8	950	2	A82986	adenylate cyclase
1262	67.5	3.8	952	2	AC0447	probable insectici
1263	67.5	3.8	963	2	T09478	ubiquitin thiolest
1264	67.5	3.8	989	2	B84532	hypothetical prote
1265	67.5	3.8	1024	1	GBEC	beta-galactosidase
1266	67.5	3.8	1052	2	H83909	cell wall-associat
1267	67.5	3.8	1069	1	KUHU	ferroxidase (EC 1.
1268	67.5	3.8	1088	1	YGBSTB	phenylalanine race
1269	67.5	3.8	1091	2	T34247	hypothetical prote
1270	67.5	3.8	1107	2	T34246	hypothetical prote

1271	67.5	3.8	1171	2	T17454	diaphanous-related
1272	67.5	3.8	1196	1	DNBEHF	DNA-binding protei
1273	67.5	3.8	1196	1	DNBEKS	DNA-binding protei
1274	67.5	3.8	1196	1	DNBEV1	major DNA-binding
1275	67.5	3.8	1206	2	S24407	formin isoform IV
1276	67.5	3.8	1212	2	T44051	hypothetical prote
1277	67.5	3.8	1238	2	T34929	hypothetical prote
1278	67.5	3.8	1305	2	T31096	cyclin G-associate
1279	67.5	3.8	1315	2	T50262	probable nucleopor
1280	67.5	3.8	1346	2	T14849	cytoadherence link
1281	67.5	3.8	1364	2	T10236	xanthine dehydroge
1282	67.5	3.8	1424	2	T03851	thyroid hormone re
1283	67.5	3.8	1495	2	S61023	hypothetical prote
1284	67.5	3.8	1541	1	S71839	canalicular multid
1285	67.5	3.8	1582	2	A56248	sulfonylurea recep
1286	67.5	3.8	1583	2	F86366	protein F26F24.8 [
1287	67.5	3.8	1613	2	F89528	protein vit-2 [imp
1288	67.5	3.8	1643	2	T05647	hypothetical prote
1289	67.5	3.8	1746	2	D83181	hypothetical prote
1290	67.5	3.8	1785	2	T22595	hypothetical prote
1291	67.5	3.8	2471	2	A49128	cell-fate determin
1292	67.5	3.8	3341	1	A42996	genome polyprotein
1293	67.5	3.8	5037	1	A54161	ryanodine-binding
1294	67.5	3.8	13055	2	T16580	hypothetical prote
1295	67	3.8	151	2	S30448	env protein - huma
1296	67	3.8	162	2	H75435	hypothetical prote
1297	67	3.8	195	2	B64359	ribosomal protein
1298	67	3.8	256	2	A54322	corticotropin / li
1299	67	3.8	261	2	A65029	rhodanese-like pro
1300	67	3.8	261	2	D91052	enhanced serine se
1301	67	3.8	263	1	S73489	probable S-adenosy
1302	67	3.8	270	2	F64050	glucosamine-6-phos
1303	67	3.8	289	2	D87496	conserved hypothet
1304	67	3.8	296	2	B96830	hypothetical prote
1305	67	3.8	298	2	F69875	pyrimidine-thiamin
1306	67	3.8	299	2	G70784	probable mmpS3 pro
1307	67	3.8	300	2	B83554	probable transfera
1308	67	3.8	309	2	T42067	polyketide synthas
1309	67	3.8	314	2	T06012	hypothetical prote
1310	67	3.8	315	2	B82229	hypothetical prote
1311	67	3.8	324	1	A48953	choloylglycine hyd
1312	67	3.8	325	2	AC1333	conjugated bile ac
1313	67	3.8	329	2	G83280	probable transcrip
1314	67	3.8	336	2	A43260	glyceraldehyde-3-p
1315	67	3.8	339	2	B86541	hypothetical prote
1316	67	3.8	339	2	C72082	hypothetical prote
1317	67	3.8	340	2	T28110	hypothetical prote
1318	67	3.8	344	2	C86507	hypothetical prote
1319	67	3.8	344	2	D72116	hypothetical prote
1320	67	3.8	346	2	A81554	hypothetical prote
1321	67	3.8	356	2	T34133	steroid/thyroid/re
1322	67	3.8	359	2	T36443	probable penicilli
1323	67	3.8	359	2	A28700	mandelate racemase
1324	67	3.8	363	2	T40350	probable polyadeny
1325	67	3.8	371	2	S75778	oligopeptide trans
1326	67	3.8	374	2	AH3522	xylose repressor [
1327	67	3.8	381	2	E86652	GTP-binding protei
1328	67	3.8	383	2	B95252	alcohol dehydrogen
1329	67	3.8	393	1	A45100	mitogen-activated
1330	67	3.8	393	1	I59571	mitogen-activated
1331	67	3.8	393	1	JN0840	mitogen-activated
1332	67	3.8	393	1	S42068	mitogen-activated
1333	67	3.8	393	1	S46361	mitogen-activated
1334	67	3.8	413	2	A54127	dolichyl-diphospho
1335	67	3.8	420	2	AB0098	diaminopimelate de
1336	67	3.8	425	2	T43454	hypothetical prote
1337	67	3.8	426	2	B90170	histidyl-tRNA synt
1338	67	3.8	430	2	I48142	B-lymphocyte antig
1339	67	3.8	430	2	F90272	phytoene dehydroge
1340	67	3.8	436	2	B70473	protoporphyrinogen
1341	67	3.8	440	2	F86385	probable lysine an
1342	67	3.8	443	2	T46127	hypothetical prote
1343	67	3.8	447	2	H89113	protein ZK742.3 [i
1344	67	3.8	450	2	C70515	probable glnA3 pro
1345	67	3.8	453	2	S37935	hypothetical prote
1346	67	3.8	462	1	A37986	interleukin-6 rece
1347	67	3.8	466	2	A95355	probable inner-mem
1348	67	3.8	473	2	D70405	glutamate-tRNA lig
1349	67	3.8	494	2	AG1231	PTS system trehalo
1350	67	3.8	502	2	T45852	hypothetical prote
1351	67	3.8	504	2	S51590	mitochondrial proc
1352	67	3.8	504	2	H84862	hypothetical prote
1353	67	3.8	506	2	D81703	conserved hypothet
1354	67	3.8	507	2	T24944	hypothetical prote
1355	67	3.8	508	2	E81723	conserved hypothet
1356	67	3.8	543	2	T32961	hypothetical prote
1357	67	3.8	559	2	AI0135	DNA repair protein
1358	67	3.8	560	2	T05278	hypothetical prote
1359	67	3.8	563	2	AH1245	DNA repair and gen
1360	67	3.8	585	1	A24168	involucrin - human
1361	67	3.8	587	2	S33951	fiber protein - hu
1362	67	3.8	588	2	AI3543	60K inner membrane
1363	67	3.8	592	2	S25705	Ig mu chain - shee
1364	67	3.8	594	2	B71893	excinuclease ABC c
1365	67	3.8	602	2	S58336	probable membrane
1366	67	3.8	625	2	T16777	hypothetical prote
1367	67	3.8	634	2	S32349	probable SNF2-type
1368	67	3.8	642	2	C96777	F25A4.24 [imported
1369	67	3.8	660	2	A24266	glutenin high mole
1370	67	3.8	677	1	CNHUB	chromogranin B pre
1371	67	3.8	682	2	T10319	envelope protein E
1372	67	3.8	691	2	E83027	hypothetical prote
1373	67	3.8	710	2	T21339	hypothetical prote
1374	67	3.8	734	1	A2NTP7	photosystem I P700
1375	67	3.8	752	2	H97191	uncharacterized pr
1376	67	3.8	759	2	D95129	pullulanase, proba
1377	67	3.8	759	2	A98000	pullulanase (EC 3.
1378	67	3.8	760	1	JXHU	transferrin recept
1379	67	3.8	792	2	A83303	phenylalanyl-tRNA
1380	67	3.8	801	1	A44165	1-phosphatidylinos
1381	67	3.8	829	2	B27211	virA protein - Agr
1382	67	3.8	837	2	A97557	dimethylglycine de
1383	67	3.8	837	2	AD2777	dimethylglycine de
1384	67	3.8	866	1	JC4305	dynamin II - human
1385	67	3.8	890	2	T00800	disease resistance
1386	67	3.8	896	2	I56563	interleukin-3 rece
1387	67	3.8	917	1	A31869	hexokinase (EC 2.7
1388	67	3.8	930	2	A84668	Argonaute (AGO1)-1
1389	67	3.8	942	2	C81139	probable oxoglutar
1390	67	3.8	1071	2	T18597	hypothetical prote
1391	67	3.8	1078	2	T30860	traI protein - Sal
1392	67	3.8	1120	2	T38431	DNA-directed RNA p
1393	67	3.8	1130	2	T34081	hypothetical prote
1394	67	3.8	1215	2	I52882	autoantigen - huma
1395	67	3.8	1217	2	A45493	phospholipase C-be
1396	67	3.8	1241	2	S01827	period clock prote
1397	67	3.8	1242	2	S78061	DNA-directed RNA p
1398	67	3.8	1264	2	S64146	probable membrane
1399	67	3.8	1267	1	MWXR31	lambda 3 protein -
1400	67	3.8	1279	2	T13613	hypothetical prote
1401	67	3.8	1289	2	B72354	conserved hypothet
1402	67	3.8	1290	2	JC5473	dextransucrase (EC
1403	67	3.8	1309	2	F82207	ATP-dependent heli
1404	67	3.8	1317	2	T03748	apoptosis associat
1405	67	3.8	1352	2	T13150	neuroblastoma-ampl
1406	67	3.8	1464	2	T07050	hypothetical prote
1407	67	3.8	1496	2	AH0447	insecticidal toxin
1408	67	3.8	1510	2	T33100	hypothetical prote
1409	67	3.8	1571	2	T00062	hypothetical prote
1410	67	3.8	1893	2	A56158	eye development pr
1411	67	3.8	2013	2	AI1489	probable peptidogl
1412	67	3.8	2195	2	S61103	SEC16 protein - ye
1413	67	3.8	2211	1	KFBO5	coagulation factor
1414	67	3.8	2223	2	S65074	pyrimidine synthes
1415	67	3.8	2265	1	FNBO	fibronectin - bovi
1416	67	3.8	2359	2	T03094	A-kinase anchor pr

1417	67	3.8	2531	2	T31070	notch homolog - se
1418	67	3.8	2819	2	A90551	conserved hypothet
1419	67	3.8	4684	2	A59404	plectin [imported]
1420	67	3.8	5762	2	A41819	proline-rich pepti
1421	66.5	3.7	131	2	S49351	profilin 1 - kidne
1422	66.5	3.7	151	2	S30455	env protein - huma
1423	66.5	3.7	151	2	S30454	env protein - huma
1424	66.5	3.7	164	2	A81341	phosphoribosylamin
1425	66.5	3.7	207	2	B75294	DNA-binding stress
1426	66.5	3.7	220	2	B90974	probable phage rep
1427	66.5	3.7	220	2	D85821	unknown protein en
1428	66.5	3.7	224	2	AF0838	transcription regu
1429	66.5	3.7	228	2	T22259	hypothetical prote
1430	66.5	3.7	247	2	AB0545	probable transmemb
1431	66.5	3.7	269	2	H75214	hypothetical prote
1432	66.5	3.7	281	2	A87661	conserved hypothet
1433	66.5	3.7	286	2	A84063	hypothetical prote
1434	66.5	3.7	287	2	A69838	transcription regu
1435	66.5	3.7	300	2	H69260	thiamin biosynthes
1436	66.5	3.7	301	2	C84474	hypothetical prote
1437	66.5	3.7	303	2	H97742	hypothetical prote
1438	66.5	3.7	304	2	H90466	oxidoreductase [im
1439	66.5	3.7	322	2	A69963	hypothetical prote
1440	66.5	3.7	331	2	A70884	probable ribF prot
1441	66.5	3.7	331	2	S70212	hypothetical prote
1442	66.5	3.7	332	2	E71105	hypothetical prote
1443	66.5	3.7	345	2	T29981	hypothetical prote
1444	66.5	3.7	355	2	C86592	aminopeptidase P [
1445	66.5	3.7	355	2	B72032	proline dipeptidas
1446	66.5	3.7	361	2	A35390	mobilization prote
1447	66.5	3.7	370	2	C82553	homoserine O-acety
1448	66.5	3.7	370	2	C64645	hypothetical prote
1449	66.5	3.7	372	2	T45524	regulatory protein
1450	66.5	3.7	373	1	DEHUHS	3beta-hydroxy-Delt
1451	66.5	3.7	374	1	TVMVM	protein kinase (EC
1452	66.5	3.7	374	2	T05923	glutenin low molec
1453	66.5	3.7	380	2	JC5217	site-specific DNA-
1454	66.5	3.7	383	2	C95186	hypothetical prote
1455	66.5	3.7	383	2	D98053	hypothetical prote
1456	66.5	3.7	389	2	D75389	membrane-bound pro
1457	66.5	3.7	398	2	S74347	hypothetical prote
1458	66.5	3.7	405	2	T07699	hypothetical prote
1459	66.5	3.7	406	2	A75344	pilin biogenesis p
1460	66.5	3.7	410	2	C84827	hypothetical prote
1461	66.5	3.7	411	2	B69006	phosphoglycerate k
1462	66.5	3.7	414	2	F29826	hypothetical prote
1463	66.5	3.7	416	2	A71095	probable sugar-pho
1464	66.5	3.7	423	2	T20857	hypothetical prote
1465	66.5	3.7	429	2	S45459	TOM34 protein - ye
1466	66.5	3.7	430	2	C83975	O-acetylhomoserine
1467	66.5	3.7	434	2	E96826	hypothetical prote
1468	66.5	3.7	461	2	A32008	site-specific DNA-
1469	66.5	3.7	469	2	A90166	conserved hypothet
1470	66.5	3.7	494	2	A33952	58K mobilization p
1471	66.5	3.7	515	2	A42140	box B-binding fact
1472	66.5	3.7	526	2	D87532	alpha amylase fami
1473	66.5	3.7	557	2	T44843	glucose-6-phosphat
1474	66.5	3.7	557	2	T41631	hypothetical prote
1475	66.5	3.7	566	2	AF1803	Sucrose phosphoryl
1476	66.5	3.7	573	2	H82257	phosphoenolpyruvat
1477	66.5	3.7	573	2	S75748	flavoprotein, 63.5
1478	66.5	3.7	583	2	D82634	acetolactate synth
1479	66.5	3.7	588	1	FWCNAB	alpha-globulin B p
1480	66.5	3.7	594	2	JT0766	transcription fact
1481	66.5	3.7	594	2	C81011	conserved hypothet
1482	66.5	3.7	604	2	S56027	hypothetical prote
1483	66.5	3.7	610	2	S58885	derailed receptor
1484	66.5	3.7	616	2	A46230	RNA-binding protei
1485	66.5	3.7	619	2	A45625	phosphoenolpyruvat
1486	66.5	3.7	619	2	E86466	protein F23M19.10
1487	66.5	3.7	625	2	D87793	protein C27A12.2 [
1488	66.5	3.7	631	1	A36749	transcription fact
1489	66.5	3.7	640	1	SYHUAL	5-aminolevulinate
1490	66.5	3.7	646	2	G70032	ABC transporter (p
1491	66.5	3.7	686	1	S28050	transforming prote
1492	66.5	3.7	707	2	A54846	fibroblast growth
1493	66.5	3.7	715	2	AB2210	anthranilate synth
1494	66.5	3.7	720	2	S50920	hypothetical prote
1495	66.5	3.7	722	1	VCPVME	coat protein VP1 -
1496	66.5	3.7	722	2	F82482	hypothetical prote
1497	66.5	3.7	727	1	VCPV1F	coat protein VP1 -
1498	66.5	3.7	728	2	S48569	hypothetical prote
1499	66.5	3.7	731	2	S18243	photosystem I prot
1500	66.5	3.7	733	2	S78376	photosystem I P700

ALIGNMENTS

RESULT 1
I38013
p54/58N - human
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: I38013
R;Pastorek, J.; Pastorekova, S.; Callebaut, I.; Mornon, J.; Zelnik, V.; Opavsky, R.; Zat
Oncogene 9, 2877-2888, 1994
A;Title: Cloning and characterization of MN, a human tumor-associated protein with a dom
A;Reference number: I38013; MUID:94366734; PMID:8084592
A;Accession: I38013
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: UNIPROT:Q16790; EMBL:X66839; NID:g1000701; PIDN:CAA47315.1; PID:g100
C;Genetics:
A;Gene: MaTuMN
F;141-390/Domain: carbonic anhydrase homology <CAH>

Query Match 31.6%; Score 562; DB 2; Length 459;
Best Local Similarity 38.8%; Pred. No. 2.2e-38;
Matches 128; Conservative 47; Mismatches 129; Indels 26; Gaps 7;

```
Qy         17 DGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEP 76
              |   || |    |   ||   | |    |||:||:     | | |  |:  |:  |
Db        136 DDQSHWRY---GGDPPWPRVSPACAGRFQSPVDIRPQLAAFCPALRPLELLGFQLPPLPE 192

Qy         77 LDLHNNGHTVQLSLPSTLYLG-GLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELH 135
              | | ||||:|||:||  | :  |  |:| | |||||||  | | |||| :      ||:|
Db        193 LRLRNNGHSVQLTLPPGLEMALGPGREYRALQLHLHWGAAGRP-GSEHTVEGHRFPAEIH 251

Qy        136 IVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP 195
              :||  | ::  : ||  || |||||   :| |  :| ||| :|| | |:  :  :| ||
Db        252 VVHL-STAFARVDEALGRPGGLAVLAAFLEEGPEENSAYEQLLSRLEEIAEEGSETQVPG 310

Qy        196 FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEP 255
              ::  |||    :||:| |||||||| | |:|||| :   :| :||  |  ||:   :
Db        311 LDISALLPSDFSRYFQYEGSLTTPPCAQGVIWTVFNQTVMLSAKQLHTLSDTLWGPGDSR 370

Qy        256 SKLLVQNYRALQPLNQRMVFASF------------IQAGSSYTTGEMLSLGVGILVGCL 302
              :|   |:|| |||| |:: |||             :|  |    |::|:|  |:|
Db        371 LQL---NFRATQPLNGRVIEASFPAGVDSSPRAAEPVQLNSCLAAGDILALVFGLLFA-- 425

Qy        303 CLLLAVYFIARKIRKKRLENRKSVVFTSAQ 332
              : :| |: :  |: |   :  | :  |:
Db        426 --VTSVAFLVQMRRQHRRGTKGGVSYRPAE 453
```

RESULT 2
A29993
carbonate dehydratase (EC 4.2.1.1) VI - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29993
R;Fernley, R.T.; Wright, R.D.; Coghlan, J.P.
Biochemistry 27, 2815-2820, 1988
A;Title: Complete amino acid sequence of ovine salivary carbonic anhydrase.

```
A;Reference number: A29993; MUID:88294021; PMID:3135834
A;Accession: A29993
A;Molecule type: protein
A;Residues: 1-307 <FER>
A;Cross-references: UNIPROT:P08060
A;Experimental source: parotid gland
A;Note: 63-Met and 297-Ile were also found
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; zinc
F;6-261/Domain: carbonic anhydrase homology <CAH>

  Query Match             29.9%;  Score 532.5;  DB 2;  Length 307;
  Best Local Similarity   39.9%;  Pred. No. 3.4e-36;
  Matches  124;  Conservative   55;  Mismatches  117;  Indels   15;  Gaps   11;

Qy         19 GQHWTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYD-QPGTEP 76
              |  ||| ||   : |||  ||:||   |||||:|   | ::| | ||   ||    |  |
Db          3 GVEWTYSEGMLDEAHWPLEYPKCGGRRQSPIDLQMKKVQYNPSLRALNLTGYGLWHGEFP 62

Qy         77 LDLHNNGHTVQLSLPSTLYLGGLP-RKYVAAQLHLHWGQKGSP-GGSEHQINSEATFAEL 134
              :   |||||||:|||||: :      :|:| |:| |||   |   ||||  ::      |:
Db         63 VT--NNGHTVQISLPSTMSMTTSDGTQYLAKQMHFHWGGASSEISGSEHTVDGMRYVIEI 120

Qy        135 HIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGE-TKNIAYEHILSHLHEVRHKDQKTSV 193
              |:|||:|  |:|  || : | |||||  |:|| : |:|  |   :||| ::|:  | | :
Db        121 HVVHYNS-KYNSYEEAQKEPDGLAVLAALVEVKDYTENAYYSKFISHLEDIRYAGQSTVL 179

Qy        194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
                 :: ::||  |   |: | |||||||| ::| | |     ::|  |:|||: :| : :
Db        180 RGLDIEDMLPGDLRYYYSYLGSLTTPPCTENVHWFVVADTVKLSKTQVEKLENSLLNHQ- 238

Qy        254 EPSKLLVQNYRALQPLNQRMVFASFI-QAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIA 312
              :| :  :||  |||| |:| |:|: :    ||    |  :  :   |  |    ||
Db        239 --NKTIQNDYRRTQPLNHRVVEANFMSRPHQEYTLASKLHFYLNNIDQTLEYLRR--FIE 294

Qy        313 RKI-RKKRLEN 322
              :|: ::|: ||
Db        295 QKMPKRKKQEN 305


RESULT 3
S71877
carbonate dehydratase (EC 4.2.1.1) isoform VI precursor - bovine
N;Alternate names: carbonic anhydrase VI
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71877; S03862
R;Jiang, W.; Woitach, J.T.; Gupta, D.
Biochem. J. 318, 291-296, 1996
A;Title: Sequence of bovine carbonic anhydrase VI: potential recognition sites for N-ace
A;Reference number: S71877; MUID:96358528; PMID:8761494
A;Accession: S71877
A;Molecule type: mRNA
A;Residues: 1-319 <JIA>
A;Cross-references: UNIPROT:P18915; EMBL:X96503; NID:g1526571; PIDN:CAA65357.1; PID:g152
A;Experimental source: submaxillary gland
R;Fernley, R.T.; Darling, P.; Aldred, P.; Wright, R.D.; Coghlan, J.P.
Biochem. J. 259, 91-96, 1989
A;Title: Tissue and species distribution of the secreted carbonic anhydrase isoenzyme.
A;Reference number: S03862; MUID:89246331; PMID:2497732
A;Accession: S03862
A;Molecule type: protein
A;Residues: 15,'S',17-36,'X',38-39 <FER>
C;Genetics:
A;Gene: CAH6
C;Function:
A;Description: catalyses the reversible dissociation of carbonic acid to carbon dioxide
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; glycoprotein; hydro-lyase; metalloprotein; zinc
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-319/Product: carbonate dehydratase isoform VI #status experimental <MAT>
F;18-273/Domain: carbonic anhydrase homology <CAH>
F;37-219/Disulfide bonds: #status predicted
F;62,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;106,108,133/Binding site: zinc (His) #status predicted

  Query Match             29.8%;  Score 530;  DB 2;  Length 319;
  Best Local Similarity   37.8%;  Pred. No. 5.8e-36;
  Matches  123;  Conservative   57;  Mismatches  125;  Indels   20;  Gaps   11;

Qy          6 LLLEVIWILAADGGQHWTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPAL 64
              : |  : :: |     ||| ||   : ||   ||:||   |||||::   | ::| | ||
Db          2 ITLLFLLVVGAQAQHEWTYSEGVLDEKHWRLQYPDCGGTRQSPIDLKMKKVRYNPSLRAL 61

Qy         65 QPHGYD-QPGTEPLDLHNNGHTVQLSLPSTLYL----GGLPRKYVAAQLHLHWGQKGSP- 118
                 ||  : |  |:   |||||||:||||:: :    |    :|:| |:| |||   |
Db         62 NLTGYGLRQGEFPMT--NNGHTVQISLPSSMRMTTSDGS---QYLAKQMHFHWGGDSSEI 116

Qy        119 GGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGE-TKNIAYEHI 177
              |||| ::      |:|:||| |  | |  ||   | |||||  |:|| :  :|  | :
Db        117 SGSEHTVDGMRYIIEIHVVHYHS-KYGSYEEAQNEPDGLAVLAALVEVKDYAENTYYSNF 175

Qy        178 LSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQIS 237
              :||| ::|:  | | :   :::::||  |  |: | |||||| | ::| | |     ::|
Db        176 ISHLEDIRYAGQSTVLRDLDIQDMLPGDLRYYYSYLGSLTTPSCTENVHWFVVADTVKLS 235

Qy        238 MEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFI-QAGSSYTTGEMLSLGVG 296
               |:|||: :| : : |    :  |||: |||| |:| |:|:      || |  |   :
Db        236 KTQIEKLENSLLNHQNE---TIQNNYRSTQPLNHRVVEANFVSHPHQEYTLGSKLHFYLN 292

Qy        297 ILVGCLCLLLAVYFIARKIRKKRLE 321
              :   |  |     || :|| |:: |
Db        293 NIDQNLEYLRR--FIEQKITKRKKE 315


RESULT 4
CRHU6
carbonate dehydratase (EC 4.2.1.1) VI precursor - human
N;Alternate names: carbonic anhydrase VI; salivary carbonic anhydrase; secreted carbonic
C;Species: Homo sapiens (man)
C;Date: 31-May-1991 #sequence_revision 05-May-1995 #text_change 02-Sep-1997
C;Accession: A37917
R;Aldred, P.; Fu, P.; Barrett, G.; Penschow, J.D.; Wright, R.D.; Coghlan, J.P.; Fernley,
Biochemistry 30, 569-575, 1991
A;Title: Human secreted carbonic anhydrase: cDNA cloning, nucleotide sequence, and hybri
A;Reference number: A37917; MUID:91105141; PMID:1899030
A;Accession: A37917
A;Molecule type: mRNA
A;Residues: 1-308 <ALD>
A;Cross-references: GB:M57892; GB:J05305
A;Experimental source: salivary gland
A;Note: the authors translated the codon GAG for residue 248 as Gln
C;Genetics:
A;Gene: GDB:CA6
A;Cross-references: GDB:125350; OMIM:114780
A;Map position: 1p36-1p36
C;Function:
A;Description: catalyzes the reversible dissociation of carbonic acid to carbon dioxide
A;Note: this form is expressed in salivary, parotid, and submandibular glands; it is exc
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; glycoprotein; hydro-lyase; metalloprotein; pyroglutamic
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-308/Product: carbonate dehydratase VI #status predicted <MAT>
F;23-278/Domain: carbonic anhydrase homology <CAH>
F;18/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;42-224/Disulfide bonds: #status predicted
F;67,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;111,113,138/Binding site: zinc (His) #status predicted

  Query Match             28.4%;  Score 505;  DB 1;  Length 308;
  Best Local Similarity   38.8%;  Pred. No. 6.3e-34;
  Matches  114;  Conservative   53;  Mismatches  107;  Indels   20;  Gaps   11;

Qy          5 ALLLEVIWILAADGGQH---WTY-EGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPD 60
              ||:| :   |      ||   ||| ||   : |||  || ||   ||||::|   | ::|
Db          3 ALVLLLSLFLLGGQAQHVSDWTYSEGALDEAHWPQHYPACGGQRQSPINLQRTKVRYNPS 62
```

```
Qy          61 LPALQPHGYD-QPGTEPLDLHNNGHTVQLSLPSTLYL---GGLPRKYVAAQLHLHWGQKG 116
               |  |   ||: | |  |  : |||||||: ||||: :    |:   |:| |:| |||
Db          63 LKGLNMTGYETQAGEFP--MVNNGHTVQIGLPSTMRMTVADGI--VYIAQQMHFHWGGAS 118

Qy         117 SP-GGSEHQINSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEV-GETKNIAY 174
               |   |||| ::      |:|||||:|  | :   | : | |||||   :||    :|  |
Db         119 SEISGSEHTVDGIRHVIEIHIVHYNS-KYKTYDIAQDAPDGLAVLAAFVEVKNYPENTYY 177

Qy         175 EHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRS 234
                : :|||  :::  |:|::   :::::||: |  |: |:|||||||| ::| | |
Db         178 SNFISHLANIKYPGQRTTLTGLDVQDMLPRNLQHYYTYHGSLTTPPCTENVHWFVLADFV 237

Qy         235 QISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTG 288
               ::|  |: ||: :|    :  :| :  :||  |||| |:| ::|      || |
Db         238 KLSRTQVWKLENSLL---DHRNKTIHNDYRRTQPLNHRVVESNF--PNQEYTLG 286


RESULT 5
B48148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B48148
R;Barnea, G.; Silvennoinen, O.; Shaanan, B.; Honegger, A.M.; Canoll, P.D.; D'Eustachio,
Mol. Cell. Biol. 13, 1497-1506, 1993
A;Title: Identification of a carbonic anhydrase-like domain in the extracellular region
A;Reference number: A48148; MUID:93180796; PMID:8382771
A;Accession: B48148
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1442 <BAR>
A;Cross-references: UNIPROT:Q05909; GB:L09562; NID:g293773; PIDN:AAA40022.1; PID:g293774
C;Genetics:
A;Gene: Ptprg
A;Map position: 14
A;Note: extensively polymorphic
C;Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom
ne-phosphatase homology
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; polymorphism; receptor; tran
F;60-321/Domain: carbonic anhydrase homology <CAH>
F;346-434/Domain: fibronectin type III repeat homology <3FR>
F;871-1105/Domain: protein-tyrosine-phosphatase homology <PTP>
F;1172-1396/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1057/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1063/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             25.8%;  Score 458.5;  DB 1;  Length 1442;
  Best Local Similarity   32.1%;  Pred. No. 3.5e-29;
  Matches  100;  Conservative   53;  Mismatches  152;  Indels    7;  Gaps    3;

Qy          16 ADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE 75
               | |  :| | | :| :||  |   || : ||||||        :   ||  |:|   :
Db          54 ASGDPYWAYSGAYGPEHWVTSSVSCGGSHQSPIDILDHHARVGDEYQELQLDGFDNESSN 113

Qy          76 PLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAE 133
                  : | | || : |    ::   ||| :: | ::  |||       |||| :|      |
Db         114 KTWMKNTGKTVAILLKDDYFVSGAGLPGRFKAEKVEFHWGHSNGSAGSEHSVNGRRFPVE 173

Qy         134 LHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSV 193
               : |  |: | :||    |    : :  : |  :|  |  | :|:  |:|::| :
Db         174 MQIFFYNPDDFDSFQTAISENRIIGAMAIFFQVSPRDNSALDPIIHGLKGVVHHEKETFL 233

Qy         194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
                || ||:|||  || |:|| |||||||| : | | || |   ||  |||    ::|:||:
Db         234 DPFILRDLLPASLGSYYRYTGSLTTPPCSEIVEWIVFRRPVPISYHQLEAFY-SIFTTEQ 292

Qy         254 EPS----KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVY 309
               :      : |  |:|  | || |:|  | ::   ::   : |   :|     :|    ::
Db         293 QDHVKSVEYLRNNFRPQQALNDRVVSKSAVRDAWNHDLADFLDNPLGTEASKVCSSPPIH 352

Qy         310 FIARKIRKKRLE 321
                  : : :  |:
Db         353 MKVQPLNQTALQ 364


RESULT 6
T42636
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42636
R;Qinghua, X.; Xiaojun, G.; Cong, S.; Zong, S.M.; Jong, Y.J.; Chan, J.; Wang, L.H.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z22226
A;Accession: T42636
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1422 <QIN>
A;Cross-references: UNIPROT:Q98936; EMBL:U38349; NID:g1617477; PID:g1617478; PIDN:AAB169
A;Experimental source: kidney and brain
C;Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom
ne-phosphatase homology
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot

  Query Match             25.4%;  Score 452.5;  DB 2;  Length 1422;
  Best Local Similarity   32.2%;  Pred. No. 1.1e-28;
  Matches  105;  Conservative   54;  Mismatches  154;  Indels   13;  Gaps    4;

Qy          16 ADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE 75
               | |  :| | | :| :||  |  :|| : ||||||          :   ||  |:|   :
Db          54 ASGDPYWGYSGTYGPEHWVTSSEKCGGSHQSPIDIVDHQAHVLYEYQELQLDGFDNESSN 113

Qy          76 PLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAE 133
                  : | | || : |    ::   ||| :: | ::  ||||      |||| || :     |
Db         114 KTWMKNTGKTVAILLKDDYFVSGAGLPGRFKAEKVEFHWGQSNGSAGSEHSINGKRFPVE 173

Qy         134 LHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSV 193
               : |  |: | :||    |    : :  : :  :| :  | | : |:  |  | | :::| :
Db         174 MQIYFYNPDDFDSFGTAVLENREVGAMAVFFQVSQRDNSALDPIIRGLKGVVHHEKETFL 233

Qy         194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
                || ||:|||  || |:|| |||||||| : | | :| :   ||  |||    ::|:||:
Db         234 DPFVLRDLLPTSLGSYYRYTGSLTTPPCSEIVEWIIFRKPVPISYHQLEAFY-SIFTTEQ 292

Qy         254 EPS----KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVY 309
               :      : |  |:|  | || | :|  | ::   |    ::|    :|     |    |
Db         293 QDHVKSVEYLRNNFRPQQRLNNRKVSKSAVKDAWSQDMTDILENPLGTEASKACSTPPVN 352

Qy         310 FIARKIRKKRLENRKSVVFTSAQATT 335
                  : :      || ::: |  |  |
Db         353 MKVQPV------NRTALLVTWNQPET 372


RESULT 7
A48148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A48148; C36065; S12051
R;Barnea, G.; Silvennoinen, O.; Shaanan, B.; Honegger, A.M.; Canoll, P.D.; D'Eustachio, P
Mol. Cell. Biol. 13, 1497-1506, 1993
A;Title: Identification of a carbonic anhydrase-like domain in the extracellular region c
A;Reference number: A48148; MUID:93180796; PMID:8382771
A;Accession: A48148
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1445 <BAR>
A;Cross-references: UNIPROT:P23470
A;Note: sequence extracted from NCBI backbone (NCBIP:125788)
R;Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Howk, R.; Ravera, M.; Ricca, G.; Jaye, M
Proc. Natl. Acad. Sci. U.S.A. 87, 7000-7004, 1990
A;Title: Cloning of three human tyrosine phosphatases reveals a multigene family of recep
A;Reference number: A36065; MUID:90384936; PMID:2169617
A;Accession: C36065
A;Status: preliminary; not compared with conceptual translation
```

```
A;Molecule type: mRNA
A;Residues: 874-1118;1175-1409 <KAP>
R;Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A;Reference number: S12049; MUID:91006018; PMID:2170109
A;Accession: S12051
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 836-1406,'M',1408-1445 <KRU>
A;Cross-references: GB:X54132; NID:g35793; PIDN:CAA38067.1; PID:g35794
C;Genetics:
A;Gene: GDB:PTPRG; D3S1249
A;Cross-references: GDB:127351; OMIM:176886
A;Map position: 3p14.2-3p14.2
C;Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom
ne-phosphatase homology
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
F;60-321/Domain: carbonic anhydrase homology <CAH>
F;346-434/Domain: fibronectin type III repeat homology <3FN>
F;742-758/Domain: transmembrane #status predicted <TMN>
F;874-1108/Domain: protein-tyrosine-phosphatase homology <PTP>
F;1175-1399/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1060/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1066/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             25.3%;  Score 449.5;  DB 1;  Length 1445;
  Best Local Similarity   32.1%;  Pred. No. 2e-28;
  Matches  100;  Conservative   53;  Mismatches  152;  Indels    7;  Gaps    3;

Qy         16 ADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE 75
Db         54 ASGDPYWAYSGAYGPEHWVTSSVSCGSRHQSPIDILDQYARVGEEYQELQLDGFDNESSN 113

Qy         76 PLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAE 133
Db        114 KTWMKNTGKTVAILLKDDYFVSGAGLPGRFKAEKVEFHWGHSNGSAGSEHSINGRRFPVE 173

Qy        134 LHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSV 193
Db        174 MQIFFYNPDDFDSFQTAISEWRIIGAMAIFFQVSPRDNSALDPIIHGLKGVVHHEKETFL 233

Qy        194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
Db        234 DPFVLRDLLPASLGSYYRYTGSLTTPPCSEIVEWIVFRRPVPISYHQLEAFY-SIFTTEQ 292

Qy        254 EPS----KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVY 309
Db        293 QDHVKSVEYLRNNFRPQQRLHDRVVSKSAVRDSWNHDMTDFLENPLGTEASKVCSSPPIH 352

Qy        310 FIARKIRKKRLE 321
Db        353 MKVQPLNQTALQ 364


RESULT 8
CRRB2
carbonate dehydratase (EC 4.2.1.1) II - rabbit (tentative sequence)
N;Alternate names: carbonic anhydrase II
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 31-Mar-2000
C;Accession: A01142
R;Ferrell, R.E.; Stroup, S.K.; Tanis, R.J.; Tashian, R.E.
Biochim. Biophys. Acta 533, 1-11, 1978
A;Title: Amino acid sequence of rabbit carbonic anhydrase II.
A;Reference number: A01142; MUID:78144871; PMID:416851
A;Accession: A01142
A;Molecule type: protein
A;Residues: 1-259 <FER>
A;Note: 203-Glu was also found
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; zinc
F;4-258/Domain: carbonic anhydrase homology <CAH>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;93,95,118/Binding site: zinc (His) #status predicted

  Query Match             23.9%;  Score 425;  DB 1;  Length 259;
  Best Local Similarity   37.4%;  Pred. No. 1.9e-27;
  Matches   99;  Conservative   39;  Mismatches  113;  Indels   14;  Gaps    8;

Qy         21 HWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLH 80
Db          3 HWGYGKHNGPEHWHKDFPIADGERQSPIDIDTDAAKHDPSLKPLRV-SYEHPISR--RII 59

Qy         81 NNGHTVQLSL-----PSTLYLGGLPRKYVAAQLHLHWGQKGSPG-GSEHQINSEATFAEL 134
Db         60 NNGHSFNVEFDDSHDKSVLKEGPLEGTYRLIQFHFHWG--SSDGEGSEHTVNKKKYAAEL 117

Qy        135 HIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVP 194
Db        118 HLVHWNT-KYGDFGKAVKHPDGLAVLGIFLKIG-SATPGLQKVVDTLSSIKTKGKSVDFT 175

Qy        195 PFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEE 254
Db        176 NFDPRGLLPESL-DYWTYPGSLTTPPLLQCVTWIVLKEPITVSSEQMLKFRNLNFNKEAE 234

Qy        255 PSKLLVQNYRALQPLNQRMVFASFI 279
Db        235 PEEPMVDNWRPTQPLKGRQVKASFV 259


RESULT 9
I51900
carbonic anhydrase IV - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51900; A42589
R;Fleming, R.E.; Crouch, E.C.; Ruzicka, C.A.; Sly, W.S.
Am. J. Physiol. 265, L627-L635, 1993
A;Title: Pulmonary carbonic anhydrase IV: developmental regulation and cell-specific expr
A;Reference number: I51900; MUID:94106650; PMID:8279579
A;Accession: I51900
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-309 <RES>
A;Cross-references: UNIPROT:P48284; GB:S68245; NID:g544725; PIDN:AAB29505.1; PID:g544726
R;Waheed, A.; Zhu, X.L.; Sly, W.S.
J. Biol. Chem. 267, 3308-3311, 1992
A;Title: Membrane-associated carbonic anhydrase from rat lung. Purification, characteriza
A;Reference number: A42589; MUID:92147688; PMID:1737787
A;Accession: A42589
A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-22,'X',24-33,'XX',36-38 <WAH>
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:81133)
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
F;22-282/Domain: carbonic anhydrase homology <CAH>

  Query Match             23.8%;  Score 423;  DB 2;  Length 309;
  Best Local Similarity   34.0%;  Pred. No. 3.5e-27;
  Matches  111;  Conservative   54;  Mismatches  113;  Indels   48;  Gaps   13;

Qy          7 LLEVIWILAADGGQHWTYE------GPH--GQDHWPASYPECGNNAQSPIDIQTDSVTFD 58
Db          7 LLALAYVAPSTEDSHWCYEIQAKEPNSHCSGPEQWTG---DCKKNQQSPINIVTSKTKLN 63

Qy         59 PDLPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKG 116
Db         64 PSLTPFTFVGYDQ--KKKWEVKNNQHSVEMSLGEDIYIFGGDLPTQYKAIQLHLHWSEE- 120

Qy        117 SPGGSEHQINSEATFAELHIVH---------YDSDSYDSLSEAAERPQGLAVLGILIEVG 167
Db        121 SNKGSEHSIDGKHFAMEMHVVHKKMTTGDKVQDSDSKDK----------IAVLAFMVEVG 170

Qy        168 ETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLP--KQLGQYFRYNGSLTTPPCYQSV 225
```

```
Db        171 NEVNEGFQPLVEALSRLSKPFTNSTVSESCLQDMLPEKKKLSAYFRYQGSLTTPGCDETV 230

Qy        226 LWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKL-LVQNYRALQPLNQRMVFASFIQAGSS 284

Db        231 IWTVFEEPIKIHKDQFLEFSKKLYYDQEQ--KLNMKDNVRPLQPLGNRQVF-------RS 281

Qy        285 YTTGEMLSLGV-GILVGCLCLLLAVY 309

Db        282 HASGRLLSLPLPTLLVPTLTCLVASF 307


RESULT 10
CRHU2
carbonate dehydratase (EC 4.2.1.1) II [validated] - human
N;Alternate names: carbonic anhydrase II; hepatic carbonic anhydrase
C;Species: Homo sapiens (man)
C;Date: 07-May-1981 #sequence_revision 05-May-1995 #text_change 09-Jul-2004
C;Accession: A27175; A23202; A92194; A92147; I37214; I51863; I51871; A01141
R;Murakami, H.; Marelich, G.P.; Grubb, J.H.; Kyle, J.W.; Sly, W.S.
Genomics 1, 159-166, 1987
A;Title: Cloning, expression, and sequence homologies of cDNA for human carbonic anhydra
A;Reference number: A27175; MUID:88085190; PMID:3121496
A;Accession: A27175
A;Molecule type: mRNA
A;Residues: 1-260 <MUR>
A;Cross-references: UNIPROT:P00918; GB:J03037; NID:g179771; PIDN:AAA51908.1; PID:g179772
R;Venta, P.J.; Montgomery, C.; Hewett-Emmett, D.; Tashian, R.E.
Biochim. Biophys. Acta 826, 195-201, 1985
A;Title: Comparison of the 5' regions of human and mouse carbonic anhydrase II genes and
A;Reference number: A90655; MUID:86077780; PMID:3000449
A;Accession: A23202
A;Molecule type: DNA
A;Residues: 1-77 <VEN>
A;Cross-references: GB:X03251; GB:M18100; GB:M77181; NID:g179778; PIDN:AAA51909.1; PID:g
R;Henderson, L.E.; Henriksson, D.; Nyman, P.O.
J. Biol. Chem. 251, 5457-5463, 1976
A;Title: The primary structure of human carbonic anhydrase C.
A;Reference number: A92194; MUID:77006079; PMID:823150
A;Accession: A92194
A;Molecule type: protein
A;Residues: 2-260 <HEN>
R;Lin, K.T.D.; Deutsch, H.F.
J. Biol. Chem. 249, 2329-2337, 1974
A;Title: Human carbonic anhydrases. XII. The complete primary structure of the C isozyme
A;Reference number: A92147; MUID:74143468; PMID:4207120
A;Accession: A92147
A;Molecule type: protein
A;Residues: 2-260 <LIN>
R;Montgomery, J.C.; Venta, P.J.; Tashian, R.E.; Hewett-Emmett, D.
Nucleic Acids Res. 15, 4687, 1987
A;Title: Nucleotide sequence of human liver carbonic anhydrase II cDNA.
A;Reference number: I37214; MUID:87231043; PMID:3108857
A;Accession: I37214
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-260 <RE3>
A;Cross-references: EMBL:Y00339; NID:g29586; PIDN:CAA68426.1; PID:g29587
A;Experimental source: liver
A;Note: submitted to the EMBL/GenBank/DDBJ databases by David Hewett-Emmett 01-JUL-1987
R;Venta, P.J.; Welty, R.J.; Johnson, T.M.; Sly, W.S.; Tashian, R.E.
Am. J. Hum. Genet. 49, 1082-1090, 1991
A;Title: Carbonic anhydrase II deficiency syndrome in a Belgian family is caused by a po
e.
A;Reference number: I51863; MUID:92026087; PMID:1928091
A;Accession: I51863
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <RES>
A;Cross-references: GB:M77181; NID:g179778; PIDN:AAA51909.1; PID:g179780
A;Note: the complete nucleotide sequence is not shown
R;Hu, P.Y.; Ernst, A.R.; Sly, W.S.; Venta, P.J.; Skaggs, L.A.; Tashian, R.E.
Am. J. Hum. Genet. 54, 602-608, 1994
A;Title: Carbonic anhydrase II deficiency: single-base deletion in exon 7 is the predomi
A;Reference number: I51871; MUID:94175074; PMID:8128957
A;Accession: I51871
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 225-242 <RE2>
A;Cross-references: GB:S69526; NID:g545850; PIDN:AAB30170.1; PID:g545851
A;Note: wild type shown; mutant contains frameshift after residue 226
R;Eriksson, A.E.; Jones, T.A.; Liljas, A.
submitted to the Brookhaven Protein Data Bank, February 1989
A;Reference number: A50085; PDB:1CA2
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 4-259
R;Liljas, A.; Kannan, K.K.; Bergsten, P.C.; Waara, I.; Fridborg, K.; Strandberg, B.; Car
Nature New Biol. 235, 131-137, 1972
A;Title: Crystal structure of human carbonic anhydrase C.
A;Reference number: A93404; MUID:72111787; PMID:4621826
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
A;Note: other residues at the active site are His-64, Asn-67, Tyr-127, Leu-197, Thr-198,
C;Genetics:
A;Gene: GDB:CA2
A;Cross-references: GDB:119739; OMIM:259730
A;Map position: 8q13-8q22.1
A;Introns: 12/1; 78/1; 117/3; 148/3; 169/3; 221/3
C;Function:
A;Description: catalyzes the reversible dissociation of carbonic acid to carbon dioxide
A;Note: this form is expressed in erythrocytes and other tissues; deficiency of this form
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; metalloprotein; monor
F;2-260/Product: carbonate dehydratase II #status experimental <MAT>
F;5-259/Domain: carbonic anhydrase homology <CAH>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F;94,96,119/Binding site: zinc (His) #status experimental

  Query Match             23.6%;  Score 420;  DB 1;  Length 260;
  Best Local Similarity   36.5%;  Pred. No. 4.9e-27;
  Matches   96;  Conservative   39;  Mismatches  116;  Indels   12;  Gaps    7;

Qy         21 HWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLH 80

Db          4 HWGYGKHNGPEHWHKDFPIAKGERQSPVDIDTHTAKYDPSLKPLSV-SYDQ--ATSLRIL 60

Qy         81 NNGHTVQLSL-----PSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELH 135

Db         61 NNGHAFNVEFDDSQDKAVLKGGPLDGTYRLIQFHFHWGSLDGQ-GSEHTVDKKKYAAELH 119

Qy        136 IVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP 195

Db        120 LVHWNT-KYGDFGKAVQQPDGLAVLGIFLKVGSAKP-GLQKVVDVLDSIKTKGKSADFTN 177

Qy        196 FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEP 255

Db        178 FDPRGLLPESL-DYWTYPGSLTTPPLLECVTWIVLKEPISVSSEQVLKFRKLNFNGEGEP 236

Qy        256 SKLLVQNYRALQPLNQRMVFASF 278

Db        237 EELMVDNWRPAQPLKNRQIKASF 259


RESULT 11
JC2580
carbonate dehydratase (EC 4.2.1.1) II - chicken
N;Alternate names: carbonic anhydrase II
C;Species: Gallus gallus (chicken)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: JC2580; S10229; S01078; A26415; I50181; S31987
R;Mezquita, W.; Pau, M.; Mezquita, C.
Gene 147, 231-235, 1994
A;Title: A novel carbonic anhydrase II mRNA isolated from mature chicken testis displays
A;Reference number: JC2580; MUID:95011620; PMID:7926806
A;Accession: JC2580
A;Molecule type: mRNA
A;Residues: 1-260 <MEZ>
A;Cross-references: UNIPROT:P07630; EMBL:Z14957; NID:g65331; PIDN:CAA78681.1; PID:g65332
```

```
A;Experimental source: testis
R;Godbout, R.; Andison, R.; Upton, C.; Day, R.
Nucleic Acids Res. 18, 1049, 1990
A;Title: Utilization of the second polyadenylation signal at the 3' end of the chicken c
A;Reference number: S10229; MUID:90192090; PMID:1969140
A;Accession: S10229
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 222-260 <GOD>
A;Cross-references: EMBL:X17378; NID:g63127; PIDN:CAA35250.1; PID:g63128
R;Yoshihara, C.M.; Lee, J.D.; Dodgson, J.B.
Nucleic Acids Res. 15, 753-770, 1987
A;Title: The chicken carbonic anhydrase II gene: evidence for a recent shift in intron p
A;Reference number: S01078; MUID:87146391; PMID:3029691
A;Accession: S01078
A;Molecule type: DNA
A;Residues: 1-249,'V',251-260 <YOS>
A;Cross-references: EMBL:X06000; NID:g63115; PIDN:CAA29417.1; PID:g1289219
A;Note: the authors translated the codon GTA for residue 250 as Leu
R;Rogers, J.H.
Eur. J. Biochem. 162, 119-122, 1987
A;Title: Sequence of carbonic anhydrase II cDNA from chick retina.
A;Reference number: A26415; MUID:87133522; PMID:3102231
A;Accession: A26415
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'L',6-260 <ROG>
A;Cross-references: EMBL:X04810; NID:g63129; PIDN:CAA28501.1; PID:g833606
R;Yoshihara, C.M.; Federspiel, M.; Dodgson, J.B.
Ann. N. Y. Acad. Sci. 429, 332-334, 1984
A;Title: Isolation of the chicken carbonic anhydrase II gene.
A;Reference number: I50181; MUID:84255154; PMID:6331256
A;Accession: I50181
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'GX',10-16,'X',18,'X',20-43,'X',45-78,'X',80-86,'S' <YO2>
A;Cross-references: GB:M25943; NID:g211369; PIDN:AAA48646.1; PID:g211370
C;Genetics:
A;Introns: 12/1; 78/1; 117/3; 148/3; 169/3; 221/3
C;Function:
A;Description: catalyzes the reversible dissociation of carbonic acid to carbon dioxide
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; metalloprotein; zinc
F;5-259/Domain: carbonic anhydrase homology <CAH>
F;94,96,119/Binding site: zinc (His) #status predicted

  Query Match             23.3%;  Score 415;  DB 2;  Length 260;
  Best Local Similarity   37.5%;  Pred. No. 1.3e-26;
  Matches   99;  Conservative   39;  Mismatches  112;  Indels   14;  Gaps    7;

Qy          21 HWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLH 80
               || |:  :|  ||   :|       |||| | | :  :|   |||:|  :         :
Db           4 HWGYDSHNGPAHWHEHFPIANGERQSPIAISTKAARYD---PALKPLSFSYDAGTAKAIV 60

Qy          81 NNGHTVQL-----SLPSTLYLGGLPRKYVAAQLHLHWGQ-KGSPGGSEHQINSEATFAEL 134
               ||||:  :     |  | |  | |    |   | |:|||  :|   ||||  ::     |||
Db          61 NNGHSFNVEFDDSSDKSVLQGGALDGVYRLVQFHIHWGSCEGQ--GSEHTVDGVKYDAEL 118

Qy         135 HIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVP 194
               ||||::    |   :|| : | ||||:|| ::||  |    : ::  |: :: | :: |
Db         119 HIVHWNV-KYGKFAEALKHPDGLAVVGIFMKVGNAKP-EIQKVVDALNSIQTKGKQASFT 176

Qy         195 PFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEE 254
                |:   |||      |: | ||||||| :: |:| |      :| ||: ||:|  || | |
Db         177 NFDPTGLLP-PCRDYWTYPGSLTTPPLHECVIWHVLKEPITVSSEQMCKLRGLCFSAENE 235

Qy         255 PSKLLVQNYRALQPLNQRMVFASF 278
               |   :| |:|  |||  | | |||
Db         236 PVCRMVDNWRPCQPLKSREVRASF 259


RESULT 12
CRHU7
carbonate dehydratase (EC 4.2.1.1) VII - human
N;Alternate names: carbonic anhydrase VII
C;Species: Homo sapiens (man)
C;Date: 10-Feb-1995 #sequence_revision 05-May-1995 #text_change 09-Jul-2004
C;Accession: A55272
R;Montgomery, J.C.; Venta, P.J.; Eddy, R.L.; Fukushima, Y.S.; Shows, T.B.; Tashian, R.E.
Genomics 11, 835-848, 1991
A;Title: Characterization of the human gene for a newly discovered carbonic anhydrase, CA
A;Reference number: A55272; MUID:92147127; PMID:1783392
A;Accession: A55272
A;Molecule type: DNA
A;Residues: 1-264 <MON>
A;Cross-references: UNIPROT:P43166; GB:M76423; NID:g179964; PIDN:AAA51923.1; PID:g179967
A;Note: sequence extracted from NCBI backbone (NCBIN:80199, NCBIN:80201, NCBIN:80205, NCB
C;Genetics:
A;Gene: GDB:CA7
A;Cross-references: GDB:119741; OMIM:114770
A;Map position: 16q22.1-16q22.1
A;Introns: 14/1; 80/1; 119/3; 151/3; 172/3; 224/3
C;Function:
A;Description: catalyzes the reversible dissociation of carbonic acid to carbon dioxide a
A;Note: this form is expressed in salivary gland and other tissues
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; metalloprotein; zinc
F;2-264/Product: carbonate dehydratase VII #status predicted <MAT>
F;7-262/Domain: carbonic anhydrase homology <CAH>
F;96,98,121/Binding site: zinc (His) #status predicted

  Query Match             23.1%;  Score 411;  DB 1;  Length 264;
  Best Local Similarity   37.2%;  Pred. No. 2.8e-26;
  Matches   99;  Conservative   41;  Mismatches  114;  Indels   12;  Gaps    7;

Qy          19 GQH-WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPL 77
               | | | |    |  ||   ||    : ||||:| :    :    |:|||        |
Db           3 GHHGWGYGQDDGPSHWHKLYPIAQGDRQSPINIISSQAVYS---PSLQPLELSYEACMSL 59

Qy          78 DLHNNGHTVQL----SLPSTLYLGG-LPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFA 132
               : ||||:||:    |   |:  || |   |   | | |||:|    |||| :: ::  :
Db          60 SITNNGHSVQVDFNDSDDRTVVTGGPLEGPYRLKQFHFHWGKKHDV-GSEHTVDGKSFPS 118

Qy         133 ELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTS 192
               |||:||:::  | :  |||  | ||||:|: :| |: :: :   :   |: || | |
Db         119 ELHLVHWNAKKYSTFGEAASAPDGLAVVGVFLETGD-EHPSMNRLTDALYMVRFKGTKAQ 177

Qy         193 VPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE 252
                 || : |||     |: | |||||||  :|| | |      ||  |: | :  ||::|
Db         178 FSCFNPKCLLPAS-RHYWTYPGSLTTPPLSESVTWIVLREPICISERQMGKFRSLLFTSE 236

Qy         253 EEPSKLLVQNYRALQPLNQRMVFASF 278
               ::    :| |:|  |||  |:| |||
Db         237 DDERIHMVNNFRPPQPLKGRVVKASF 262


RESULT 13
A26344
carbonate dehydratase (EC 4.2.1.1) I - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: A26344; I49573
R;Fraser, P.J.; Curtis, P.J.
J. Mol. Evol. 23, 294-299, 1986
A;Title: Molecular evolution of the carbonic anhydrase genes: calculation of divergence t
A;Reference number: A26344; MUID:87169766; PMID:3104601
A;Accession: A26344
A;Molecule type: mRNA
A;Residues: 1-261 <FRA>
A;Cross-references: UNIPROT:P13634
R;Fraser, P.; Cummings, P.; Curtis, P.
Mol. Cell. Biol. 9, 3308-3313, 1989
A;Title: The mouse carbonic anhydrase I gene contains two tissue-specific promoters.
A;Reference number: I49573; MUID:90014784; PMID:2571923
A;Accession: I49573
A;Status: preliminary; translated from GB/EMBL/DDBJ
```

```
A;Molecule type: DNA
A;Residues: 1-82,'G',83-100,102-261 <RES>
A;Cross-references: GB:L36655; NID:g556293; PIDN:AAA50291.1; PID:g556295
C;Genetics:
A;Gene: Car1
A;Introns: 13/1; 79/1; 118/3; 150/3; 171/3; 223/3
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; zinc
F;6-261/Domain: carbonic anhydrase homology <CAH>

  Query Match             23.0%;  Score 409.5;  DB 2;  Length 261;
  Best Local Similarity   37.2%;  Pred. No. 3.6e-26;
  Matches   97;  Conservative   39;  Mismatches  116;  Indels    9;  Gaps    6;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              | |   :| | |   ||    | ||||||:|     |  |  |     |: | |   :: |
Db          6 WGYGSENGPDQWSKLYPIANGNNQSPIDIKTSEANHDSSLKPLS-ISYN-PATAK-EIVN 62

Qy         82 NGHTVQL----SLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIV 137
               ||:  :    |   ::  | |   |   | | |||   :  |||| ::      |||:|
Db         63 VGHSFHVIFDDSSNQSVLKGPLADSYRLTQFHFHWGNSSNDHGSEHTVDGTRYSGELHLV 122

Qy        138 HYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197
              |::|  | | |||  :  |||:||:|::||   | : : :|  |: |: | ::     |:
Db        123 HWNSAKYSSASEAISKADGLAILGVLMKVGPA-NPSLQKVLDALNSVKTKGKRAPFTNFD 181

Qy        198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSK 257
                 |||  |  |: | |||| || ::|| | :      :| ||| :|:| | | | | :
Db        182 PSSLLPSSL-DYWTYFGSLTHPPLHESVTWVICKDSISLSPEQLAQLRGLLSSAEGESAV 240

Qy        258 LLVQNYRALQPLNQRMVFASF 278
               :: |:|  |||  | | |||
Db        241 PVLSNHRPPQPLKGRTVRASF 261


RESULT 14
A48993
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma precursor (allelic varia
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 16-Feb-1996 #text_change 20-Mar-1998
C;Accession: A48993
R;Wary, K.K.; Lou, Z.; Buchberg, A.M.; Siracusa, L.D.; Druck, T.; LaForgia, S.; Huebner,
Cancer Res. 53, 1498-1502, 1993
A;Title: A homozygous deletion within the carbonic anhydrase-like domain of the Ptprg ge
A;Reference number: A48993; MUID:93201530; PMID:8453613
A;Accession: A48993
A;Molecule type: mRNA; DNA
A;Residues: 1-306 <WAR>
A;Experimental source: B6/CBA mouse lung cDNA library and genomic library
A;Note: authors translated the codon TTC for residue 274 as Ala
A;Note: sequence extracted from NCBI backbone (NCBIN:127780, NCBIP:127784) and corrected
C;Genetics:
A;Gene: Ptprg
A;Map position: 14
A;Introns: 92/1; 158/1; 198/3; 226/1; 252/3; 305/3 #status incomplete
A;Note: extensively polymorphic
C;Superfamily: protein-tyrosine-phosphatase, receptor type gamma; carbonic anhydrase hom
ne-phosphatase homology
C;Keywords: phosphoric monoester hydrolase; polymorphism; receptor; transmembrane protei
F;85-306/Domain: carbonic anhydrase homology (fragment) <CAH>

  Query Match             23.0%;  Score 409;  DB 2;  Length 306;
  Best Local Similarity   36.0%;  Pred. No. 5e-26;
  Matches   82;  Conservative   34;  Mismatches  110;  Indels    2;  Gaps    1;

Qy         16 ADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE 75
              | |  :| | | :| :||  |   || : ||||||          :   || :|:|   :
Db         79 ASGDPYWAYSGAYGPEHWVTSSVSCGGSHQSPIDILDHHARVGDEYQELQLYGFDNESSN 138

Qy         76 PLDLHNNGHTVQLSLPSTLYL--GGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAE 133
                 : | | || : |    ::   ||| :: | ::  |||      |||| :|      |
Db        139 KTWMKNTGKTVAILLKDDYFVSGAGLPGRFKAEKVEFHWGHSNGSAGSEHSVNGRRFPVE 198

Qy        134 LHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSV 193
              : |  |: | :||   |    : :  : |  :|    | | : |:  |  | | :::| :
Db        199 MQIFFYNPDDFDSFQTAISENRIIGAMAIFFQVSPRDNSALDPIIHGLKGVVHHEKETFL 258

Qy        194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQL 241
              || ||:|||  || |:|| |||||||| : | | || |   ||  |:
Db        259 DPFILRDLLPASLGSYYRYTGSLTTPPCSEIVEWIVFRRPVPISYHQV 306


RESULT 15
CRSH2
carbonate dehydratase (EC 4.2.1.1) II - sheep (tentative sequence)
N;Alternate names: carbonic anhydrase II
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C;Accession: A01145
R;Tanis, R.J.; Ferrell, R.E.; Tashian, R.E.
Biochim. Biophys. Acta 371, 534-548, 1974
A;Title: Amino acid sequence of sheep carbonic anhydrase C.
A;Reference number: A90598; MUID:75054988; PMID:4215456
A;Accession: A01145
A;Molecule type: protein
A;Residues: 1-259 <TAN>
A;Cross-references: UNIPROT:P00922
R;Mallet, B.; Gulian, J.M.; Sciaky, M.; Laurent, G.; Charrel, M.
Biochim. Biophys. Acta 576, 290-304, 1979
A;Title: Formes moleculaires multiples de l'anhydrase carbonique erythrocytaire ovine.
A;Reference number: A90628; MUID:79145542; PMID:106895
A;Contents: annotation
A;Note: one minor and three major forms were isolated chromatographically. One of these
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; zinc
F;4-258/Domain: carbonic anhydrase homology <CAH>
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;93,95,118/Binding site: zinc (His) #status predicted

  Query Match             22.8%;  Score 406;  DB 1;  Length 259;
  Best Local Similarity   35.6%;  Pred. No. 7e-26;
  Matches   93;  Conservative   44;  Mismatches  108;  Indels   16;  Gaps    9;

Qy         21 HWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHG--YDQPGTEPLD 78
              || |   :| :||   :|      |||:|| | :|   || |||:|    |:|  :
Db          3 HWGYGEHNGPEHWHKDFPIADGERQSPVDIDTKAVV--PD-PALKPLALLYEQAASR--R 57

Qy         79 LHNNGHTVQLSL-----PSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAE 133
              : ||||:  :        : |  | |   |   | | |||      |||| :: :   ||
Db         58 MVNNGHSFNVEFDDSQDKAVLKDGPLTGTYRLVQFHFHWGSSDDQ-GSEHTVDRKKYAAE 116

Qy        134 LHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSV 193
              ||:||:::  |     ||::| ||||:|: ::||:  | | : :|  |  :: | :
Db        117 LHLVHWNT-KYGDFGTAAQQPDGLAVVGVFLKVGDA-NPALQKVLDVLDSIKTKGKSADF 174

Qy        194 PPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEE 253
              |.|:   || : |  |: | |||| ||  :|| | |    : :| :|: | :   |: |
Db        175 PNFDPSSLLKRAL-NYWTYPGSLTNPPLLESVTWVVLKEPTSVSSQQMLKFRSLNFNAEG 233

Qy        254 EPSKLLVQNYRALQPLNQRMV 274
              ||  |:: |:|  |||  | |
Db        234 EPELLMLANWRPAQPLKNRQV 254


Search completed: May  4, 2005, 15:14:04
Job time : 77 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:31:00 ; Search time 43 Seconds
(without alignments)
585.040 Million cell updates/sec

Title: US-10-063-583-74
Perfect score: 1779
Sequence: 1 MLFSALLLEVIWILAADGGQ.....KRLENRKSVVFTSAQATTEA 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	696.5	39.2	354	1	US-08-276-919-2	Sequence 2, Appli
2	696.5	39.2	354	1	US-08-776-088-2	Sequence 2, Appli
3	696.5	39.2	354	1	US-08-776-088-6	Sequence 6, Appli
4	696.5	39.2	354	3	US-09-325-320-2	Sequence 2, Appli
5	696.5	39.2	354	3	US-09-585-109-2	Sequence 2, Appli
6	696.5	39.2	354	4	US-09-949-016-6043	Sequence 6043, Ap
7	696.5	39.2	354	5	PCT-US95-09145A-2	Sequence 2, Appli
8	696.5	39.2	354	5	PCT-US95-09145A-6	Sequence 6, Appli
9	696.5	39.2	392	4	US-09-949-016-9900	Sequence 9900, Ap
10	691.5	38.9	325	1	US-08-276-919-4	Sequence 4, Appli
11	691.5	38.9	325	1	US-08-776-088-4	Sequence 4, Appli
12	691.5	38.9	325	5	PCT-US95-09145A-4	Sequence 4, Appli
13	689.5	38.8	325	1	US-08-276-919-13	Sequence 13, Appl
14	689.5	38.8	325	1	US-08-776-088-18	Sequence 18, Appl
15	689.5	38.8	325	5	PCT-US95-09145A-18	Sequence 18, Appl
16	654.5	36.8	274	1	US-08-776-088-15	Sequence 15, Appl
17	654.5	36.8	274	5	PCT-US95-09145A-15	Sequence 15, Appl
18	648.5	36.5	271	1	US-08-276-919-10	Sequence 10, Appl
19	648.5	36.5	271	1	US-08-776-088-13	Sequence 13, Appl
20	648.5	36.5	271	5	PCT-US95-09145A-13	Sequence 13, Appl
21	562	31.6	422	3	US-08-335-469-2	Sequence 2, Appli
22	562	31.6	422	4	US-08-260-190-2	Sequence 2, Appli
23	562	31.6	459	2	US-08-481-658B-2	Sequence 2, Appli
24	562	31.6	459	2	US-08-477-504A-2	Sequence 2, Appli
25	562	31.6	459	2	US-08-486-756A-2	Sequence 2, Appli
26	562	31.6	459	2	US-08-485-862B-2	Sequence 2, Appli
27	562	31.6	459	3	US-08-787-739-2	Sequence 2, Appli
28	562	31.6	459	3	US-08-487-077A-2	Sequence 2, Appli
29	562	31.6	459	3	US-08-485-863A-2	Sequence 2, Appli
30	562	31.6	459	3	US-08-485-049D-2	Sequence 2, Appli
31	562	31.6	459	3	US-09-178-115-2	Sequence 2, Appli
32	562	31.6	459	3	US-09-177-776-2	Sequence 2, Appli
33	562	31.6	459	4	US-09-772-719B-2	Sequence 2, Appli
34	562	31.6	459	4	US-08-260-190-6	Sequence 6, Appli
35	562	31.6	459	4	US-09-949-016-6042	Sequence 6042, Ap
36	562	31.6	473	4	US-09-949-016-10203	Sequence 10203, A
37	535	30.1	377	3	US-08-787-739-87	Sequence 87, Appl
38	535	30.1	377	3	US-09-178-115-87	Sequence 87, Appl
39	535	30.1	377	3	US-09-177-776-87	Sequence 87, Appl
40	533.5	30.0	256	2	US-08-481-658B-51	Sequence 51, Appl
41	533.5	30.0	256	2	US-08-477-504A-51	Sequence 51, Appl
42	533.5	30.0	256	2	US-08-486-756A-51	Sequence 51, Appl
43	533.5	30.0	256	2	US-08-485-862B-51	Sequence 51, Appl
44	533.5	30.0	256	3	US-08-487-077A-51	Sequence 51, Appl
45	533.5	30.0	256	3	US-08-485-863A-51	Sequence 51, Appl
46	533.5	30.0	256	3	US-08-485-049D-51	Sequence 51, Appl
47	533.5	30.0	256	4	US-09-772-719B-51	Sequence 51, Appl
48	533.5	30.0	257	3	US-08-787-739-51	Sequence 51, Appl
49	533.5	30.0	257	3	US-09-178-115-51	Sequence 51, Appl
50	533.5	30.0	257	3	US-09-177-776-51	Sequence 51, Appl
51	519.5	29.2	262	1	US-08-015-986A-11	Sequence 11, Appl
52	519.5	29.2	262	2	US-08-446-363-11	Sequence 11, Appl
53	493	27.7	262	1	US-08-015-973-8	Sequence 8, Appli
54	493	27.7	262	2	US-08-448-164-8	Sequence 8, Appli
55	493	27.7	262	3	US-08-081-929-8	Sequence 8, Appli
56	493	27.7	262	4	US-10-000-954-8	Sequence 8, Appli
57	458.5	25.8	1442	1	US-08-015-986A-3	Sequence 3, Appli
58	458.5	25.8	1442	2	US-08-446-363-3	Sequence 3, Appli
59	451.5	25.4	1445	1	US-08-015-986A-2	Sequence 2, Appli
60	451.5	25.4	1445	2	US-08-446-363-2	Sequence 2, Appli
61	439.5	24.7	267	1	US-08-015-973-3	Sequence 3, Appli
62	439.5	24.7	267	2	US-08-448-164-3	Sequence 3, Appli
63	439.5	24.7	267	3	US-08-081-929-3	Sequence 3, Appli
64	439.5	24.7	267	4	US-10-000-954-3	Sequence 3, Appli
65	421	23.7	287	4	US-09-949-016-10412	Sequence 10412, A
66	420	23.6	259	1	US-08-015-973-5	Sequence 5, Appli
67	420	23.6	259	2	US-08-448-164-5	Sequence 5, Appli
68	420	23.6	259	3	US-08-081-929-5	Sequence 5, Appli
69	420	23.6	259	4	US-10-000-954-5	Sequence 5, Appli
70	420	23.6	260	1	US-08-015-986A-9	Sequence 9, Appli
71	420	23.6	260	2	US-08-446-363-9	Sequence 9, Appli
72	420	23.6	260	3	US-08-927-128-4	Sequence 4, Appli
73	420	23.6	260	4	US-09-976-594-644	Sequence 644, App
74	414	23.3	429	1	US-07-964-589-2	Sequence 2, Appli
75	414	23.3	429	5	PCT-US93-02024-2	Sequence 2, Appli
76	411	23.1	264	4	US-09-949-016-6599	Sequence 6599, Ap
77	410	23.0	288	2	US-08-595-868C-12	Sequence 12, Appl
78	410	23.0	288	3	US-09-139-819A-12	Sequence 12, Appl
79	410	23.0	288	4	US-09-750-913-12	Sequence 12, Appl
80	406	22.8	259	1	US-08-015-986A-10	Sequence 10, Appl
81	406	22.8	259	1	US-08-015-973-6	Sequence 6, Appli
82	406	22.8	259	2	US-08-446-363-10	Sequence 10, Appl
83	406	22.8	259	2	US-08-448-164-6	Sequence 6, Appli
84	406	22.8	259	3	US-08-081-929-6	Sequence 6, Appli
85	406	22.8	259	4	US-10-000-954-6	Sequence 6, Appli
86	406	22.8	364	4	US-09-949-016-8113	Sequence 8113, Ap
87	405	22.8	421	4	US-09-938-270B-1	Sequence 1, Appli
88	393	22.1	261	1	US-08-015-973-9	Sequence 9, Appli
89	393	22.1	261	2	US-08-448-164-9	Sequence 9, Appli
90	393	22.1	261	3	US-08-081-929-9	Sequence 9, Appli
91	393	22.1	261	4	US-10-000-954-9	Sequence 9, Appli
92	387	21.8	288	4	US-09-949-016-8850	Sequence 8850, Ap
93	385.5	21.7	170	2	US-08-481-658B-54	Sequence 54, Appl
94	385.5	21.7	170	2	US-08-477-504A-54	Sequence 54, Appl
95	385.5	21.7	170	2	US-08-486-756A-54	Sequence 54, Appl
96	385.5	21.7	170	2	US-08-485-862B-54	Sequence 54, Appl
97	385.5	21.7	170	3	US-08-487-077A-54	Sequence 54, Appl
98	385.5	21.7	170	3	US-08-485-863A-54	Sequence 54, Appl
99	385.5	21.7	170	3	US-08-485-049D-54	Sequence 54, Appl
100	385.5	21.7	170	4	US-09-772-719B-54	Sequence 54, Appl

101	380.5	21.4	260	1	US-08-015-973-4	Sequence 4, Appli
102	380.5	21.4	260	2	US-08-448-164-4	Sequence 4, Appli
103	380.5	21.4	260	3	US-08-081-929-4	Sequence 4, Appli
104	380.5	21.4	260	4	US-10-000-954-4	Sequence 4, Appli
105	380.5	21.4	261	1	US-08-015-986A-8	Sequence 8, Appli
106	380.5	21.4	261	2	US-08-446-363-8	Sequence 8, Appli
107	374.5	21.1	260	3	US-08-081-929-10	Sequence 10, Appl
108	374.5	21.1	260	4	US-10-000-954-10	Sequence 10, Appl
109	373	21.0	268	1	US-08-015-973-7	Sequence 7, Appli
110	373	21.0	268	2	US-08-448-164-7	Sequence 7, Appli
111	373	21.0	268	3	US-08-081-929-7	Sequence 7, Appli
112	373	21.0	268	4	US-10-000-954-7	Sequence 7, Appli
113	365	20.5	373	1	US-08-015-986A-14	Sequence 14, Appl
114	365	20.5	373	2	US-08-446-363-14	Sequence 14, Appl
115	365	20.5	2308	1	US-08-015-973-1	Sequence 1, Appli
116	365	20.5	2308	2	US-08-448-164-1	Sequence 1, Appli
117	365	20.5	2308	3	US-08-081-929-2	Sequence 2, Appli
118	365	20.5	2308	4	US-10-000-954-2	Sequence 2, Appli
119	365	20.5	2314	4	US-09-816-703A-2	Sequence 2, Appli
120	363	20.4	344	4	US-09-270-767-41438	Sequence 41438, A
121	362	20.3	266	1	US-08-015-986A-12	Sequence 12, Appl
122	362	20.3	266	2	US-08-446-363-12	Sequence 12, Appl
123	360.5	20.3	270	1	US-08-452-052-1	Sequence 1, Appli
124	288.5	16.2	328	2	US-08-977-767-1	Sequence 1, Appli
125	288.5	16.2	385	4	US-09-949-016-11213	Sequence 11213, A
126	280.5	15.8	201	1	US-08-469-667-18	Sequence 18, Appl
127	280.5	15.8	201	3	US-09-224-110-18	Sequence 18, Appl
128	280.5	15.8	201	4	US-09-988-292A-18	Sequence 18, Appl
129	280.5	15.8	201	5	PCT-US95-07289-18	Sequence 18, Appl
130	266	15.0	235	1	US-08-015-986A-13	Sequence 13, Appl
131	266	15.0	235	2	US-08-446-363-13	Sequence 13, Appl
132	257.5	14.5	782	4	US-09-270-767-44626	Sequence 44626, A
133	250.5	14.1	486	4	US-09-270-767-60075	Sequence 60075, A
134	243.5	13.7	132	4	US-09-513-999C-4373	Sequence 4373, Ap
135	176	9.9	147	4	US-09-270-767-33301	Sequence 33301, A
136	169.5	9.5	443	4	US-09-270-767-33409	Sequence 33409, A
137	169.5	9.5	443	4	US-09-270-767-48626	Sequence 48626, A
138	163.5	9.2	430	2	US-08-945-848-8	Sequence 8, Appli
139	160.5	9.0	106	4	US-09-270-767-33324	Sequence 33324, A
140	158.5	8.9	234	4	US-09-107-532A-5283	Sequence 5283, Ap
141	156	8.8	105	4	US-09-513-999C-5350	Sequence 5350, Ap
142	150.5	8.5	144	4	US-09-621-976-5098	Sequence 5098, Ap
143	119	6.7	123	4	US-09-270-767-33649	Sequence 33649, A
144	119	6.7	123	4	US-09-270-767-48866	Sequence 48866, A
145	114.5	6.4	3647	4	US-09-949-016-10932	Sequence 10932, A
146	112	6.3	140	4	US-09-270-767-33338	Sequence 33338, A
147	112	6.3	140	4	US-09-270-767-48555	Sequence 48555, A
148	105.5	5.9	1439	2	US-08-449-644-2	Sequence 2, Appli
149	105.5	5.9	1439	2	US-08-087-244A-2	Sequence 2, Appli
150	103.5	5.8	1457	2	US-08-652-971-3	Sequence 3, Appli
151	103.5	5.8	1457	2	US-08-449-644-1	Sequence 1, Appli
152	103.5	5.8	1457	2	US-08-087-244A-1	Sequence 1, Appli
153	103.5	5.8	1457	2	US-08-991-258A-3	Sequence 3, Appli
154	103.5	5.8	1457	2	US-08-769-399-3	Sequence 3, Appli
155	103.5	5.8	1457	3	US-08-991-953A-3	Sequence 3, Appli
156	100	5.6	104	4	US-09-270-767-33498	Sequence 33498, A
157	100	5.6	104	4	US-09-270-767-48715	Sequence 48715, A
158	98	5.5	530	4	US-08-486-049-3	Sequence 3, Appli
159	97	5.5	518	3	US-09-113-309-19	Sequence 19, Appl
160	97	5.5	518	3	US-09-521-109-19	Sequence 19, Appl
161	97	5.5	518	3	US-09-562-332-19	Sequence 19, Appl
162	97	5.5	545	3	US-08-974-180-15	Sequence 15, Appl
163	97	5.5	856	4	US-09-248-796A-16089	Sequence 16089, A
164	96	5.4	374	4	US-09-638-937-2	Sequence 2, Appli
165	95.5	5.4	346	4	US-09-270-767-45452	Sequence 45452, A
166	95	5.3	810	4	US-09-538-092-1275	Sequence 1275, Ap
167	95	5.3	953	4	US-09-845-583A-4	Sequence 4, Appli
168	92	5.2	746	4	US-09-252-991A-29228	Sequence 29228, A
169	91	5.1	534	3	US-09-087-134-11	Sequence 11, Appl
170	91	5.1	694	4	US-09-328-352-7276	Sequence 7276, Ap
171	89	5.0	560	3	US-09-139-064-6	Sequence 6, Appli
172	89	5.0	560	3	US-09-487-370-6	Sequence 6, Appli
173	89	5.0	560	4	US-09-248-796A-22980	Sequence 22980, A
174	88	4.9	328	4	US-09-489-847-310	Sequence 310, App
175	87.5	4.9	424	4	US-10-029-180-104	Sequence 104, App
176	87.5	4.9	624	4	US-09-877-730-24	Sequence 24, Appl
177	87.5	4.9	712	4	US-09-877-730-22	Sequence 22, Appl
178	87.5	4.9	793	4	US-09-877-730-28	Sequence 28, Appl
179	87.5	4.9	991	4	US-09-877-730-12	Sequence 12, Appl
180	87.5	4.9	1069	4	US-09-877-730-2	Sequence 2, Appli
181	87.5	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl
182	87.5	4.9	1150	4	US-09-877-730-8	Sequence 8, Appli
183	86.5	4.9	307	2	US-08-807-861A-56	Sequence 56, Appl
184	86.5	4.9	307	3	US-09-210-681-56	Sequence 56, Appl
185	86.5	4.9	307	3	US-08-946-719A-56	Sequence 56, Appl
186	86.5	4.9	307	4	US-09-547-983-56	Sequence 56, Appl
187	85.5	4.8	1457	4	US-09-436-874-2	Sequence 2, Appli
188	85	4.8	351	4	US-09-252-991A-29992	Sequence 29992, A
189	85	4.8	984	2	US-08-449-645A-19	Sequence 19, Appl
190	85	4.8	984	2	US-08-702-367A-19	Sequence 19, Appl
191	85	4.8	984	5	PCT-US95-04681-19	Sequence 19, Appl
192	85	4.8	2273	3	US-09-426-998-5	Sequence 5, Appli
193	84.5	4.7	1184	1	US-08-446-038B-20	Sequence 20, Appl
194	84.5	4.7	1184	1	US-08-446-010B-20	Sequence 20, Appl
195	84.5	4.7	1184	2	US-08-805-445-20	Sequence 20, Appl
196	84.5	4.7	1184	2	US-08-064-067D-20	Sequence 20, Appl
197	84.5	4.7	1184	2	US-09-066-208-20	Sequence 20, Appl
198	84.5	4.7	1299	3	US-08-460-900C-62	Sequence 62, Appl
199	84.5	4.7	1299	3	US-08-674-509B-48	Sequence 48, Appl
200	84.5	4.7	1299	3	US-08-954-698-48	Sequence 48, Appl
201	84.5	4.7	1299	4	US-09-639-695-62	Sequence 62, Appl
202	84.5	4.7	1299	4	US-09-448-188-48	Sequence 48, Appl
203	84.5	4.7	1299	4	US-08-954-128-48	Sequence 48, Appl
204	84.5	4.7	1299	4	US-08-954-740-48	Sequence 48, Appl
205	84.5	4.7	1457	4	US-09-713-273A-18	Sequence 18, Appl
206	84	4.7	697	4	US-09-949-016-9660	Sequence 9660, Ap
207	83.5	4.7	501	3	US-08-857-076-102	Sequence 102, App
208	83.5	4.7	547	4	US-09-877-730-26	Sequence 26, Appl
209	83.5	4.7	628	4	US-09-877-730-30	Sequence 30, Appl
210	83.5	4.7	686	4	US-09-328-352-4303	Sequence 4303, Ap
211	83.5	4.7	826	4	US-09-877-730-16	Sequence 16, Appl
212	83.5	4.7	904	4	US-09-877-730-6	Sequence 6, Appli
213	83.5	4.7	907	4	US-09-877-730-20	Sequence 20, Appl
214	83.5	4.7	985	4	US-09-877-730-10	Sequence 10, Appl
215	83.5	4.7	1187	1	US-08-357-598-8	Sequence 8, Appli
216	83.5	4.7	1187	1	US-08-097-997A-13	Sequence 13, Appl
217	83.5	4.7	1187	2	US-09-003-289-8	Sequence 8, Appli
218	83.5	4.7	1187	3	US-08-665-574C-13	Sequence 13, Appl
219	83.5	4.7	1187	3	US-08-946-994-13	Sequence 13, Appl
220	83.5	4.7	1187	4	US-09-972-800A-18	Sequence 18, Appl
221	83.5	4.7	1187	5	PCT-US95-16435-8	Sequence 8, Appli
222	83.5	4.7	1469	4	US-09-713-273A-16	Sequence 16, Appl
223	83	4.7	457	4	US-09-394-142B-22	Sequence 22, Appl
224	83	4.7	579	4	US-09-244-805-38	Sequence 38, Appl
225	83	4.7	984	2	US-08-673-789-9	Sequence 9, Appli
226	83	4.7	2907	4	US-09-698-295-1	Sequence 1, Appli
227	82.5	4.6	479	3	US-09-004-838-123	Sequence 123, App
228	82.5	4.6	635	4	US-10-101-464A-932	Sequence 932, App
229	81.5	4.6	372	4	US-09-638-937-4	Sequence 4, Appli
230	81.5	4.6	664	4	US-09-107-532A-7252	Sequence 7252, Ap
231	81.5	4.6	994	4	US-09-949-016-6779	Sequence 6779, Ap
232	81	4.6	189	4	US-09-902-540-16173	Sequence 16173, A
233	81	4.6	411	1	US-08-399-561-2	Sequence 2, Appli
234	81	4.6	513	4	US-09-252-991A-32658	Sequence 32658, A
235	81	4.6	561	4	US-09-902-540-15714	Sequence 15714, A
236	81	4.6	1055	4	US-09-949-016-9776	Sequence 9776, Ap
237	81	4.6	1187	1	US-08-201-697-2	Sequence 2, Appli
238	80.5	4.5	552	4	US-09-248-796A-25337	Sequence 25337, A
239	80.5	4.5	658	4	US-09-252-991A-26319	Sequence 26319, A
240	80.5	4.5	777	4	US-09-949-016-7158	Sequence 7158, Ap
241	80.5	4.5	857	2	US-08-659-251-2	Sequence 2, Appli
242	80.5	4.5	857	3	US-09-256-490-2	Sequence 2, Appli
243	80.5	4.5	857	5	PCT-US96-11445-2	Sequence 2, Appli
244	80.5	4.5	1261	1	US-08-764-100-26	Sequence 26, Appl
245	80.5	4.5	1290	3	US-09-150-460B-6	Sequence 6, Appli
246	80	4.5	631	3	US-09-310-463-20	Sequence 20, Appl

247	80	4.5	631	4	US-08-842-248A-20	Sequence 20, Appl
248	80	4.5	719	4	US-09-949-016-7766	Sequence 7766, Ap
249	80	4.5	725	4	US-09-724-653-10	Sequence 10, Appl
250	80	4.5	739	1	US-07-618-946B-22	Sequence 22, Appl
251	80	4.5	814	1	US-07-618-946B-23	Sequence 23, Appl
252	79.5	4.5	365	4	US-09-328-352-6107	Sequence 6107, Ap
253	79.5	4.5	524	4	US-09-171-553B-4	Sequence 4, Appli
254	79.5	4.5	743	4	US-09-724-653-8	Sequence 8, Appli
255	79.5	4.5	748	3	US-09-061-764A-19	Sequence 19, Appl
256	79.5	4.5	808	4	US-09-917-254-52	Sequence 52, Appl
257	79.5	4.5	823	4	US-09-107-532A-5667	Sequence 5667, Ap
258	79.5	4.5	850	4	US-09-129-603-2	Sequence 2, Appli
259	79.5	4.5	1285	2	US-08-540-406-6	Sequence 6, Appli
260	79.5	4.5	1285	3	US-08-656-055-6	Sequence 6, Appli
261	79.5	4.5	1285	3	US-08-954-668-6	Sequence 6, Appli
262	79.5	4.5	1285	4	US-08-918-658-6	Sequence 6, Appli
263	79.5	4.5	1285	4	US-09-724-631-6	Sequence 6, Appli
264	79.5	4.5	1285	4	US-08-954-701A-6	Sequence 6, Appli
265	79.5	4.5	1285	5	PCT-US95-13233-6	Sequence 6, Appli
266	79.5	4.5	1286	3	US-09-268-140-3	Sequence 3, Appli
267	79.5	4.5	1307	1	US-08-395-246C-2	Sequence 2, Appli
268	79	4.4	357	5	PCT-US91-00899-14	Sequence 14, Appl
269	79	4.4	370	4	US-09-540-236-2696	Sequence 2696, Ap
270	79	4.4	382	4	US-09-252-991A-20201	Sequence 20201, A
271	79	4.4	573	4	US-09-248-796A-17549	Sequence 17549, A
272	79	4.4	631	3	US-09-345-468-12	Sequence 12, Appl
273	79	4.4	631	3	US-09-414-453A-12	Sequence 12, Appl
274	79	4.4	655	3	US-09-228-986-70	Sequence 70, Appl
275	79	4.4	655	4	US-10-101-464A-70	Sequence 70, Appl
276	79	4.4	1423	3	US-08-810-712-10	Sequence 10, Appl
277	79	4.4	1431	4	US-09-538-092-1198	Sequence 1198, Ap
278	79	4.4	2343	3	US-09-324-867-2	Sequence 2, Appli
279	79	4.4	3118	2	US-08-457-273B-8	Sequence 8, Appli
280	78.5	4.4	197	4	US-09-270-767-46202	Sequence 46202, A
281	78.5	4.4	381	1	US-08-585-758A-2	Sequence 2, Appli
282	78.5	4.4	381	1	US-08-977-818-2	Sequence 2, Appli
283	78.5	4.4	381	2	US-08-670-274B-2	Sequence 2, Appli
284	78.5	4.4	381	2	US-08-786-999-3	Sequence 3, Appli
285	78.5	4.4	381	3	US-09-146-187-2	Sequence 2, Appli
286	78.5	4.4	381	4	US-09-216-387-3	Sequence 3, Appli
287	78.5	4.4	381	4	US-09-804-690-2	Sequence 2, Appli
288	78.5	4.4	391	4	US-09-886-319A-1	Sequence 1, Appli
289	78.5	4.4	448	4	US-09-949-016-9938	Sequence 9938, Ap
290	78.5	4.4	845	4	US-09-949-016-11413	Sequence 11413, A
291	78.5	4.4	1028	4	US-09-949-016-9650	Sequence 9650, Ap
292	78.5	4.4	1424	4	US-09-388-221B-12	Sequence 12, Appl
293	78.5	4.4	1454	4	US-09-388-221B-10	Sequence 10, Appl
294	78	4.4	254	4	US-09-248-796A-27114	Sequence 27114, A
295	78	4.4	280	4	US-10-101-464A-614	Sequence 614, App
296	78	4.4	400	4	US-09-538-092-1146	Sequence 1146, Ap
297	78	4.4	852	4	US-09-206-551-19	Sequence 19, Appl
298	78	4.4	905	4	US-09-340-620A-52	Sequence 52, Appl
299	78	4.4	1152	2	US-08-476-062A-43	Sequence 43, Appl
300	78	4.4	1152	5	PCT-US96-01314-43	Sequence 43, Appl
301	78	4.4	1152	6	5424399-2	Patent No. 5424399
302	78	4.4	1152	6	5424399-2	Patent No. 5424399
303	77.5	4.4	227	4	US-09-248-796A-15723	Sequence 15723, A
304	77.5	4.4	364	4	US-09-198-452A-423	Sequence 423, App
305	77.5	4.4	364	4	US-09-438-185A-406	Sequence 406, App
306	77.5	4.4	563	4	US-09-252-991A-28996	Sequence 28996, A
307	77.5	4.4	716	2	US-08-766-982-1	Sequence 1, Appli
308	77.5	4.4	716	3	US-09-296-219-1	Sequence 1, Appli
309	77.5	4.4	1176	4	US-09-976-594-793	Sequence 793, App
310	77	4.3	509	1	US-08-030-096-2	Sequence 2, Appli
311	77	4.3	514	4	US-09-252-991A-29276	Sequence 29276, A
312	77	4.3	573	4	US-09-902-540-12155	Sequence 12155, A
313	77	4.3	751	4	US-09-252-991A-29893	Sequence 29893, A
314	77	4.3	802	4	US-09-252-991A-23824	Sequence 23824, A
315	77	4.3	963	4	US-09-328-352-4544	Sequence 4544, Ap
316	77	4.3	1419	4	US-09-252-991A-31822	Sequence 31822, A
317	77	4.3	2220	4	US-09-949-016-9730	Sequence 9730, Ap
318	76.5	4.3	260	4	US-09-540-236-2594	Sequence 2594, Ap
319	76.5	4.3	318	4	US-09-888-623-16	Sequence 16, Appl
320	76.5	4.3	424	4	US-09-902-540-10575	Sequence 10575, A
321	76.5	4.3	472	4	US-09-134-000C-3893	Sequence 3893, Ap
322	76.5	4.3	484	4	US-09-270-767-42785	Sequence 42785, A
323	76.5	4.3	566	3	US-09-023-731-1	Sequence 1, Appli
324	76.5	4.3	566	4	US-09-911-969-1	Sequence 1, Appli
325	76.5	4.3	696	4	US-09-252-991A-20587	Sequence 20587, A
326	76.5	4.3	752	4	US-09-693-542-89	Sequence 89, Appl
327	76.5	4.3	792	4	US-09-949-016-10798	Sequence 10798, A
328	76.5	4.3	833	4	US-09-489-039A-8936	Sequence 8936, Ap
329	76.5	4.3	1587	3	US-09-000-094-46	Sequence 46, Appl
330	76.5	4.3	1587	4	US-10-011-749-46	Sequence 46, Appl
331	76	4.3	336	4	US-09-902-540-16050	Sequence 16050, A
332	76	4.3	370	3	US-09-142-551A-4	Sequence 4, Appli
333	76	4.3	416	4	US-09-949-016-7756	Sequence 7756, Ap
334	76	4.3	451	4	US-09-902-540-13289	Sequence 13289, A
335	76	4.3	457	3	US-09-416-213-2	Sequence 2, Appli
336	76	4.3	457	4	US-09-416-214-2	Sequence 2, Appli
337	76	4.3	457	4	US-09-035-676-2	Sequence 2, Appli
338	76	4.3	457	4	US-10-161-346-2	Sequence 2, Appli
339	76	4.3	506	2	US-08-845-161A-18	Sequence 18, Appl
340	76	4.3	506	3	US-09-270-751-18	Sequence 18, Appl
341	76	4.3	525	4	US-09-543-681A-4364	Sequence 4364, Ap
342	76	4.3	553	1	US-08-651-572-2	Sequence 2, Appli
343	76	4.3	553	3	US-09-066-544-2	Sequence 2, Appli
344	76	4.3	553	3	US-08-951-086-2	Sequence 2, Appli
345	76	4.3	553	3	US-09-430-669-2	Sequence 2, Appli
346	76	4.3	646	4	US-09-949-016-7344	Sequence 7344, Ap
347	76	4.3	1055	4	US-09-489-039A-9150	Sequence 9150, Ap
348	76	4.3	2509	4	US-09-252-991A-16642	Sequence 16642, A
349	75.5	4.2	300	3	US-09-099-041A-4	Sequence 4, Appli
350	75.5	4.2	300	3	US-09-245-281-4	Sequence 4, Appli
351	75.5	4.2	300	4	US-09-207-359B-4	Sequence 4, Appli
352	75.5	4.2	300	4	US-09-340-620A-4	Sequence 4, Appli
353	75.5	4.2	300	4	US-09-865-364-4	Sequence 4, Appli
354	75.5	4.2	304	4	US-09-270-767-43346	Sequence 43346, A
355	75.5	4.2	482	1	US-08-135-510-5	Sequence 5, Appli
356	75.5	4.2	482	1	US-08-483-852-5	Sequence 5, Appli
357	75.5	4.2	482	1	US-08-477-953-5	Sequence 5, Appli
358	75.5	4.2	482	2	US-08-477-952-5	Sequence 5, Appli
359	75.5	4.2	504	1	US-08-135-511-28	Sequence 28, Appl
360	75.5	4.2	504	1	US-08-483-852-8	Sequence 8, Appli
361	75.5	4.2	504	1	US-08-361-458-3	Sequence 3, Appli
362	75.5	4.2	504	1	US-08-477-953-8	Sequence 8, Appli
363	75.5	4.2	504	1	US-08-187-453-28	Sequence 28, Appl
364	75.5	4.2	504	2	US-08-477-952-8	Sequence 8, Appli
365	75.5	4.2	504	4	US-09-762-415-4	Sequence 4, Appli
366	75.5	4.2	507	4	US-09-949-016-10802	Sequence 10802, A
367	75.5	4.2	531	4	US-09-252-991A-17650	Sequence 17650, A
368	75.5	4.2	540	3	US-09-019-942-1	Sequence 1, Appli
369	75.5	4.2	540	3	US-09-099-041A-2	Sequence 2, Appli
370	75.5	4.2	540	3	US-09-069-023-27	Sequence 27, Appl
371	75.5	4.2	540	3	US-09-245-281-2	Sequence 2, Appli
372	75.5	4.2	540	4	US-09-470-271-1	Sequence 1, Appli
373	75.5	4.2	540	4	US-09-207-359B-2	Sequence 2, Appli
374	75.5	4.2	540	4	US-09-340-620A-2	Sequence 2, Appli
375	75.5	4.2	540	4	US-09-345-473E-28	Sequence 28, Appl
376	75.5	4.2	540	4	US-09-865-364-2	Sequence 2, Appli
377	75.5	4.2	540	4	US-09-748-537-1	Sequence 1, Appli
378	75.5	4.2	541	4	US-09-134-000C-5420	Sequence 5420, Ap
379	75.5	4.2	586	4	US-09-339-159B-10	Sequence 10, Appl
380	75.5	4.2	758	1	US-07-756-250-16	Sequence 16, Appl
381	75.5	4.2	766	4	US-09-949-016-10058	Sequence 10058, A
382	75	4.2	66	4	US-09-513-999C-5649	Sequence 5649, Ap
383	75	4.2	211	4	US-09-543-681A-7263	Sequence 7263, Ap
384	75	4.2	284	4	US-09-786-240-7	Sequence 7, Appli
385	75	4.2	393	2	US-08-837-593-3	Sequence 3, Appli
386	75	4.2	720	3	US-09-480-921B-8	Sequence 8, Appli
387	75	4.2	998	4	US-09-540-236-3801	Sequence 3801, Ap
388	74.5	4.2	229	4	US-09-394-142B-8	Sequence 8, Appli
389	74.5	4.2	342	4	US-09-538-092-776	Sequence 776, App
390	74.5	4.2	354	3	US-09-338-907-74	Sequence 74, Appl
391	74.5	4.2	354	3	US-09-218-207-74	Sequence 74, Appl
392	74.5	4.2	387	1	US-08-314-596-40	Sequence 40, Appl

393	74.5	4.2	387	1	US-08-314-596-42	Sequence 42, Appl
394	74.5	4.2	387	1	US-08-320-982-40	Sequence 40, Appl
395	74.5	4.2	387	1	US-08-320-982-42	Sequence 42, Appl
396	74.5	4.2	387	2	US-08-872-302-6	Sequence 6, Appli
397	74.5	4.2	387	3	US-08-819-037-40	Sequence 40, Appl
398	74.5	4.2	387	3	US-08-819-037-42	Sequence 42, Appl
399	74.5	4.2	387	3	US-08-530-862B-5	Sequence 5, Appli
400	74.5	4.2	387	3	US-08-597-313D-5	Sequence 5, Appli
401	74.5	4.2	387	3	US-09-059-769-14	Sequence 14, Appl
402	74.5	4.2	387	3	US-09-161-994A-18	Sequence 18, Appl
403	74.5	4.2	387	4	US-09-045-940-40	Sequence 40, Appl
404	74.5	4.2	387	4	US-09-045-940-42	Sequence 42, Appl
405	74.5	4.2	387	4	US-09-638-937-6	Sequence 6, Appli
406	74.5	4.2	396	3	US-09-142-551A-3	Sequence 3, Appli
407	74.5	4.2	459	4	US-09-543-681A-5116	Sequence 5116, Ap
408	74.5	4.2	469	4	US-09-252-991A-26584	Sequence 26584, A
409	74.5	4.2	487	4	US-09-583-110-3252	Sequence 3252, Ap
410	74.5	4.2	491	4	US-09-107-433-4631	Sequence 4631, Ap
411	74.5	4.2	522	1	US-08-625-322-2	Sequence 2, Appli
412	74.5	4.2	547	4	US-09-134-000C-5974	Sequence 5974, Ap
413	74.5	4.2	627	4	US-09-071-035-452	Sequence 452, App
414	74.5	4.2	678	4	US-09-196-270-1	Sequence 1, Appli
415	74.5	4.2	696	4	US-09-134-000C-4874	Sequence 4874, Ap
416	74.5	4.2	752	3	US-08-975-762-61	Sequence 61, Appl
417	74.5	4.2	752	3	US-09-295-028-61	Sequence 61, Appl
418	74.5	4.2	752	3	US-09-106-582-61	Sequence 61, Appl
419	74.5	4.2	752	4	US-09-159-469-61	Sequence 61, Appl
420	74.5	4.2	752	4	US-09-693-542-61	Sequence 61, Appl
421	74.5	4.2	815	4	US-09-196-270-7	Sequence 7, Appli
422	74.5	4.2	823	4	US-09-491-356C-23	Sequence 23, Appl
423	74.5	4.2	846	3	US-09-134-001C-3067	Sequence 3067, Ap
424	74.5	4.2	933	4	US-09-949-016-8386	Sequence 8386, Ap
425	74.5	4.2	953	4	US-09-949-016-8387	Sequence 8387, Ap
426	74.5	4.2	969	4	US-09-949-016-8059	Sequence 8059, Ap
427	74.5	4.2	1053	3	US-08-863-118-3	Sequence 3, Appli
428	74.5	4.2	1313	4	US-09-071-035-450	Sequence 450, App
429	74.5	4.2	1313	4	US-09-071-035-454	Sequence 454, App
430	74	4.2	146	4	US-09-732-210-616	Sequence 616, App
431	74	4.2	290	3	US-09-134-001C-3401	Sequence 3401, Ap
432	74	4.2	301	4	US-09-902-540-13071	Sequence 13071, A
433	74	4.2	330	3	US-09-145-391-2	Sequence 2, Appli
434	74	4.2	330	4	US-09-794-591-2	Sequence 2, Appli
435	74	4.2	330	4	US-09-725-945-5	Sequence 5, Appli
436	74	4.2	414	4	US-09-248-796A-16417	Sequence 16417, A
437	74	4.2	497	4	US-09-248-796A-16678	Sequence 16678, A
438	74	4.2	677	4	US-09-248-796A-16017	Sequence 16017, A
439	74	4.2	692	4	US-10-101-464A-897	Sequence 897, App
440	74	4.2	696	4	US-09-710-279-2922	Sequence 2922, Ap
441	74	4.2	789	4	US-09-252-991A-27011	Sequence 27011, A
442	74	4.2	989	4	US-09-079-030-218	Sequence 218, App
443	74	4.2	1183	3	US-09-134-001C-3530	Sequence 3530, Ap
444	74	4.2	2781	4	US-09-698-295-10	Sequence 10, Appl
445	74	4.2	2867	4	US-09-902-540-12593	Sequence 12593, A
446	74	4.2	3119	1	US-08-246-982A-16	Sequence 16, Appl
447	74	4.2	3119	1	US-08-453-265-16	Sequence 16, Appl
448	74	4.2	3623	4	US-09-341-461-2	Sequence 2, Appli
449	73.5	4.1	123	4	US-09-134-000C-6096	Sequence 6096, Ap
450	73.5	4.1	297	4	US-09-248-796A-22761	Sequence 22761, A
451	73.5	4.1	309	3	US-08-530-862B-8	Sequence 8, Appli
452	73.5	4.1	309	3	US-08-597-313D-8	Sequence 8, Appli
453	73.5	4.1	363	4	US-08-914-372C-37	Sequence 37, Appl
454	73.5	4.1	365	1	US-08-447-500-4	Sequence 4, Appli
455	73.5	4.1	365	1	US-08-454-097-4	Sequence 4, Appli
456	73.5	4.1	365	1	US-08-453-866-4	Sequence 4, Appli
457	73.5	4.1	365	3	US-09-100-664A-13	Sequence 13, Appl
458	73.5	4.1	365	3	US-08-185-359-4	Sequence 4, Appli
459	73.5	4.1	365	4	US-09-335-983-13	Sequence 13, Appl
460	73.5	4.1	365	4	US-09-553-867A-13	Sequence 13, Appl
461	73.5	4.1	495	4	US-09-543-681A-5589	Sequence 5589, Ap
462	73.5	4.1	499	3	US-08-985-492-14	Sequence 14, Appl
463	73.5	4.1	499	4	US-09-949-016-5906	Sequence 5906, Ap
464	73.5	4.1	608	3	US-09-134-001C-3395	Sequence 3395, Ap
465	73.5	4.1	611	4	US-09-710-279-2586	Sequence 2586, Ap
466	73.5	4.1	657	1	US-08-264-534-34	Sequence 34, Appl
467	73.5	4.1	657	1	US-08-083-590A-13	Sequence 13, Appl
468	73.5	4.1	657	1	US-08-465-500-34	Sequence 34, Appl
469	73.5	4.1	657	2	US-08-346-128-34	Sequence 34, Appl
470	73.5	4.1	657	3	US-08-532-384-13	Sequence 13, Appl
471	73.5	4.1	657	3	US-08-893-828-34	Sequence 34, Appl
472	73.5	4.1	664	4	US-09-248-796A-26707	Sequence 26707, A
473	73.5	4.1	746	4	US-09-248-796A-20280	Sequence 20280, A
474	73.5	4.1	749	4	US-09-913-955A-1	Sequence 1, Appli
475	73.5	4.1	803	2	US-08-951-648-4	Sequence 4, Appli
476	73.5	4.1	803	3	US-09-174-437-4	Sequence 4, Appli
477	73.5	4.1	803	4	US-09-686-055A-4	Sequence 4, Appli
478	73.5	4.1	1047	4	US-09-252-991A-29125	Sequence 29125, A
479	73.5	4.1	1180	4	US-09-543-681A-6436	Sequence 6436, Ap
480	73.5	4.1	2471	1	US-08-185-432-16	Sequence 16, Appl
481	73.5	4.1	2471	1	US-08-083-590A-19	Sequence 19, Appl
482	73.5	4.1	2471	3	US-08-532-384-19	Sequence 19, Appl
483	73.5	4.1	2471	4	US-08-899-232-1	Sequence 1, Appli
484	73.5	4.1	2471	4	US-09-121-457-1	Sequence 1, Appli
485	73	4.1	243	4	US-09-248-796A-15919	Sequence 15919, A
486	73	4.1	284	4	US-09-248-796A-24957	Sequence 24957, A
487	73	4.1	318	4	US-09-107-532A-5738	Sequence 5738, Ap
488	73	4.1	321	4	US-09-248-796A-20146	Sequence 20146, A
489	73	4.1	368	4	US-09-902-540-15739	Sequence 15739, A
490	73	4.1	382	2	US-08-872-302-2	Sequence 2, Appli
491	73	4.1	383	3	US-09-059-769-12	Sequence 12, Appl
492	73	4.1	383	3	US-09-161-994A-16	Sequence 16, Appl
493	73	4.1	420	4	US-09-902-540-10528	Sequence 10528, A
494	73	4.1	569	4	US-09-618-425-7	Sequence 7, Appli
495	73	4.1	584	4	US-09-270-767-43419	Sequence 43419, A
496	73	4.1	605	4	US-09-248-796A-15879	Sequence 15879, A
497	73	4.1	631	4	US-09-252-991A-26007	Sequence 26007, A
498	73	4.1	648	3	US-09-031-563-5	Sequence 5, Appli
499	73	4.1	648	4	US-09-392-277-5	Sequence 5, Appli
500	73	4.1	648	4	US-09-258-000-5	Sequence 5, Appli
501	73	4.1	807	4	US-09-177-650-3	Sequence 3, Appli
502	73	4.1	884	2	US-08-474-067-8	Sequence 8, Appli
503	73	4.1	884	2	US-08-474-068A-8	Sequence 8, Appli
504	73	4.1	884	2	US-08-472-481-7	Sequence 7, Appli
505	73	4.1	984	4	US-09-328-352-6926	Sequence 6926, Ap
506	73	4.1	1078	4	US-09-248-796A-20284	Sequence 20284, A
507	73	4.1	3892	4	US-09-328-352-5503	Sequence 5503, Ap
508	72.5	4.1	210	4	US-09-997-165-6	Sequence 6, Appli
509	72.5	4.1	367	4	US-09-198-452A-604	Sequence 604, App
510	72.5	4.1	368	4	US-09-540-236-3172	Sequence 3172, Ap
511	72.5	4.1	376	1	US-08-303-238-1	Sequence 1, Appli
512	72.5	4.1	376	3	US-08-458-834-1	Sequence 1, Appli
513	72.5	4.1	385	4	US-09-328-352-4372	Sequence 4372, Ap
514	72.5	4.1	387	3	US-09-133-962A-12	Sequence 12, Appl
515	72.5	4.1	400	4	US-09-543-681A-5821	Sequence 5821, Ap
516	72.5	4.1	403	4	US-09-438-185A-567	Sequence 567, App
517	72.5	4.1	431	4	US-09-710-279-1474	Sequence 1474, Ap
518	72.5	4.1	450	3	US-09-134-001C-4811	Sequence 4811, Ap
519	72.5	4.1	479	3	US-08-852-782-3	Sequence 3, Appli
520	72.5	4.1	633	4	US-09-949-016-11734	Sequence 11734, A
521	72.5	4.1	639	4	US-09-543-681A-6148	Sequence 6148, Ap
522	72.5	4.1	700	4	US-09-976-594-67	Sequence 67, Appl
523	72.5	4.1	700	4	US-09-538-092-893	Sequence 893, App
524	72.5	4.1	715	4	US-09-252-991A-19235	Sequence 19235, A
525	72.5	4.1	724	4	US-09-252-991A-30884	Sequence 30884, A
526	72.5	4.1	776	4	US-09-523-849-34	Sequence 34, Appl
527	72.5	4.1	917	4	US-09-438-185A-380	Sequence 380, App
528	72.5	4.1	1156	4	US-09-198-452A-171	Sequence 171, App
529	72.5	4.1	1434	2	US-08-540-406-10	Sequence 10, Appl
530	72.5	4.1	1434	3	US-08-656-055-10	Sequence 10, Appl
531	72.5	4.1	1434	3	US-08-954-668-10	Sequence 10, Appl
532	72.5	4.1	1434	4	US-08-918-658-10	Sequence 10, Appl
533	72.5	4.1	1434	4	US-09-724-631-10	Sequence 10, Appl
534	72.5	4.1	1434	4	US-08-954-701A-10	Sequence 10, Appl
535	72.5	4.1	1434	5	PCT-US95-13233-10	Sequence 10, Appl
536	72.5	4.1	1562	4	US-09-438-185A-152	Sequence 152, App
537	72.5	4.1	3135	1	US-08-323-170B-2	Sequence 2, Appli
538	72.5	4.1	3135	3	US-08-954-441-2	Sequence 2, Appli

539	72.5	4.1	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
540	72	4.0	244	4	US-09-807-258-20	Sequence 20, Appl
541	72	4.0	270	4	US-09-328-352-4465	Sequence 4465, Ap
542	72	4.0	322	4	US-09-949-016-8007	Sequence 8007, Ap
543	72	4.0	375	4	US-09-270-767-39877	Sequence 39877, A
544	72	4.0	375	4	US-09-270-767-55094	Sequence 55094, A
545	72	4.0	380	4	US-09-902-540-11937	Sequence 11937, A
546	72	4.0	382	3	US-08-811-177A-2	Sequence 2, Appli
547	72	4.0	383	1	US-08-314-596-41	Sequence 41, Appl
548	72	4.0	383	1	US-08-320-982-41	Sequence 41, Appl
549	72	4.0	383	3	US-08-819-037-41	Sequence 41, Appl
550	72	4.0	383	3	US-08-530-862B-6	Sequence 6, Appli
551	72	4.0	383	3	US-08-597-313D-6	Sequence 6, Appli
552	72	4.0	383	3	US-09-059-769-9	Sequence 9, Appli
553	72	4.0	383	3	US-09-161-994A-14	Sequence 14, Appl
554	72	4.0	383	3	US-09-133-962A-2	Sequence 2, Appli
555	72	4.0	383	4	US-09-045-940-41	Sequence 41, Appl
556	72	4.0	383	4	US-09-763-331-4	Sequence 4, Appli
557	72	4.0	384	3	US-09-354-231B-16	Sequence 16, Appl
558	72	4.0	384	4	US-09-128-602B-16	Sequence 16, Appl
559	72	4.0	384	4	US-09-995-297-16	Sequence 16, Appl
560	72	4.0	392	4	US-09-711-164-375	Sequence 375, App
561	72	4.0	397	4	US-09-252-991A-20668	Sequence 20668, A
562	72	4.0	400	2	US-08-878-989-17	Sequence 17, Appl
563	72	4.0	400	3	US-09-272-796-17	Sequence 17, Appl
564	72	4.0	400	4	US-09-543-681A-6151	Sequence 6151, Ap
565	72	4.0	439	4	US-09-248-796A-15969	Sequence 15969, A
566	72	4.0	462	4	US-09-252-991A-17536	Sequence 17536, A
567	72	4.0	474	4	US-09-248-796A-19995	Sequence 19995, A
568	72	4.0	479	4	US-09-198-452A-763	Sequence 763, App
569	72	4.0	479	4	US-09-438-185A-718	Sequence 718, App
570	72	4.0	498	4	US-09-902-540-10459	Sequence 10459, A
571	72	4.0	524	3	US-09-625-188-2	Sequence 2, Appli
572	72	4.0	556	4	US-09-949-016-7134	Sequence 7134, Ap
573	72	4.0	588	4	US-09-583-110-4288	Sequence 4288, Ap
574	72	4.0	638	4	US-09-134-000C-4864	Sequence 4864, Ap
575	72	4.0	647	3	US-09-031-563-7	Sequence 7, Appli
576	72	4.0	647	4	US-09-392-277-7	Sequence 7, Appli
577	72	4.0	647	4	US-09-258-000-7	Sequence 7, Appli
578	72	4.0	656	4	US-09-538-092-654	Sequence 654, App
579	72	4.0	680	4	US-09-107-532A-4798	Sequence 4798, Ap
580	72	4.0	714	2	US-08-472-534-3	Sequence 3, Appli
581	72	4.0	920	4	US-09-949-016-7178	Sequence 7178, Ap
582	72	4.0	963	1	US-08-537-002A-3	Sequence 3, Appli
583	72	4.0	963	3	US-08-863-010-3	Sequence 3, Appli
584	72	4.0	963	3	US-09-024-429-3	Sequence 3, Appli
585	72	4.0	1055	3	US-09-031-563-27	Sequence 27, Appl
586	72	4.0	1055	4	US-09-392-277-27	Sequence 27, Appl
587	72	4.0	1055	4	US-09-258-000-27	Sequence 27, Appl
588	72	4.0	1058	4	US-09-902-540-15976	Sequence 15976, A
589	72	4.0	1177	4	US-09-795-927-2	Sequence 2, Appli
590	72	4.0	1259	4	US-09-902-540-16442	Sequence 16442, A
591	72	4.0	1315	3	US-09-031-563-2	Sequence 2, Appli
592	72	4.0	1315	3	US-09-031-563-25	Sequence 25, Appl
593	72	4.0	1315	3	US-09-293-505-10	Sequence 10, Appl
594	72	4.0	1315	4	US-09-392-277-2	Sequence 2, Appli
595	72	4.0	1315	4	US-09-392-277-25	Sequence 25, Appl
596	72	4.0	1315	4	US-09-258-000-2	Sequence 2, Appli
597	72	4.0	1315	4	US-09-258-000-25	Sequence 25, Appl
598	72	4.0	1315	4	US-09-060-939A-10	Sequence 10, Appl
599	72	4.0	2304	3	US-09-324-867-4	Sequence 4, Appli
600	71.5	4.0	265	4	US-09-795-926-6	Sequence 6, Appli
601	71.5	4.0	273	4	US-09-252-991A-25511	Sequence 25511, A
602	71.5	4.0	287	1	US-08-622-353-7	Sequence 7, Appli
603	71.5	4.0	287	2	US-08-622-352A-9	Sequence 9, Appli
604	71.5	4.0	287	3	US-08-826-390-9	Sequence 9, Appli
605	71.5	4.0	303	4	US-09-795-926-2	Sequence 2, Appli
606	71.5	4.0	361	4	US-08-914-372C-7	Sequence 7, Appli
607	71.5	4.0	364	4	US-08-914-372C-10	Sequence 10, Appl
608	71.5	4.0	431	4	US-09-248-796A-17260	Sequence 17260, A
609	71.5	4.0	453	4	US-09-543-681A-5871	Sequence 5871, Ap
610	71.5	4.0	502	4	US-09-949-016-10424	Sequence 10424, A
611	71.5	4.0	519	4	US-08-956-171B-5230	Sequence 5230, Ap
612	71.5	4.0	519	4	US-08-781-986A-5230	Sequence 5230, Ap
613	71.5	4.0	560	4	US-09-614-912-130	Sequence 130, App
614	71.5	4.0	635	4	US-09-252-991A-21514	Sequence 21514, A
615	71.5	4.0	646	4	US-09-270-767-46432	Sequence 46432, A
616	71.5	4.0	703	3	US-08-646-273-25	Sequence 25, Appl
617	71.5	4.0	749	4	US-09-562-737-95	Sequence 95, Appl
618	71.5	4.0	753	3	US-08-646-273-36	Sequence 36, Appl
619	71.5	4.0	758	4	US-09-198-452A-996	Sequence 996, App
620	71.5	4.0	810	4	US-09-489-039A-9748	Sequence 9748, Ap
621	71.5	4.0	876	1	US-08-717-515-4	Sequence 4, Appli
622	71.5	4.0	915	4	US-09-198-452A-395	Sequence 395, App
623	71.5	4.0	1084	1	US-08-717-515-6	Sequence 6, Appli
624	71.5	4.0	1165	1	US-08-240-357-2	Sequence 2, Appli
625	71.5	4.0	1233	3	US-09-194-613-5	Sequence 5, Appli
626	71.5	4.0	1276	1	US-08-717-515-8	Sequence 8, Appli
627	71.5	4.0	1436	2	US-08-652-971-2	Sequence 2, Appli
628	71.5	4.0	1436	2	US-08-991-258A-2	Sequence 2, Appli
629	71.5	4.0	1436	2	US-08-769-399-2	Sequence 2, Appli
630	71.5	4.0	1436	3	US-08-991-953A-2	Sequence 2, Appli
631	71.5	4.0	1724	4	US-09-607-510-2	Sequence 2, Appli
632	71	4.0	236	4	US-09-134-000C-4896	Sequence 4896, Ap
633	71	4.0	250	4	US-09-853-450-30	Sequence 30, Appl
634	71	4.0	341	4	US-09-252-991A-18743	Sequence 18743, A
635	71	4.0	400	2	US-08-878-989-3	Sequence 3, Appli
636	71	4.0	400	3	US-09-272-796-3	Sequence 3, Appli
637	71	4.0	400	4	US-10-101-464A-939	Sequence 939, App
638	71	4.0	469	1	US-08-363-215-1	Sequence 1, Appli
639	71	4.0	469	3	US-08-807-342B-6	Sequence 6, Appli
640	71	4.0	474	4	US-09-328-352-5724	Sequence 5724, Ap
641	71	4.0	475	4	US-09-252-991A-26219	Sequence 26219, A
642	71	4.0	513	3	US-09-041-886-28	Sequence 28, Appl
643	71	4.0	530	3	US-09-041-886-29	Sequence 29, Appl
644	71	4.0	538	3	US-09-457-040B-23	Sequence 23, Appl
645	71	4.0	552	3	US-09-041-886-30	Sequence 30, Appl
646	71	4.0	589	3	US-09-041-886-31	Sequence 31, Appl
647	71	4.0	593	3	US-08-964-268-2	Sequence 2, Appli
648	71	4.0	593	4	US-09-105-254-2	Sequence 2, Appli
649	71	4.0	598	4	US-09-583-110-3070	Sequence 3070, Ap
650	71	4.0	604	4	US-09-107-433-4348	Sequence 4348, Ap
651	71	4.0	635	4	US-09-538-092-1	Sequence 1, Appli
652	71	4.0	650	4	US-09-252-991A-17330	Sequence 17330, A
653	71	4.0	706	1	US-08-484-105-16	Sequence 16, Appl
654	71	4.0	706	1	US-08-484-106-16	Sequence 16, Appl
655	71	4.0	722	4	US-09-252-991A-27003	Sequence 27003, A
656	71	4.0	724	4	US-09-724-653-9	Sequence 9, Appli
657	71	4.0	736	4	US-09-949-016-8076	Sequence 8076, Ap
658	71	4.0	738	4	US-09-538-092-818	Sequence 818, App
659	71	4.0	765	4	US-09-252-991A-19778	Sequence 19778, A
660	71	4.0	877	4	US-09-492-709A-353	Sequence 353, App
661	71	4.0	895	1	US-08-123-161A-8	Sequence 8, Appli
662	71	4.0	895	1	US-08-483-278-8	Sequence 8, Appli
663	71	4.0	895	4	US-09-949-016-6490	Sequence 6490, Ap
664	71	4.0	908	4	US-09-949-016-8542	Sequence 8542, Ap
665	71	4.0	1092	4	US-09-252-991A-28476	Sequence 28476, A
666	71	4.0	1531	4	US-09-949-016-6740	Sequence 6740, Ap
667	71	4.0	1543	4	US-09-904-987-7	Sequence 7, Appli
668	71	4.0	1626	4	US-09-252-991A-23805	Sequence 23805, A
669	71	4.0	2319	1	US-08-212-133A-8	Sequence 8, Appli
670	71	4.0	2319	1	US-08-474-503-6	Sequence 6, Appli
671	71	4.0	2319	2	US-08-670-707A-6	Sequence 6, Appli
672	71	4.0	2319	3	US-09-037-601-6	Sequence 6, Appli
673	71	4.0	2319	3	US-09-315-179-6	Sequence 6, Appli
674	71	4.0	2319	4	US-09-523-656-28	Sequence 28, Appl
675	71	4.0	2319	5	PCT-US94-13200-6	Sequence 6, Appli
676	71	4.0	3144	1	US-08-246-982A-6	Sequence 6, Appli
677	71	4.0	3144	1	US-08-453-265-6	Sequence 6, Appli
678	71	4.0	3144	2	US-08-457-273B-42	Sequence 42, Appl
679	71	4.0	3144	3	US-08-556-419-21	Sequence 21, Appl
680	71	4.0	3144	3	US-09-041-886-15	Sequence 15, Appl
681	71	4.0	3144	4	US-09-538-092-1118	Sequence 1118, Ap
682	70.5	4.0	219	4	US-09-648-004-16	Sequence 16, Appl
683	70.5	4.0	219	4	US-10-272-419-16	Sequence 16, Appl
684	70.5	4.0	255	2	US-08-592-214A-10	Sequence 10, Appl

685	70.5	4.0	255	3	US-08-659-188-10	Sequence 10, Appl
686	70.5	4.0	255	3	US-08-655-227-10	Sequence 10, Appl
687	70.5	4.0	255	3	US-08-655-241-10	Sequence 10, Appl
688	70.5	4.0	255	3	US-09-149-976-10	Sequence 10, Appl
689	70.5	4.0	255	3	US-09-398-326-10	Sequence 10, Appl
690	70.5	4.0	255	4	US-09-853-450-10	Sequence 10, Appl
691	70.5	4.0	262	4	US-09-270-767-41926	Sequence 41926, A
692	70.5	4.0	286	4	US-09-205-258-1012	Sequence 1012, Ap
693	70.5	4.0	349	6	5510466-2	Patent No. 5510466
694	70.5	4.0	349	6	5510466-2	Patent No. 5510466
695	70.5	4.0	355	4	US-09-811-673-2	Sequence 2, Appli
696	70.5	4.0	388	1	US-08-232-519-2	Sequence 2, Appli
697	70.5	4.0	388	1	US-08-456-956-2	Sequence 2, Appli
698	70.5	4.0	390	4	US-09-107-532A-4749	Sequence 4749, Ap
699	70.5	4.0	453	6	5510466-4	Patent No. 5510466
700	70.5	4.0	453	6	5510466-4	Patent No. 5510466
701	70.5	4.0	461	4	US-09-252-991A-19307	Sequence 19307, A
702	70.5	4.0	485	4	US-09-543-681A-7443	Sequence 7443, Ap
703	70.5	4.0	493	4	US-08-979-847B-106	Sequence 106, App
704	70.5	4.0	506	3	US-08-942-012B-26	Sequence 26, Appl
705	70.5	4.0	506	4	US-09-252-991A-27119	Sequence 27119, A
706	70.5	4.0	507	4	US-09-252-991A-23541	Sequence 23541, A
707	70.5	4.0	617	4	US-09-252-991A-22318	Sequence 22318, A
708	70.5	4.0	626	4	US-09-949-016-6776	Sequence 6776, Ap
709	70.5	4.0	700	4	US-09-902-540-11256	Sequence 11256, A
710	70.5	4.0	773	4	US-09-252-991A-19916	Sequence 19916, A
711	70.5	4.0	848	4	US-09-491-356C-22	Sequence 22, Appl
712	70.5	4.0	850	4	US-09-328-352-6583	Sequence 6583, Ap
713	70.5	4.0	971	4	US-09-538-092-1332	Sequence 1332, Ap
714	70.5	4.0	1113	4	US-09-618-425-9	Sequence 9, Appli
715	70.5	4.0	1118	2	US-08-724-354D-2	Sequence 2, Appli
716	70.5	4.0	1118	3	US-09-270-984A-2	Sequence 2, Appli
717	70.5	4.0	1183	4	US-09-248-796A-14987	Sequence 14987, A
718	70.5	4.0	1315	4	US-09-902-540-16086	Sequence 16086, A
719	70.5	4.0	1376	4	US-09-252-991A-29515	Sequence 29515, A
720	70.5	4.0	1447	2	US-08-540-406-19	Sequence 19, Appl
721	70.5	4.0	1447	3	US-08-656-055-19	Sequence 19, Appl
722	70.5	4.0	1447	3	US-08-954-668-19	Sequence 19, Appl
723	70.5	4.0	1447	3	US-09-268-140-5	Sequence 5, Appli
724	70.5	4.0	1447	4	US-08-918-658-19	Sequence 19, Appl
725	70.5	4.0	1447	4	US-09-724-631-19	Sequence 19, Appl
726	70.5	4.0	1447	4	US-08-954-701A-19	Sequence 19, Appl
727	70.5	4.0	1447	5	PCT-US95-13233-19	Sequence 19, Appl
728	70.5	4.0	1586	4	US-09-543-681A-5329	Sequence 5329, Ap
729	70.5	4.0	1778	4	US-09-252-991A-18159	Sequence 18159, A
730	70	3.9	278	4	US-09-248-796A-20610	Sequence 20610, A
731	70	3.9	288	4	US-09-270-767-42632	Sequence 42632, A
732	70	3.9	306	4	US-09-252-991A-20009	Sequence 20009, A
733	70	3.9	323	4	US-09-543-681A-6916	Sequence 6916, Ap
734	70	3.9	343	4	US-09-252-991A-26240	Sequence 26240, A
735	70	3.9	368	3	US-09-000-092-2	Sequence 2, Appli
736	70	3.9	368	3	US-09-000-092-4	Sequence 4, Appli
737	70	3.9	368	3	US-09-000-092-8	Sequence 8, Appli
738	70	3.9	368	3	US-09-000-092-10	Sequence 10, Appl
739	70	3.9	419	4	US-09-276-438-13	Sequence 13, Appl
740	70	3.9	543	2	US-08-224-482-4	Sequence 4, Appli
741	70	3.9	543	4	US-09-702-705-337	Sequence 337, App
742	70	3.9	543	4	US-09-736-457-337	Sequence 337, App
743	70	3.9	543	4	US-09-614-124B-337	Sequence 337, App
744	70	3.9	543	4	US-09-671-325-337	Sequence 337, App
745	70	3.9	543	4	US-09-589-184-337	Sequence 337, App
746	70	3.9	543	4	US-09-658-824-337	Sequence 337, App
747	70	3.9	543	4	US-09-538-092-953	Sequence 953, App
748	70	3.9	605	3	US-09-394-645-2	Sequence 2, Appli
749	70	3.9	605	3	US-09-243-560B-2	Sequence 2, Appli
750	70	3.9	625	4	US-09-196-270-6	Sequence 6, Appli
751	70	3.9	625	4	US-09-538-092-377	Sequence 377, App
752	70	3.9	656	4	US-09-248-796A-15211	Sequence 15211, A
753	70	3.9	703	3	US-09-433-043B-124	Sequence 124, App
754	70	3.9	760	4	US-09-107-532A-5490	Sequence 5490, Ap
755	70	3.9	1007	4	US-09-538-092-736	Sequence 736, App
756	70	3.9	1088	4	US-09-233-857-4	Sequence 4, Appli
757	70	3.9	1190	1	US-08-337-690A-2	Sequence 2, Appli
758	70	3.9	1190	3	US-09-048-887-2	Sequence 2, Appli
759	70	3.9	1455	2	US-08-726-012B-2	Sequence 2, Appli
760	70	3.9	1527	3	US-09-376-330-2	Sequence 2, Appli
761	69.5	3.9	108	3	US-09-199-637A-391	Sequence 391, App
762	69.5	3.9	157	4	US-09-270-767-32528	Sequence 32528, A
763	69.5	3.9	223	4	US-09-949-016-10045	Sequence 10045, A
764	69.5	3.9	285	4	US-09-886-319A-82	Sequence 82, Appl
765	69.5	3.9	296	4	US-09-248-796A-16691	Sequence 16691, A
766	69.5	3.9	344	3	US-09-134-001C-4175	Sequence 4175, Ap
767	69.5	3.9	346	3	US-09-199-637A-313	Sequence 313, App
768	69.5	3.9	355	4	US-09-616-506-3	Sequence 3, Appli
769	69.5	3.9	355	4	US-09-616-506-4	Sequence 4, Appli
770	69.5	3.9	355	4	US-09-574-377-31	Sequence 31, Appl
771	69.5	3.9	355	4	US-09-811-673-4	Sequence 4, Appli
772	69.5	3.9	364	4	US-09-270-767-43896	Sequence 43896, A
773	69.5	3.9	375	4	US-09-638-937-13	Sequence 13, Appl
774	69.5	3.9	376	4	US-09-538-092-1276	Sequence 1276, Ap
775	69.5	3.9	380	1	US-08-585-758A-4	Sequence 4, Appli
776	69.5	3.9	380	1	US-08-977-818-4	Sequence 4, Appli
777	69.5	3.9	380	2	US-08-670-274B-4	Sequence 4, Appli
778	69.5	3.9	380	3	US-09-146-187-4	Sequence 4, Appli
779	69.5	3.9	380	4	US-09-804-690-4	Sequence 4, Appli
780	69.5	3.9	387	2	US-08-837-593-4	Sequence 4, Appli
781	69.5	3.9	388	2	US-08-894-772-2	Sequence 2, Appli
782	69.5	3.9	388	2	US-09-207-844-2	Sequence 2, Appli
783	69.5	3.9	388	4	US-09-248-796A-23255	Sequence 23255, A
784	69.5	3.9	390	2	US-08-786-999-1	Sequence 1, Appli
785	69.5	3.9	390	4	US-09-216-387-1	Sequence 1, Appli
786	69.5	3.9	390	4	US-09-886-319A-2	Sequence 2, Appli
787	69.5	3.9	403	4	US-09-949-016-11251	Sequence 11251, A
788	69.5	3.9	438	4	US-09-902-540-10924	Sequence 10924, A
789	69.5	3.9	472	4	US-09-252-991A-32479	Sequence 32479, A
790	69.5	3.9	494	4	US-09-614-912-128	Sequence 128, App
791	69.5	3.9	552	4	US-09-270-767-33451	Sequence 33451, A
792	69.5	3.9	552	4	US-09-270-767-48668	Sequence 48668, A
793	69.5	3.9	587	1	US-07-955-905A-23	Sequence 23, Appl
794	69.5	3.9	602	3	US-09-257-490-15	Sequence 15, Appl
795	69.5	3.9	632	1	US-08-443-104-4	Sequence 4, Appli
796	69.5	3.9	632	1	US-08-442-859-4	Sequence 4, Appli
797	69.5	3.9	632	2	US-08-398-489-4	Sequence 4, Appli
798	69.5	3.9	632	5	PCT-US95-05534-4	Sequence 4, Appli
799	69.5	3.9	640	4	US-09-248-796A-16129	Sequence 16129, A
800	69.5	3.9	665	4	US-09-248-796A-14200	Sequence 14200, A
801	69.5	3.9	718	4	US-09-252-991A-28229	Sequence 28229, A
802	69.5	3.9	824	2	US-08-785-310A-7	Sequence 7, Appli
803	69.5	3.9	854	4	US-09-206-551-16	Sequence 16, Appl
804	69.5	3.9	863	4	US-09-894-927B-9	Sequence 9, Appli
805	69.5	3.9	879	4	US-09-872-733A-16	Sequence 16, Appl
806	69.5	3.9	905	4	US-09-902-540-10223	Sequence 10223, A
807	69.5	3.9	906	4	US-09-107-532A-6450	Sequence 6450, Ap
808	69.5	3.9	923	4	US-09-270-767-45546	Sequence 45546, A
809	69.5	3.9	972	4	US-09-469-200E-9	Sequence 9, Appli
810	69.5	3.9	1264	1	US-07-789-915A-6	Sequence 6, Appli
811	69.5	3.9	1264	1	US-08-005-002C-6	Sequence 6, Appli
812	69.5	3.9	1264	1	US-08-487-203A-6	Sequence 6, Appli
813	69.5	3.9	1484	4	US-09-902-540-14332	Sequence 14332, A
814	69.5	3.9	1493	4	US-09-713-273A-20	Sequence 20, Appl
815	69	3.9	222	2	US-08-927-230A-2	Sequence 2, Appli
816	69	3.9	222	3	US-09-151-052-2	Sequence 2, Appli
817	69	3.9	238	4	US-09-270-767-33105	Sequence 33105, A
818	69	3.9	238	4	US-09-270-767-48322	Sequence 48322, A
819	69	3.9	301	4	US-09-270-767-40023	Sequence 40023, A
820	69	3.9	301	4	US-09-270-767-55239	Sequence 55239, A
821	69	3.9	305	4	US-09-902-540-11093	Sequence 11093, A
822	69	3.9	334	4	US-09-198-452A-70	Sequence 70, Appl
823	69	3.9	364	4	US-09-755-665-64	Sequence 64, Appl
824	69	3.9	393	2	US-08-837-593-2	Sequence 2, Appli
825	69	3.9	395	4	US-09-755-665-34	Sequence 34, Appl
826	69	3.9	400	1	US-08-530-950-12	Sequence 12, Appl
827	69	3.9	400	3	US-08-888-429A-12	Sequence 12, Appl
828	69	3.9	400	3	US-09-149-879-12	Sequence 12, Appl
829	69	3.9	400	4	US-09-057-009-12	Sequence 12, Appl
830	69	3.9	400	4	US-09-593-653-12	Sequence 12, Appl

831	69	3.9	400	4	US-09-134-000C-3791	Sequence 3791, Ap
832	69	3.9	461	4	US-09-328-352-7746	Sequence 7746, Ap
833	69	3.9	567	4	US-09-583-110-4823	Sequence 4823, Ap
834	69	3.9	570	4	US-09-923-684-4	Sequence 4, Appli
835	69	3.9	576	4	US-09-107-433-4103	Sequence 4103, Ap
836	69	3.9	579	4	US-09-902-540-16017	Sequence 16017, A
837	69	3.9	599	1	US-08-222-619-2	Sequence 2, Appli
838	69	3.9	599	3	US-08-221-767-24	Sequence 24, Appl
839	69	3.9	599	5	PCT-US95-04075-2	Sequence 2, Appli
840	69	3.9	604	4	US-09-902-540-14691	Sequence 14691, A
841	69	3.9	608	3	US-09-134-001C-3855	Sequence 3855, Ap
842	69	3.9	611	4	US-09-248-796A-16130	Sequence 16130, A
843	69	3.9	647	4	US-09-543-681A-5240	Sequence 5240, Ap
844	69	3.9	660	4	US-09-462-606-54	Sequence 54, Appl
845	69	3.9	662	4	US-09-252-991A-18392	Sequence 18392, A
846	69	3.9	667	4	US-09-923-684-3	Sequence 3, Appli
847	69	3.9	729	3	US-09-625-188-20	Sequence 20, Appl
848	69	3.9	744	4	US-09-785-381-1	Sequence 1, Appli
849	69	3.9	770	4	US-09-270-767-43871	Sequence 43871, A
850	69	3.9	797	4	US-09-949-016-6761	Sequence 6761, Ap
851	69	3.9	915	4	US-09-817-514A-6	Sequence 6, Appli
852	69	3.9	935	3	US-09-271-438A-3	Sequence 3, Appli
853	69	3.9	935	3	US-09-271-438A-8	Sequence 8, Appli
854	69	3.9	935	4	US-10-078-107-1	Sequence 1, Appli
855	69	3.9	935	4	US-10-077-751-1	Sequence 1, Appli
856	69	3.9	951	4	US-09-328-352-4456	Sequence 4456, Ap
857	69	3.9	965	4	US-09-437-277-3	Sequence 3, Appli
858	69	3.9	976	2	US-08-449-645A-18	Sequence 18, Appl
859	69	3.9	976	2	US-08-702-367A-18	Sequence 18, Appl
860	69	3.9	976	4	US-09-949-016-6499	Sequence 6499, Ap
861	69	3.9	976	5	PCT-US95-04681-18	Sequence 18, Appl
862	69	3.9	977	2	US-08-673-789-8	Sequence 8, Appli
863	69	3.9	1013	4	US-09-949-016-7991	Sequence 7991, Ap
864	69	3.9	1016	4	US-09-252-991A-25429	Sequence 25429, A
865	69	3.9	1142	2	US-08-993-118-7	Sequence 7, Appli
866	69	3.9	1142	3	US-08-845-528C-7	Sequence 7, Appli
867	69	3.9	1142	3	US-09-061-709-2	Sequence 2, Appli
868	69	3.9	1142	4	US-09-066-281B-7	Sequence 7, Appli
869	69	3.9	1142	4	US-09-899-651-2	Sequence 2, Appli
870	69	3.9	1142	4	US-09-468-433C-7	Sequence 7, Appli
871	69	3.9	1142	4	US-09-392-714-26	Sequence 26, Appl
872	69	3.9	1142	4	US-09-270-437D-2	Sequence 2, Appli
873	69	3.9	1153	1	US-08-173-497-3	Sequence 3, Appli
874	69	3.9	1153	1	US-08-286-889-3	Sequence 3, Appli
875	69	3.9	1153	1	US-08-485-618-3	Sequence 3, Appli
876	69	3.9	1153	1	US-08-362-652-3	Sequence 3, Appli
877	69	3.9	1153	2	US-08-605-672-3	Sequence 3, Appli
878	69	3.9	1153	2	US-08-482-293A-3	Sequence 3, Appli
879	69	3.9	1153	2	US-08-943-363-3	Sequence 3, Appli
880	69	3.9	1153	3	US-09-193-043-3	Sequence 3, Appli
881	69	3.9	1153	4	US-09-688-307A-3	Sequence 3, Appli
882	69	3.9	1153	4	US-09-350-259-3	Sequence 3, Appli
883	69	3.9	1296	4	US-08-857-636-60	Sequence 60, Appl
884	69	3.9	1358	4	US-08-943-144-2	Sequence 2, Appli
885	69	3.9	1739	4	US-09-976-594-76	Sequence 76, Appl
886	69	3.9	1739	4	US-09-538-092-824	Sequence 824, App
887	69	3.9	1740	4	US-09-949-016-8860	Sequence 8860, Ap
888	69	3.9	2704	4	US-09-538-092-1260	Sequence 1260, Ap
889	69	3.9	3165	2	US-08-459-146-3	Sequence 3, Appli
890	69	3.9	3165	2	US-08-459-065-3	Sequence 3, Appli
891	69	3.9	3913	4	US-09-949-016-10933	Sequence 10933, A
892	69	3.9	4377	4	US-09-949-016-6978	Sequence 6978, Ap
893	68.5	3.9	243	4	US-09-198-452A-284	Sequence 284, App
894	68.5	3.9	244	4	US-09-134-000C-4358	Sequence 4358, Ap
895	68.5	3.9	245	4	US-09-438-185A-273	Sequence 273, App
896	68.5	3.9	266	3	US-08-983-502-20	Sequence 20, Appl
897	68.5	3.9	266	4	US-09-516-747-20	Sequence 20, Appl
898	68.5	3.9	266	5	PCT-US96-10521-20	Sequence 20, Appl
899	68.5	3.9	267	4	US-09-107-433-3575	Sequence 3575, Ap
900	68.5	3.9	286	3	US-09-360-017-1	Sequence 1, Appli
901	68.5	3.9	287	4	US-09-583-110-4372	Sequence 4372, Ap
902	68.5	3.9	306	5	PCT-US94-09799-1	Sequence 1, Appli
903	68.5	3.9	331	4	US-09-543-681A-6822	Sequence 6822, Ap
904	68.5	3.9	335	3	US-08-983-502-16	Sequence 16, Appl
905	68.5	3.9	335	4	US-09-516-747-16	Sequence 16, Appl
906	68.5	3.9	335	5	PCT-US96-10521-16	Sequence 16, Appl
907	68.5	3.9	377	4	US-09-949-016-7949	Sequence 7949, Ap
908	68.5	3.9	378	4	US-09-638-937-14	Sequence 14, Appl
909	68.5	3.9	389	2	US-08-618-408B-4	Sequence 4, Appli
910	68.5	3.9	406	4	US-09-252-991A-19195	Sequence 19195, A
911	68.5	3.9	443	4	US-09-328-352-7566	Sequence 7566, Ap
912	68.5	3.9	464	3	US-08-983-502-18	Sequence 18, Appl
913	68.5	3.9	464	4	US-09-516-747-18	Sequence 18, Appl
914	68.5	3.9	464	5	PCT-US96-10521-18	Sequence 18, Appl
915	68.5	3.9	474	4	US-09-902-540-16368	Sequence 16368, A
916	68.5	3.9	476	3	US-09-561-756-27	Sequence 27, Appl
917	68.5	3.9	476	3	US-09-227-721-27	Sequence 27, Appl
918	68.5	3.9	476	4	US-09-954-697-27	Sequence 27, Appl
919	68.5	3.9	478	4	US-09-009-893A-3	Sequence 3, Appli
920	68.5	3.9	478	4	US-09-489-155-3	Sequence 3, Appli
921	68.5	3.9	479	2	US-08-807-200-12	Sequence 12, Appl
922	68.5	3.9	479	3	US-09-382-155-26	Sequence 26, Appl
923	68.5	3.9	479	3	US-09-382-155-28	Sequence 28, Appl
924	68.5	3.9	479	3	US-09-001-777-12	Sequence 12, Appl
925	68.5	3.9	479	3	US-09-074-044A-26	Sequence 26, Appl
926	68.5	3.9	479	3	US-09-074-044A-27	Sequence 27, Appl
927	68.5	3.9	479	3	US-09-074-044A-28	Sequence 28, Appl
928	68.5	3.9	479	3	US-08-983-502-7	Sequence 7, Appli
929	68.5	3.9	479	4	US-09-516-747-7	Sequence 7, Appli
930	68.5	3.9	479	4	US-09-851-873-101	Sequence 101, App
931	68.5	3.9	479	5	PCT-US96-10521-7	Sequence 7, Appli
932	68.5	3.9	488	4	US-09-540-236-3027	Sequence 3027, Ap
933	68.5	3.9	496	1	US-08-665-220-4	Sequence 4, Appli
934	68.5	3.9	496	3	US-09-291-692-4	Sequence 4, Appli
935	68.5	3.9	496	4	US-09-952-768-4	Sequence 4, Appli
936	68.5	3.9	505	4	US-09-949-016-11473	Sequence 11473, A
937	68.5	3.9	525	4	US-09-549-519-26	Sequence 26, Appl
938	68.5	3.9	532	4	US-09-252-991A-17930	Sequence 17930, A
939	68.5	3.9	538	4	US-09-134-000C-4331	Sequence 4331, Ap
940	68.5	3.9	574	4	US-09-902-540-11805	Sequence 11805, A
941	68.5	3.9	591	4	US-09-602-787A-24	Sequence 24, Appl
942	68.5	3.9	597	1	US-08-399-646-4	Sequence 4, Appli
943	68.5	3.9	597	1	US-08-607-321-4	Sequence 4, Appli
944	68.5	3.9	597	2	US-08-961-240-4	Sequence 4, Appli
945	68.5	3.9	597	2	US-08-605-501-4	Sequence 4, Appli
946	68.5	3.9	598	1	US-08-399-646-14	Sequence 14, Appl
947	68.5	3.9	598	1	US-08-607-321-14	Sequence 14, Appl
948	68.5	3.9	598	2	US-08-961-240-14	Sequence 14, Appl
949	68.5	3.9	598	2	US-08-605-501-14	Sequence 14, Appl
950	68.5	3.9	616	4	US-09-252-991A-19164	Sequence 19164, A
951	68.5	3.9	680	4	US-09-731-166-6	Sequence 6, Appli
952	68.5	3.9	761	3	US-08-928-941D-1	Sequence 1, Appli
953	68.5	3.9	761	3	US-09-280-590A-1	Sequence 1, Appli
954	68.5	3.9	761	4	US-09-892-398-1	Sequence 1, Appli
955	68.5	3.9	766	2	US-08-951-648-2	Sequence 2, Appli
956	68.5	3.9	766	3	US-09-174-437-2	Sequence 2, Appli
957	68.5	3.9	766	4	US-09-686-055A-2	Sequence 2, Appli
958	68.5	3.9	779	2	US-08-951-648-6	Sequence 6, Appli
959	68.5	3.9	779	3	US-09-174-437-6	Sequence 6, Appli
960	68.5	3.9	779	4	US-09-686-055A-6	Sequence 6, Appli
961	68.5	3.9	779	4	US-09-420-190-1	Sequence 1, Appli
962	68.5	3.9	835	4	US-09-270-767-60845	Sequence 60845, A
963	68.5	3.9	898	4	US-09-902-540-11561	Sequence 11561, A
964	68.5	3.9	935	4	US-09-902-540-16200	Sequence 16200, A
965	68.5	3.9	947	4	US-09-270-767-45347	Sequence 45347, A
966	68.5	3.9	1025	2	US-08-304-309-4	Sequence 4, Appli
967	68.5	3.9	1025	3	US-08-991-942-4	Sequence 4, Appli
968	68.5	3.9	1068	1	US-08-396-479B-12	Sequence 12, Appl
969	68.5	3.9	1068	1	US-08-818-823-12	Sequence 12, Appl
970	68.5	3.9	1078	4	US-09-949-016-9573	Sequence 9573, Ap
971	68.5	3.9	1162	2	US-08-728-323A-2	Sequence 2, Appli
972	68.5	3.9	1162	3	US-09-298-568-2	Sequence 2, Appli
973	68.5	3.9	1162	4	US-09-410-399-2	Sequence 2, Appli
974	68.5	3.9	1162	4	US-09-894-273-2	Sequence 2, Appli
975	68.5	3.9	1409	4	US-09-489-039A-10338	Sequence 10338, A
976	68.5	3.9	1729	4	US-09-696-115B-2	Sequence 2, Appli

977	68.5	3.9	1897	4	US-09-792-024-98	Sequence 98, Appl
978	68.5	3.9	2628	3	US-09-413-814-11	Sequence 11, Appl
979	68.5	3.9	3672	2	US-08-822-445-12	Sequence 12, Appl
980	68.5	3.9	3672	3	US-09-396-540-12	Sequence 12, Appl
981	68.5	3.9	3801	2	US-08-822-445-10	Sequence 10, Appl
982	68.5	3.9	3801	3	US-09-396-540-10	Sequence 10, Appl
983	68	3.8	146	4	US-09-248-796A-16057	Sequence 16057, A
984	68	3.8	189	4	US-09-902-540-9850	Sequence 9850, Ap
985	68	3.8	198	6	5240847-10	Patent No. 5240847
986	68	3.8	198	6	5240847-11	Patent No. 5240847
987	68	3.8	198	6	5240847-10	Patent No. 5240847
988	68	3.8	198	6	5240847-11	Patent No. 5240847
989	68	3.8	237	2	US-08-578-709-11	Sequence 11, Appl
990	68	3.8	251	4	US-09-248-796A-26488	Sequence 26488, A
991	68	3.8	292	4	US-09-540-236-3576	Sequence 3576, Ap
992	68	3.8	292	4	US-09-248-796A-16836	Sequence 16836, A
993	68	3.8	318	4	US-09-489-039A-13319	Sequence 13319, A
994	68	3.8	319	4	US-09-489-847-130	Sequence 130, App
995	68	3.8	356	4	US-09-489-847-257	Sequence 257, App
996	68	3.8	367	4	US-09-902-540-10526	Sequence 10526, A
997	68	3.8	368	4	US-09-248-796A-20724	Sequence 20724, A
998	68	3.8	375	4	US-09-540-236-3290	Sequence 3290, Ap
999	68	3.8	384	3	US-09-059-769-10	Sequence 10, Appl
1000	68	3.8	384	3	US-09-354-231B-8	Sequence 8, Appli
1001	68	3.8	384	4	US-09-128-602B-8	Sequence 8, Appli
1002	68	3.8	384	4	US-09-995-297-8	Sequence 8, Appli
1003	68	3.8	427	4	US-09-919-039-29	Sequence 29, Appl
1004	68	3.8	427	4	US-09-902-540-12222	Sequence 12222, A
1005	68	3.8	429	4	US-09-198-452A-189	Sequence 189, App
1006	68	3.8	431	4	US-09-388-221B-8	Sequence 8, Appli
1007	68	3.8	432	4	US-09-438-185A-173	Sequence 173, App
1008	68	3.8	445	4	US-09-270-767-46492	Sequence 46492, A
1009	68	3.8	453	4	US-09-252-991A-25869	Sequence 25869, A
1010	68	3.8	454	4	US-09-489-039A-12918	Sequence 12918, A
1011	68	3.8	474	4	US-09-489-039A-13282	Sequence 13282, A
1012	68	3.8	489	2	US-08-895-521-1	Sequence 1, Appli
1013	68	3.8	489	3	US-09-235-218-1	Sequence 1, Appli
1014	68	3.8	500	2	US-08-578-709-15	Sequence 15, Appl
1015	68	3.8	505	4	US-09-949-016-10947	Sequence 10947, A
1016	68	3.8	512	1	US-07-779-890-4	Sequence 4, Appli
1017	68	3.8	512	1	US-07-779-890-4	Sequence 4, Appli
1018	68	3.8	512	2	US-09-008-962-4	Sequence 4, Appli
1019	68	3.8	512	2	US-08-675-507-4	Sequence 4, Appli
1020	68	3.8	512	3	US-09-213-205-4	Sequence 4, Appli
1021	68	3.8	512	5	PCT-US93-05640-4	Sequence 4, Appli
1022	68	3.8	520	4	US-09-792-024-121	Sequence 121, App
1023	68	3.8	603	4	US-09-107-532A-5482	Sequence 5482, Ap
1024	68	3.8	610	1	US-08-212-188-2	Sequence 2, Appli
1025	68	3.8	610	3	US-08-970-725-2	Sequence 2, Appli
1026	68	3.8	610	3	US-09-336-447A-11	Sequence 11, Appl
1027	68	3.8	610	4	US-09-952-267B-11	Sequence 11, Appl
1028	68	3.8	610	5	PCT-US95-02708-2	Sequence 2, Appli
1029	68	3.8	611	4	US-09-949-016-7139	Sequence 7139, Ap
1030	68	3.8	626	4	US-09-252-991A-27835	Sequence 27835, A
1031	68	3.8	682	4	US-09-538-092-223	Sequence 223, App
1032	68	3.8	686	2	US-08-993-228-12	Sequence 12, Appl
1033	68	3.8	744	4	US-09-785-381-3	Sequence 3, Appli
1034	68	3.8	789	4	US-09-107-532A-6734	Sequence 6734, Ap
1035	68	3.8	816	2	US-08-785-310A-8	Sequence 8, Appli
1036	68	3.8	834	4	US-09-538-092-619	Sequence 619, App
1037	68	3.8	863	4	US-09-252-991A-20821	Sequence 20821, A
1038	68	3.8	907	4	US-09-198-452A-306	Sequence 306, App
1039	68	3.8	919	4	US-09-248-796A-18971	Sequence 18971, A
1040	68	3.8	928	4	US-09-438-185A-295	Sequence 295, App
1041	68	3.8	943	2	US-08-808-982-7	Sequence 7, Appli
1042	68	3.8	943	3	US-09-306-902A-7	Sequence 7, Appli
1043	68	3.8	1023	4	US-09-902-540-12335	Sequence 12335, A
1044	68	3.8	1111	1	US-08-317-450B-15	Sequence 15, Appl
1045	68	3.8	1111	3	US-08-800-593-15	Sequence 15, Appl
1046	68	3.8	1172	4	US-09-560-385A-28	Sequence 28, Appl
1047	68	3.8	1172	4	US-09-560-385A-32	Sequence 32, Appl
1048	68	3.8	1193	1	US-08-317-450B-13	Sequence 13, Appl
1049	68	3.8	1193	3	US-08-800-593-13	Sequence 13, Appl
1050	68	3.8	1193	4	US-09-560-385A-26	Sequence 26, Appl
1051	68	3.8	1193	4	US-09-560-385A-30	Sequence 30, Appl
1052	68	3.8	1248	3	US-08-726-214-16	Sequence 16, Appl
1053	68	3.8	1323	4	US-09-248-796A-19543	Sequence 19543, A
1054	68	3.8	1362	4	US-09-902-540-14577	Sequence 14577, A
1055	68	3.8	1441	4	US-09-252-991A-28143	Sequence 28143, A
1056	68	3.8	1461	2	US-08-993-228-10	Sequence 10, Appl
1057	68	3.8	4391	4	US-10-006-011A-2	Sequence 2, Appli
1058	68	3.8	4551	3	US-09-320-878-1	Sequence 1, Appli
1059	68	3.8	4551	4	US-09-141-908-2	Sequence 2, Appli
1060	68	3.8	4551	4	US-09-657-440-1	Sequence 1, Appli
1061	68	3.8	4613	3	US-09-105-537-31	Sequence 31, Appl
1062	68	3.8	11877	3	US-09-105-537-6	Sequence 6, Appli
1063	67.5	3.8	151	4	US-09-270-767-38682	Sequence 38682, A
1064	67.5	3.8	151	4	US-09-270-767-53899	Sequence 53899, A
1065	67.5	3.8	163	4	US-09-270-767-35907	Sequence 35907, A
1066	67.5	3.8	163	4	US-09-270-767-51124	Sequence 51124, A
1067	67.5	3.8	170	4	US-09-270-767-41268	Sequence 41268, A
1068	67.5	3.8	170	4	US-09-270-767-56484	Sequence 56484, A
1069	67.5	3.8	190	4	US-09-248-796A-16862	Sequence 16862, A
1070	67.5	3.8	203	4	US-09-107-532A-4612	Sequence 4612, Ap
1071	67.5	3.8	214	4	US-09-270-767-39842	Sequence 39842, A
1072	67.5	3.8	214	4	US-09-270-767-55059	Sequence 55059, A
1073	67.5	3.8	257	4	US-09-205-258-293	Sequence 293, App
1074	67.5	3.8	261	2	US-08-484-905-111	Sequence 111, App
1075	67.5	3.8	261	3	US-08-481-985B-111	Sequence 111, App
1076	67.5	3.8	261	3	US-08-370-476-111	Sequence 111, App
1077	67.5	3.8	271	4	US-09-248-796A-22728	Sequence 22728, A
1078	67.5	3.8	275	4	US-09-270-767-33033	Sequence 33033, A
1079	67.5	3.8	314	4	US-09-252-991A-18836	Sequence 18836, A
1080	67.5	3.8	317	4	US-09-252-991A-29701	Sequence 29701, A
1081	67.5	3.8	333	4	US-09-976-594-144	Sequence 144, App
1082	67.5	3.8	341	4	US-09-949-016-10614	Sequence 10614, A
1083	67.5	3.8	342	4	US-09-328-352-4946	Sequence 4946, Ap
1084	67.5	3.8	346	4	US-09-252-991A-21432	Sequence 21432, A
1085	67.5	3.8	354	4	US-09-252-991A-29385	Sequence 29385, A
1086	67.5	3.8	391	4	US-09-583-110-2803	Sequence 2803, Ap
1087	67.5	3.8	399	4	US-09-638-937-8	Sequence 8, Appli
1088	67.5	3.8	403	4	US-09-107-433-3191	Sequence 3191, Ap
1089	67.5	3.8	412	4	US-09-198-452A-901	Sequence 901, App
1090	67.5	3.8	413	4	US-09-438-185A-838	Sequence 838, App
1091	67.5	3.8	449	4	US-09-583-110-4686	Sequence 4686, Ap
1092	67.5	3.8	458	4	US-09-107-433-3814	Sequence 3814, Ap
1093	67.5	3.8	472	4	US-09-489-039A-10123	Sequence 10123, A
1094	67.5	3.8	472	4	US-09-540-236-2097	Sequence 2097, Ap
1095	67.5	3.8	490	4	US-09-949-016-6091	Sequence 6091, Ap
1096	67.5	3.8	498	4	US-10-142-231-91	Sequence 91, Appl
1097	67.5	3.8	516	4	US-09-248-796A-17736	Sequence 17736, A
1098	67.5	3.8	524	4	US-09-248-796A-18625	Sequence 18625, A
1099	67.5	3.8	524	4	US-09-248-796A-20498	Sequence 20498, A
1100	67.5	3.8	541	3	US-09-045-185-2	Sequence 2, Appli
1101	67.5	3.8	582	4	US-09-489-039A-10786	Sequence 10786, A
1102	67.5	3.8	584	3	US-09-022-949-2	Sequence 2, Appli
1103	67.5	3.8	598	4	US-09-198-452A-511	Sequence 511, App
1104	67.5	3.8	598	4	US-09-438-185A-476	Sequence 476, App
1105	67.5	3.8	713	4	US-09-489-039A-10668	Sequence 10668, A
1106	67.5	3.8	781	4	US-09-538-092-363	Sequence 363, App
1107	67.5	3.8	888	1	US-08-445-640-35	Sequence 35, Appl
1108	67.5	3.8	888	3	US-08-170-558-35	Sequence 35, Appl
1109	67.5	3.8	888	3	US-08-447-314-35	Sequence 35, Appl
1110	67.5	3.8	888	3	US-08-445-461-35	Sequence 35, Appl
1111	67.5	3.8	888	4	US-09-223-490-35	Sequence 35, Appl
1112	67.5	3.8	900	4	US-09-107-532A-5284	Sequence 5284, Ap
1113	67.5	3.8	933	4	US-09-311-021-22	Sequence 22, Appl
1114	67.5	3.8	935	4	US-09-107-532A-3753	Sequence 3753, Ap
1115	67.5	3.8	951	4	US-09-125-635-8	Sequence 8, Appli
1116	67.5	3.8	965	4	US-09-252-991A-24038	Sequence 24038, A
1117	67.5	3.8	1010	4	US-09-654-449-2	Sequence 2, Appli
1118	67.5	3.8	1010	4	US-09-759-152A-2	Sequence 2, Appli
1119	67.5	3.8	1044	4	US-09-252-991A-24495	Sequence 24495, A
1120	67.5	3.8	1121	1	US-07-789-915A-2	Sequence 2, Appli
1121	67.5	3.8	1121	1	US-08-005-002C-2	Sequence 2, Appli
1122	67.5	3.8	1121	1	US-08-487-203A-2	Sequence 2, Appli

1123	67.5	3.8	1302	4	US-09-949-016-10852	Sequence 10852, A
1124	67.5	3.8	1334	6	5476657-1	Patent No. 5476657
1125	67.5	3.8	1334	6	5476657-1	Patent No. 5476657
1126	67.5	3.8	1403	1	US-07-908-253-3	Sequence 3, Appli
1127	67.5	3.8	1403	2	US-08-535-837-3	Sequence 3, Appli
1128	67.5	3.8	1420	4	US-09-125-635-4	Sequence 4, Appli
1129	67.5	3.8	1452	3	US-09-127-227-2	Sequence 2, Appli
1130	67.5	3.8	1498	2	US-08-404-531B-29	Sequence 29, Appl
1131	67.5	3.8	1498	3	US-08-476-900A-29	Sequence 29, Appl
1132	67.5	3.8	1498	3	US-08-488-546A-29	Sequence 29, Appl
1133	67.5	3.8	1582	2	US-08-404-531B-9	Sequence 9, Appli
1134	67.5	3.8	1582	3	US-08-476-900A-9	Sequence 9, Appli
1135	67.5	3.8	1582	3	US-08-488-546A-9	Sequence 9, Appli
1136	67.5	3.8	1582	3	US-08-726-320-5	Sequence 5, Appli
1137	67.5	3.8	1582	3	US-09-208-716-5	Sequence 5, Appli
1138	67.5	3.8	2323	4	US-09-710-279-760	Sequence 760, App
1139	67.5	3.8	2736	4	US-09-252-991A-30227	Sequence 30227, A
1140	67	3.8	171	4	US-09-252-991A-20354	Sequence 20354, A
1141	67	3.8	222	2	US-08-365-486A-28	Sequence 28, Appl
1142	67	3.8	222	3	US-08-880-342-28	Sequence 28, Appl
1143	67	3.8	262	4	US-09-270-767-42193	Sequence 42193, A
1144	67	3.8	274	4	US-09-252-991A-22166	Sequence 22166, A
1145	67	3.8	284	4	US-09-543-681A-7910	Sequence 7910, Ap
1146	67	3.8	288	4	US-09-107-532A-7120	Sequence 7120, Ap
1147	67	3.8	310	4	US-09-248-796A-24630	Sequence 24630, A
1148	67	3.8	320	4	US-09-710-279-2988	Sequence 2988, Ap
1149	67	3.8	338	4	US-09-252-991A-31155	Sequence 31155, A
1150	67	3.8	340	4	US-09-789-300A-2	Sequence 2, Appli
1151	67	3.8	346	4	US-09-248-796A-16397	Sequence 16397, A
1152	67	3.8	347	3	US-09-134-001C-3298	Sequence 3298, Ap
1153	67	3.8	358	4	US-09-949-016-10323	Sequence 10323, A
1154	67	3.8	363	4	US-09-755-665-63	Sequence 63, Appl
1155	67	3.8	369	4	US-09-755-665-16	Sequence 16, Appl
1156	67	3.8	380	4	US-09-755-665-8	Sequence 8, Appli
1157	67	3.8	380	4	US-09-438-185A-133	Sequence 133, App
1158	67	3.8	388	4	US-09-949-016-7414	Sequence 7414, Ap
1159	67	3.8	389	4	US-09-755-665-36	Sequence 36, Appl
1160	67	3.8	392	4	US-09-755-665-35	Sequence 35, Appl
1161	67	3.8	392	4	US-09-538-092-1257	Sequence 1257, Ap
1162	67	3.8	393	1	US-08-423-399B-33	Sequence 33, Appl
1163	67	3.8	393	1	US-08-530-950-11	Sequence 11, Appl
1164	67	3.8	393	3	US-08-888-429A-11	Sequence 11, Appl
1165	67	3.8	393	3	US-09-149-879-11	Sequence 11, Appl
1166	67	3.8	393	4	US-09-057-009-11	Sequence 11, Appl
1167	67	3.8	393	4	US-09-593-653-11	Sequence 11, Appl
1168	67	3.8	394	4	US-09-755-665-33	Sequence 33, Appl
1169	67	3.8	400	4	US-09-668-097A-16	Sequence 16, Appl
1170	67	3.8	403	4	US-09-710-279-1522	Sequence 1522, Ap
1171	67	3.8	404	4	US-09-949-016-7963	Sequence 7963, Ap
1172	67	3.8	405	4	US-09-489-039A-9411	Sequence 9411, Ap
1173	67	3.8	408	4	US-09-543-681A-5372	Sequence 5372, Ap
1174	67	3.8	433	4	US-09-107-532A-6785	Sequence 6785, Ap
1175	67	3.8	449	4	US-09-270-767-57465	Sequence 57465, A
1176	67	3.8	462	4	US-09-949-016-8104	Sequence 8104, Ap
1177	67	3.8	476	4	US-09-489-039A-8487	Sequence 8487, Ap
1178	67	3.8	508	3	US-09-344-700-4	Sequence 4, Appli
1179	67	3.8	508	4	US-09-563-997A-4	Sequence 4, Appli
1180	67	3.8	508	4	US-09-270-767-45071	Sequence 45071, A
1181	67	3.8	540	4	US-09-252-991A-32271	Sequence 32271, A
1182	67	3.8	541	4	US-10-101-464A-913	Sequence 913, App
1183	67	3.8	545	4	US-09-134-000C-3545	Sequence 3545, Ap
1184	67	3.8	563	4	US-09-350-841A-1602	Sequence 1602, Ap
1185	67	3.8	564	4	US-09-902-540-14784	Sequence 14784, A
1186	67	3.8	583	3	US-09-311-311C-24	Sequence 24, Appl
1187	67	3.8	585	4	US-09-949-016-6627	Sequence 6627, Ap
1188	67	3.8	592	6	5200183-18	Patent No. 5200183
1189	67	3.8	592	6	5200183-18	Patent No. 5200183
1190	67	3.8	601	4	US-09-270-767-42194	Sequence 42194, A
1191	67	3.8	607	4	US-09-252-991A-26647	Sequence 26647, A
1192	67	3.8	608	4	US-10-003-392-2	Sequence 2, Appli
1193	67	3.8	616	1	US-08-749-882A-2	Sequence 2, Appli
1194	67	3.8	616	2	US-08-539-134-2	Sequence 2, Appli
1195	67	3.8	616	2	US-08-991-531-2	Sequence 2, Appli
1196	67	3.8	616	2	US-09-032-315-9	Sequence 9, Appli
1197	67	3.8	616	2	US-08-993-318A-9	Sequence 9, Appli
1198	67	3.8	616	3	US-09-028-887-2	Sequence 2, Appli
1199	67	3.8	616	3	US-09-399-886-9	Sequence 9, Appli
1200	67	3.8	616	3	US-09-396-260-9	Sequence 9, Appli
1201	67	3.8	616	3	US-09-518-901-2	Sequence 2, Appli
1202	67	3.8	616	3	US-09-576-281-9	Sequence 9, Appli
1203	67	3.8	616	5	PCT-US95-06816-2	Sequence 2, Appli
1204	67	3.8	639	4	US-09-949-016-9434	Sequence 9434, Ap
1205	67	3.8	679	3	US-09-257-536-2	Sequence 2, Appli
1206	67	3.8	679	3	US-09-512-230-2	Sequence 2, Appli
1207	67	3.8	694	4	US-09-252-991A-32733	Sequence 32733, A
1208	67	3.8	714	4	US-09-949-016-10296	Sequence 10296, A
1209	67	3.8	760	1	US-08-547-197-2	Sequence 2, Appli
1210	67	3.8	760	3	US-08-957-940-2	Sequence 2, Appli
1211	67	3.8	795	4	US-09-252-991A-31273	Sequence 31273, A
1212	67	3.8	854	4	US-09-949-016-11363	Sequence 11363, A
1213	67	3.8	863	4	US-09-976-594-10	Sequence 10, Appl
1214	67	3.8	863	4	US-09-538-092-1373	Sequence 1373, Ap
1215	67	3.8	968	3	US-09-228-986-76	Sequence 76, Appl
1216	67	3.8	968	4	US-10-101-464A-76	Sequence 76, Appl
1217	67	3.8	1014	4	US-09-252-991A-31338	Sequence 31338, A
1218	67	3.8	1015	4	US-09-285-385C-2	Sequence 2, Appli
1219	67	3.8	1024	4	US-09-562-737-87	Sequence 87, Appl
1220	67	3.8	1031	4	US-09-489-039A-11186	Sequence 11186, A
1221	67	3.8	1164	4	US-09-949-016-11682	Sequence 11682, A
1222	67	3.8	1317	3	US-09-083-521-7	Sequence 7, Appli
1223	67	3.8	1318	4	US-09-540-236-3623	Sequence 3623, Ap
1224	67	3.8	1464	3	US-09-045-360-2	Sequence 2, Appli
1225	67	3.8	1464	4	US-09-713-273A-21	Sequence 21, Appl
1226	67	3.8	1464	4	US-09-746-390-2	Sequence 2, Appli
1227	66.5	3.7	124	4	US-09-134-000C-4510	Sequence 4510, Ap
1228	66.5	3.7	193	4	US-09-489-039A-14196	Sequence 14196, A
1229	66.5	3.7	212	2	US-08-761-248B-2	Sequence 2, Appli
1230	66.5	3.7	212	2	US-08-761-248B-6	Sequence 6, Appli
1231	66.5	3.7	274	4	US-09-328-352-5762	Sequence 5762, Ap
1232	66.5	3.7	307	4	US-09-710-279-684	Sequence 684, App
1233	66.5	3.7	309	4	US-09-655-908-12	Sequence 12, Appl
1234	66.5	3.7	312	4	US-09-107-532A-6724	Sequence 6724, Ap
1235	66.5	3.7	322	4	US-09-248-796A-17229	Sequence 17229, A
1236	66.5	3.7	345	4	US-09-107-532A-4268	Sequence 4268, Ap
1237	66.5	3.7	353	4	US-09-949-016-7923	Sequence 7923, Ap
1238	66.5	3.7	355	4	US-09-198-452A-871	Sequence 871, App
1239	66.5	3.7	364	4	US-09-438-185A-815	Sequence 815, App
1240	66.5	3.7	373	3	US-09-347-878-40	Sequence 40, Appl
1241	66.5	3.7	380	2	US-08-904-278-8	Sequence 8, Appli
1242	66.5	3.7	380	3	US-09-222-594-8	Sequence 8, Appli
1243	66.5	3.7	380	4	US-09-977-653-8	Sequence 8, Appli
1244	66.5	3.7	383	4	US-09-583-110-3277	Sequence 3277, Ap
1245	66.5	3.7	384	2	US-08-675-650B-2	Sequence 2, Appli
1246	66.5	3.7	384	2	US-08-675-650B-4	Sequence 4, Appli
1247	66.5	3.7	384	2	US-08-675-650B-6	Sequence 6, Appli
1248	66.5	3.7	384	3	US-09-354-231B-10	Sequence 10, Appl
1249	66.5	3.7	384	3	US-09-354-231B-12	Sequence 12, Appl
1250	66.5	3.7	384	3	US-09-354-231B-14	Sequence 14, Appl
1251	66.5	3.7	384	3	US-09-133-962A-4	Sequence 4, Appli
1252	66.5	3.7	384	4	US-09-128-602B-10	Sequence 10, Appl
1253	66.5	3.7	384	4	US-09-128-602B-12	Sequence 12, Appl
1254	66.5	3.7	384	4	US-09-128-602B-14	Sequence 14, Appl
1255	66.5	3.7	384	4	US-09-995-297-10	Sequence 10, Appl
1256	66.5	3.7	384	4	US-09-995-297-12	Sequence 12, Appl
1257	66.5	3.7	384	4	US-09-995-297-14	Sequence 14, Appl
1258	66.5	3.7	389	4	US-09-949-016-7723	Sequence 7723, Ap
1259	66.5	3.7	392	4	US-09-248-796A-26630	Sequence 26630, A
1260	66.5	3.7	394	4	US-09-252-991A-25572	Sequence 25572, A
1261	66.5	3.7	394	4	US-09-252-991A-32539	Sequence 32539, A
1262	66.5	3.7	399	4	US-09-270-767-45921	Sequence 45921, A
1263	66.5	3.7	401	4	US-09-252-991A-27277	Sequence 27277, A
1264	66.5	3.7	414	4	US-09-949-016-6906	Sequence 6906, Ap
1265	66.5	3.7	432	2	US-08-904-278-6	Sequence 6, Appli
1266	66.5	3.7	432	3	US-09-222-594-6	Sequence 6, Appli
1267	66.5	3.7	432	4	US-09-977-653-6	Sequence 6, Appli
1268	66.5	3.7	438	4	US-09-380-682-58	Sequence 58, Appl

1269	66.5	3.7	439	4	US-09-248-796A-15968	Sequence 15968, A
1270	66.5	3.7	442	4	US-09-252-991A-31597	Sequence 31597, A
1271	66.5	3.7	444	4	US-09-694-519-6	Sequence 6, Appli
1272	66.5	3.7	464	4	US-09-564-367-2	Sequence 2, Appli
1273	66.5	3.7	467	4	US-09-252-991A-29057	Sequence 29057, A
1274	66.5	3.7	474	4	US-09-556-877-90	Sequence 90, Appl
1275	66.5	3.7	474	4	US-09-620-412C-90	Sequence 90, Appl
1276	66.5	3.7	474	4	US-09-410-568-90	Sequence 90, Appl
1277	66.5	3.7	474	4	US-09-598-419-90	Sequence 90, Appl
1278	66.5	3.7	475	1	US-07-715-184-4	Sequence 4, Appli
1279	66.5	3.7	475	1	US-07-876-280-7	Sequence 7, Appli
1280	66.5	3.7	475	1	US-07-876-280-28	Sequence 28, Appl
1281	66.5	3.7	475	1	US-07-935-310A-2	Sequence 2, Appli
1282	66.5	3.7	475	1	US-07-828-788A-2	Sequence 2, Appli
1283	66.5	3.7	475	1	US-08-049-783-4	Sequence 4, Appli
1284	66.5	3.7	475	1	US-08-147-189-2	Sequence 2, Appli
1285	66.5	3.7	475	1	US-08-316-301A-8	Sequence 8, Appli
1286	66.5	3.7	475	2	US-08-904-278-2	Sequence 2, Appli
1287	66.5	3.7	475	2	US-08-904-278-4	Sequence 4, Appli
1288	66.5	3.7	475	3	US-09-076-137-8	Sequence 8, Appli
1289	66.5	3.7	475	3	US-07-941-650A-6	Sequence 6, Appli
1290	66.5	3.7	475	3	US-09-222-594-2	Sequence 2, Appli
1291	66.5	3.7	475	3	US-09-222-594-4	Sequence 4, Appli
1292	66.5	3.7	475	4	US-09-738-363-8	Sequence 8, Appli
1293	66.5	3.7	475	4	US-09-977-653-2	Sequence 2, Appli
1294	66.5	3.7	475	4	US-09-977-653-4	Sequence 4, Appli
1295	66.5	3.7	475	5	PCT-US92-03624-8	Sequence 8, Appli
1296	66.5	3.7	475	5	PCT-US92-11337-2	Sequence 2, Appli
1297	66.5	3.7	475	5	PCT-US93-07409-2	Sequence 2, Appli
1298	66.5	3.7	483	2	US-08-583-562B-12	Sequence 12, Appl
1299	66.5	3.7	483	2	US-08-779-113-12	Sequence 12, Appl
1300	66.5	3.7	486	4	US-09-248-796A-18727	Sequence 18727, A
1301	66.5	3.7	491	4	US-09-248-796A-26733	Sequence 26733, A
1302	66.5	3.7	495	4	US-09-734-237B-62	Sequence 62, Appl
1303	66.5	3.7	496	4	US-09-734-237B-64	Sequence 64, Appl
1304	66.5	3.7	499	3	US-09-509-902A-12	Sequence 12, Appl
1305	66.5	3.7	500	4	US-09-949-016-8865	Sequence 8865, Ap
1306	66.5	3.7	510	4	US-09-121-211-16	Sequence 16, Appl
1307	66.5	3.7	567	3	US-08-646-273-19	Sequence 19, Appl
1308	66.5	3.7	588	3	US-09-509-902A-16	Sequence 16, Appl
1309	66.5	3.7	590	4	US-09-134-000C-4456	Sequence 4456, Ap
1310	66.5	3.7	615	3	US-08-989-299-11	Sequence 11, Appl
1311	66.5	3.7	615	4	US-09-407-427-11	Sequence 11, Appl
1312	66.5	3.7	616	3	US-09-298-367B-11	Sequence 11, Appl
1313	66.5	3.7	648	3	US-09-262-773-2	Sequence 2, Appli
1314	66.5	3.7	648	4	US-09-949-016-6365	Sequence 6365, Ap
1315	66.5	3.7	659	4	US-09-955-732A-2	Sequence 2, Appli
1316	66.5	3.7	665	4	US-09-949-016-10990	Sequence 10990, A
1317	66.5	3.7	668	4	US-09-543-681A-4508	Sequence 4508, Ap
1318	66.5	3.7	673	4	US-09-252-991A-28287	Sequence 28287, A
1319	66.5	3.7	686	4	US-09-107-532A-5118	Sequence 5118, Ap
1320	66.5	3.7	707	4	US-09-328-352-4834	Sequence 4834, Ap
1321	66.5	3.7	708	3	US-08-646-273-23	Sequence 23, Appl
1322	66.5	3.7	749	4	US-09-328-352-7588	Sequence 7588, Ap
1323	66.5	3.7	754	3	US-08-646-273-30	Sequence 30, Appl
1324	66.5	3.7	758	1	US-08-289-112-2	Sequence 2, Appli
1325	66.5	3.7	857	2	US-08-779-113-2	Sequence 2, Appli
1326	66.5	3.7	858	2	US-08-583-562B-2	Sequence 2, Appli
1327	66.5	3.7	927	4	US-09-248-796A-14284	Sequence 14284, A
1328	66.5	3.7	1049	4	US-10-018-730A-4	Sequence 4, Appli
1329	66.5	3.7	1082	3	US-09-336-643A-20	Sequence 20, Appl
1330	66.5	3.7	1287	4	US-09-252-991A-29606	Sequence 29606, A
1331	66.5	3.7	1319	4	US-09-538-092-1291	Sequence 1291, Ap
1332	66.5	3.7	1403	2	US-08-694-865-17	Sequence 17, Appl
1333	66.5	3.7	1403	3	US-09-124-491-17	Sequence 17, Appl
1334	66.5	3.7	1403	4	US-09-383-912-17	Sequence 17, Appl
1335	66.5	3.7	1421	4	US-09-252-991A-17805	Sequence 17805, A
1336	66.5	3.7	1443	2	US-08-670-707A-39	Sequence 39, Appl
1337	66.5	3.7	1443	3	US-09-037-601-39	Sequence 39, Appl
1338	66.5	3.7	1443	3	US-09-315-179-39	Sequence 39, Appl
1339	66.5	3.7	1467	4	US-09-523-656-38	Sequence 38, Appl
1340	66.5	3.7	1551	4	US-09-437-568A-46	Sequence 46, Appl
1341	66.5	3.7	1596	4	US-09-328-352-5542	Sequence 5542, Ap
1342	66.5	3.7	2133	2	US-08-670-707A-37	Sequence 37, Appl
1343	66.5	3.7	2133	3	US-09-037-601-37	Sequence 37, Appl
1344	66.5	3.7	2133	3	US-09-315-179-37	Sequence 37, Appl
1345	66.5	3.7	2133	4	US-09-523-656-30	Sequence 30, Appl
1346	66.5	3.7	2366	1	US-08-480-604A-10	Sequence 10, Appl
1347	66.5	3.7	2366	2	US-08-405-496A-10	Sequence 10, Appl
1348	66.5	3.7	2366	3	US-08-915-136-10	Sequence 10, Appl
1349	66.5	3.7	2366	3	US-08-957-310-10	Sequence 10, Appl
1350	66.5	3.7	2366	4	US-10-011-366-10	Sequence 10, Appl
1351	66.5	3.7	2366	4	US-09-084-517-10	Sequence 10, Appl
1352	66.5	3.7	5215	3	US-09-105-537-2	Sequence 2, Appli
1353	66	3.7	161	4	US-09-270-767-40150	Sequence 40150, A
1354	66	3.7	161	4	US-09-270-767-55366	Sequence 55366, A
1355	66	3.7	234	3	US-09-134-001C-3362	Sequence 3362, Ap
1356	66	3.7	241	6	5175383-7	Patent No. 5175383
1357	66	3.7	241	6	5175383-7	Patent No. 5175383
1358	66	3.7	249	4	US-09-248-796A-16223	Sequence 16223, A
1359	66	3.7	249	4	US-09-438-185A-1057	Sequence 1057, Ap
1360	66	3.7	259	4	US-09-107-433-4239	Sequence 4239, Ap
1361	66	3.7	260	4	US-09-270-767-32401	Sequence 32401, A
1362	66	3.7	260	4	US-09-270-767-47618	Sequence 47618, A
1363	66	3.7	268	4	US-09-461-325-346	Sequence 346, App
1364	66	3.7	268	4	US-10-012-542-346	Sequence 346, App
1365	66	3.7	268	4	US-10-115-123-346	Sequence 346, App
1366	66	3.7	274	4	US-09-543-681A-4708	Sequence 4708, Ap
1367	66	3.7	285	4	US-09-543-681A-8131	Sequence 8131, Ap
1368	66	3.7	321	4	US-09-270-767-46190	Sequence 46190, A
1369	66	3.7	332	4	US-09-543-681A-5560	Sequence 5560, Ap
1370	66	3.7	341	4	US-09-270-767-46147	Sequence 46147, A
1371	66	3.7	348	2	US-09-031-485-28	Sequence 28, Appl
1372	66	3.7	348	2	US-08-847-429A-28	Sequence 28, Appl
1373	66	3.7	348	3	US-09-065-474-28	Sequence 28, Appl
1374	66	3.7	348	3	US-09-557-034-28	Sequence 28, Appl
1375	66	3.7	355	4	US-09-902-540-12250	Sequence 12250, A
1376	66	3.7	378	4	US-09-902-540-12143	Sequence 12143, A
1377	66	3.7	383	4	US-09-583-110-4287	Sequence 4287, Ap
1378	66	3.7	384	4	US-09-071-035-276	Sequence 276, App
1379	66	3.7	386	4	US-09-902-540-15437	Sequence 15437, A
1380	66	3.7	402	4	US-09-134-000C-4382	Sequence 4382, Ap
1381	66	3.7	430	4	US-09-071-035-274	Sequence 274, App
1382	66	3.7	447	3	US-09-070-356-7	Sequence 7, Appli
1383	66	3.7	448	2	US-08-878-989-2	Sequence 2, Appli
1384	66	3.7	448	3	US-09-272-796-2	Sequence 2, Appli
1385	66	3.7	459	1	US-08-403-545-5	Sequence 5, Appli
1386	66	3.7	459	3	US-08-404-381-5	Sequence 5, Appli
1387	66	3.7	459	4	US-09-902-540-15100	Sequence 15100, A
1388	66	3.7	466	4	US-09-949-016-7701	Sequence 7701, Ap
1389	66	3.7	468	4	US-09-710-279-1666	Sequence 1666, Ap
1390	66	3.7	474	3	US-09-134-001C-3241	Sequence 3241, Ap
1391	66	3.7	476	4	US-09-252-991A-28457	Sequence 28457, A
1392	66	3.7	477	4	US-09-134-000C-6123	Sequence 6123, Ap
1393	66	3.7	491	3	US-08-942-012B-27	Sequence 27, Appl
1394	66	3.7	498	4	US-09-134-000C-5128	Sequence 5128, Ap
1395	66	3.7	501	4	US-09-248-796A-15119	Sequence 15119, A
1396	66	3.7	520	4	US-09-252-991A-17942	Sequence 17942, A
1397	66	3.7	528	2	US-08-793-229-35	Sequence 35, Appl
1398	66	3.7	528	3	US-09-285-957-35	Sequence 35, Appl
1399	66	3.7	529	4	US-09-248-796A-25874	Sequence 25874, A
1400	66	3.7	584	4	US-09-949-016-8587	Sequence 8587, Ap
1401	66	3.7	589	4	US-09-543-681A-7643	Sequence 7643, Ap
1402	66	3.7	607	3	US-08-486-099-116	Sequence 116, App
1403	66	3.7	607	3	US-08-484-223B-116	Sequence 116, App
1404	66	3.7	607	3	US-08-919-597-116	Sequence 116, App
1405	66	3.7	607	3	US-08-475-668A-116	Sequence 116, App
1406	66	3.7	607	3	US-08-485-551A-116	Sequence 116, App
1407	66	3.7	607	3	US-08-471-913A-116	Sequence 116, App
1408	66	3.7	607	3	US-09-335-409-9	Sequence 9, Appli
1409	66	3.7	607	3	US-08-485-264A-116	Sequence 116, App
1410	66	3.7	607	3	US-08-474-349A-116	Sequence 116, App
1411	66	3.7	607	3	US-09-568-102-9	Sequence 9, Appli
1412	66	3.7	607	3	US-09-567-969-9	Sequence 9, Appli
1413	66	3.7	607	3	US-09-568-480-9	Sequence 9, Appli
1414	66	3.7	607	3	US-09-568-486-9	Sequence 9, Appli

1415	66	3.7	607	3	US-09-568-472-9	Sequence 9, Appli
1416	66	3.7	607	3	US-09-567-899-9	Sequence 9, Appli
1417	66	3.7	607	4	US-08-470-896-116	Sequence 116, App
1418	66	3.7	607	4	US-08-485-546A-116	Sequence 116, App
1419	66	3.7	607	4	US-08-487-266A-116	Sequence 116, App
1420	66	3.7	610	4	US-09-949-016-7510	Sequence 7510, Ap
1421	66	3.7	620	4	US-09-578-441-4	Sequence 4, Appli
1422	66	3.7	660	4	US-09-462-606-56	Sequence 56, Appl
1423	66	3.7	704	4	US-09-252-991A-22353	Sequence 22353, A
1424	66	3.7	704	4	US-09-248-796A-19464	Sequence 19464, A
1425	66	3.7	714	4	US-09-328-352-5347	Sequence 5347, Ap
1426	66	3.7	716	4	US-09-312-283C-183	Sequence 183, App
1427	66	3.7	771	3	US-09-188-930-183	Sequence 183, App
1428	66	3.7	797	4	US-09-949-016-9676	Sequence 9676, Ap
1429	66	3.7	811	4	US-09-489-039A-11609	Sequence 11609, A
1430	66	3.7	947	4	US-09-719-190-2	Sequence 2, Appli
1431	66	3.7	1271	4	US-09-270-767-45803	Sequence 45803, A
1432	66	3.7	1452	4	US-09-252-991A-18118	Sequence 18118, A
1433	66	3.7	1529	4	US-09-312-283C-396	Sequence 396, App
1434	66	3.7	1715	4	US-09-696-115B-17	Sequence 17, Appl
1435	66	3.7	1745	2	US-09-031-485-33	Sequence 33, Appl
1436	66	3.7	1745	2	US-08-847-429A-33	Sequence 33, Appl
1437	66	3.7	1745	3	US-09-065-474-33	Sequence 33, Appl
1438	66	3.7	1745	3	US-09-557-034-33	Sequence 33, Appl
1439	66	3.7	1838	3	US-09-120-663-2	Sequence 2, Appli
1440	66	3.7	1838	4	US-09-431-614-8	Sequence 8, Appli
1441	66	3.7	2004	1	US-08-375-709-15	Sequence 15, Appl
1442	66	3.7	2004	1	US-08-752-929-15	Sequence 15, Appl
1443	66	3.7	2004	3	US-09-090-793-9	Sequence 9, Appli
1444	66	3.7	2004	4	US-09-231-899-9	Sequence 9, Appli
1445	66	3.7	3066	3	US-08-952-127-12	Sequence 12, Appl
1446	66	3.7	3665	2	US-08-222-617A-13	Sequence 13, Appl
1447	66	3.7	3712	2	US-08-222-617A-4	Sequence 4, Appli
1448	66	3.7	3712	2	US-08-222-617A-25	Sequence 25, Appl
1449	65.5	3.7	218	4	US-09-252-991A-22469	Sequence 22469, A
1450	65.5	3.7	238	4	US-09-328-352-5013	Sequence 5013, Ap
1451	65.5	3.7	263	4	US-09-252-991A-27644	Sequence 27644, A
1452	65.5	3.7	282	3	US-08-910-820-5	Sequence 5, Appli
1453	65.5	3.7	282	4	US-09-844-908-5	Sequence 5, Appli
1454	65.5	3.7	304	4	US-09-134-000C-5217	Sequence 5217, Ap
1455	65.5	3.7	304	4	US-09-270-767-33347	Sequence 33347, A
1456	65.5	3.7	304	4	US-09-270-767-48564	Sequence 48564, A
1457	65.5	3.7	310	4	US-09-976-594-807	Sequence 807, App
1458	65.5	3.7	311	4	US-09-248-796A-27203	Sequence 27203, A
1459	65.5	3.7	314	4	US-09-107-532A-4919	Sequence 4919, Ap
1460	65.5	3.7	341	3	US-09-412-600B-2	Sequence 2, Appli
1461	65.5	3.7	341	3	US-09-412-600B-4	Sequence 4, Appli
1462	65.5	3.7	345	4	US-09-902-540-13152	Sequence 13152, A
1463	65.5	3.7	366	4	US-09-252-991A-27837	Sequence 27837, A
1464	65.5	3.7	366	4	US-09-107-433-4252	Sequence 4252, Ap
1465	65.5	3.7	378	4	US-09-441-411-8	Sequence 8, Appli
1466	65.5	3.7	384	4	US-09-328-352-5901	Sequence 5901, Ap
1467	65.5	3.7	390	3	US-09-561-322-2	Sequence 2, Appli
1468	65.5	3.7	392	3	US-08-861-774E-92	Sequence 92, Appl
1469	65.5	3.7	398	4	US-09-328-352-6136	Sequence 6136, Ap
1470	65.5	3.7	422	1	US-08-403-545-4	Sequence 4, Appli
1471	65.5	3.7	422	3	US-08-404-381-4	Sequence 4, Appli
1472	65.5	3.7	475	3	US-09-009-494-6	Sequence 6, Appli
1473	65.5	3.7	475	3	US-09-010-233-2	Sequence 2, Appli
1474	65.5	3.7	475	3	US-09-010-232-6	Sequence 6, Appli
1475	65.5	3.7	475	4	US-10-138-701-29	Sequence 29, Appl
1476	65.5	3.7	504	3	US-09-126-420A-23	Sequence 23, Appl
1477	65.5	3.7	510	3	US-08-948-564-4	Sequence 4, Appli
1478	65.5	3.7	511	4	US-09-252-991A-19728	Sequence 19728, A
1479	65.5	3.7	514	4	US-09-543-681A-5352	Sequence 5352, Ap
1480	65.5	3.7	531	3	US-09-069-023-1	Sequence 1, Appli
1481	65.5	3.7	532	1	US-08-657-192-9	Sequence 9, Appli
1482	65.5	3.7	532	3	US-08-523-373-7	Sequence 7, Appli
1483	65.5	3.7	537	4	US-09-198-452A-246	Sequence 246, App
1484	65.5	3.7	543	4	US-09-438-185A-238	Sequence 238, App
1485	65.5	3.7	543	4	US-09-902-540-12545	Sequence 12545, A
1486	65.5	3.7	554	4	US-09-540-236-3778	Sequence 3778, Ap
1487	65.5	3.7	572	4	US-09-949-016-6366	Sequence 6366, Ap
1488	65.5	3.7	575	4	US-09-394-142B-20	Sequence 20, Appl
1489	65.5	3.7	578	4	US-09-252-991A-17776	Sequence 17776, A
1490	65.5	3.7	621	2	US-08-969-714-1	Sequence 1, Appli
1491	65.5	3.7	626	4	US-09-949-016-6361	Sequence 6361, Ap
1492	65.5	3.7	630	4	US-09-248-796A-19619	Sequence 19619, A
1493	65.5	3.7	631	3	US-08-927-219-127	Sequence 127, App
1494	65.5	3.7	636	4	US-09-949-016-7908	Sequence 7908, Ap
1495	65.5	3.7	640	4	US-09-134-000C-3871	Sequence 3871, Ap
1496	65.5	3.7	645	2	US-08-969-714-3	Sequence 3, Appli
1497	65.5	3.7	648	3	US-08-800-291B-8	Sequence 8, Appli
1498	65.5	3.7	660	4	US-09-902-540-16293	Sequence 16293, A
1499	65.5	3.7	671	4	US-09-252-991A-16922	Sequence 16922, A
1500	65.5	3.7	675	4	US-09-270-767-46383	Sequence 46383, A

ALIGNMENTS

```
RESULT 1
US-08-276-919-2
; Sequence 2, Application US/08276919
; Patent No. 5589579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,919
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelligan, Mark C.
;      REGISTRATION NUMBER:  36,389
;      REFERENCE/DOCKET NUMBER:  B35792
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-276-919-2

  Query Match             39.2%;  Score 696.5;  DB 1;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 5.5e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :
Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
              | ||||:|:|:||| ::: ||  :| | ||||||     | |||| :: :   |||||||
Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:|| |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||:
Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207
```

```
Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
              ||||::  :|:|| |||||||| :|||||    ||| ||| |:  |: |  ::||
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
              : :: |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
                ||  ||   : | |::  | :  |||
Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352


RESULT 2
US-08-776-088-2
; Sequence 2, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-776-088-2

  Query Match             39.2%;  Score 696.5;  DB 1;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 5.5e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :
Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
              | ||||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   |||||||
Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:|| |   | |: : :|||| :|||:| : | :|: | |||  |::| |:  || ||:
Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
              ||||::  :|:|| |||||||| :||||||    ||| ||| |:  |: |  ::||
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
              : :: |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
                ||  ||   : | |::  | :  |||
Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352


RESULT 3
US-08-776-088-6
; Sequence 6, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-776-088-6

  Query Match             39.2%;  Score 696.5;  DB 1;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 5.5e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :
Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
              | ||||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   |||||||
Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:|| |   | |: : :|||| :|||:| : | :|: | |||  |::| |:  || ||:
Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
              ||||::  :|:|| |||||||| :||||||    ||| ||| |:  |: |  ::||
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
              : :: |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325
```

```
Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352
```

RESULT 4
US-09-325-320-2
; Sequence 2, Application US/09325320
; Patent No. 6117981
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06101
; CURRENT APPLICATION NUMBER: US/09/325,320
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-325-320-2

Query Match 39.2%; Score 696.5; DB 3; Length 354;
Best Local Similarity 43.5%; Pred. No. 5.5e-65;
Matches 143; Conservative 62; Mismatches 109; Indels 15; Gaps 7;

```
Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :
Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
              | ||||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   |||||||
Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:|| |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||:
Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
              ||||::  :|:|| |||||||  :||||||    ||| |||  |:  |: |  ::||
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
              : :: |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352

RESULT 5
US-09-585-109-2
; Sequence 2, Application US/09585109
; Patent No. 6242204
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06104
; CURRENT APPLICATION NUMBER: US/09/585,109
; CURRENT FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-585-109-2

Query Match 39.2%; Score 696.5; DB 3; Length 354;
Best Local Similarity 43.5%; Pred. No. 5.5e-65;
Matches 143; Conservative 62; Mismatches 109; Indels 15; Gaps 7;

```
Qy 19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
 | ||| || |:: | || || |||||: :| : :| | |: ||: :
Db 29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy 79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
 | ||||:|:|:||| ::: || :| | ||||||| | |||| :: : |||||||
Db 89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy 139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
 |:|| | | |: : :||||| :|||:| : | :|: | ||| |::| |: || ||:
Db 149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy 199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
 ||||:: :|:|| ||||||| :|||||| ||| ||| |: |: | ::||
Db 208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy 257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
 : :: |:| :| ::|:|: || | | ||||: ||| |: ::::::
Db 268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy 310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
 || || : | |:: | : |||
Db 326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352
```

RESULT 6
US-09-949-016-6043
; Sequence 6043, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6043
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6043

Query Match 39.2%; Score 696.5; DB 4; Length 354;
Best Local Similarity 43.5%; Pred. No. 5.5e-65;
Matches 143; Conservative 62; Mismatches 109; Indels 15; Gaps 7;

```
Qy 19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
 | ||| || |:: | || || |||||: :| : :| | |: ||: :
Db 29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy 79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
 | ||||:|:|:||| ::: || :| | ||||||| | |||| :: : |||||||
Db 89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy 139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
 |:|| | | |: : :||||| :|||:| : | :|: | ||| |::| |: || ||:
Db 149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy 199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
```
```

```
Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309

Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337

Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352


RESULT 7
PCT-US95-09145A-2
; Sequence 2, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-09145A-2

  Query Match             39.2%;  Score 696.5;  DB 5;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 5.5e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78

Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138

Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198

Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256

Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309

Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337

Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352


RESULT 8
PCT-US95-09145A-6
; Sequence 6, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  354 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-09145A-6

  Query Match             39.2%;  Score 696.5;  DB 5;  Length 354;
  Best Local Similarity   43.5%;  Pred. No. 5.5e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78

Db         29 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 88

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138

Db         89 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 148

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198

Db        149 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 207

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256

Db        208 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 267

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309

Db        268 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 325

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337

Db        326 LFRRKSIKK--GDNKGVIYKPATKMETEA 352
```

```
RESULT 9
US-09-949-016-9900
; Sequence 9900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9900
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9900

  Query Match             39.2%;  Score 696.5;  DB 4;  Length 392;
  Best Local Similarity   43.5%;  Pred. No. 6.4e-65;
  Matches  143;  Conservative   62;  Mismatches  109;  Indels   15;  Gaps    7;

Qy         19 GQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLD 78
              |  ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :
Db         67 GSKWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFL 126

Qy         79 LHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVH 138
              | ||||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   |||||||
Db        127 LTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVH 186

Qy        139 YDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNL 198
              |:|| |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||:
Db        187 YNSDLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNI 245

Qy        199 RELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS- 256
               ||||::  :|:|| |||||||  :||||||    ||| |||  |:  |: |  ::||
Db        246 EELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSP 305

Qy        257 KLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVY 309
              : :: |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        306 REMINNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIW 363

Qy        310 FIARKIRKKRLENRKSVVFTSA-QATTEA 337
                 ||  ||   : | |::  | :  |||
Db        364 LFRRKSIKK--GDNKGVIYKPATKMETEA 390


RESULT 10
US-08-276-919-4
; Sequence 4, Application US/08276919
; Patent No. 5589579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,919
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelligan, Mark C.
;      REGISTRATION NUMBER:  36,389
;      REFERENCE/DOCKET NUMBER:  B35792
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-276-919-4

  Query Match             38.9%;  Score 691.5;  DB 1;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 1.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :  | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| ||||||||  :||||||    ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |       |   ||||:       |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKSIKK--GDNKGVIYKPATKMETEA 323


RESULT 11
US-08-776-088-4
; Sequence 4, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
```

```
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-776-088-4

  Query Match             38.9%;  Score 691.5;  DB 1;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 1.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||  ||||: :| : :|  | |:  ||:    :  | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| |||||||||  :||||||    ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKSIKK--GDNKGVIYKPATKMETEA 323


RESULT 12
PCT-US95-09145A-4
; Sequence 4, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-09145A-4

  Query Match             38.9%;  Score 691.5;  DB 5;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 1.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||  ||||: :| : :|  | |:  ||:    :  | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| |||||||||  :||||||    ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKSIKK--GDNKGVIYKPATKMETEA 323


RESULT 13
US-08-276-919-13
; Sequence 13, Application US/08276919
; Patent No. 5589579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,919
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelligan, Mark C.
;      REGISTRATION NUMBER:  36,389
;      REFERENCE/DOCKET NUMBER:  B35792
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  13:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-276-919-13

  Query Match             38.8%;  Score 689.5;  DB 1;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 2.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :   | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| |||||||  :||||||     ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |      |   ||||:        |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKGIKK--GDNKGVIYKPATKMETEA 323


RESULT 14
US-08-776-088-18
; Sequence 18, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-776-088-18

  Query Match             38.8%;  Score 689.5;  DB 1;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 2.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;

Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :   | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| |||||||  :||||||     ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |      |   ||||:        |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKGIKK--GDNKGVIYKPATKMETEA 323


RESULT 15
PCT-US95-09145A-18
; Sequence 18, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  325 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-09145A-18

  Query Match             38.8%;  Score 689.5;  DB 5;  Length 325;
  Best Local Similarity   43.6%;  Pred. No. 2.6e-64;
  Matches  142;  Conservative   62;  Mismatches  107;  Indels   15;  Gaps    7;
```

```
Qy         22 WTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPLDLHN 81
              ||| || |:: |   || ||   |||||: :| : :|  |  |:  ||:    :   | |
Db          3 WTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTN 62

Qy         82 NGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDS 141
              |||:|:|:||| ::: ||  :| | |||||||    | |||| :: :   ||||||||:|
Db         63 NGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNS 122

Qy        142 DSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLREL 201
              | |   | |: : :||||| :|||:| : | :|: | |||  |::| |:  || ||: ||
Db        123 DLYPDASTASNKSEGLAVLAVLIEMG-SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEEL 181

Qy        202 LPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTE-EEPS-KLL 259
              ||::  :|:|| |||||||  :||||||    ||| |||  |:  |: |  ::|| : :
Db        182 LPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREM 241

Qy        260 VQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGV-------GILVGCLCLLLAVYFIA 312
              : |:| :|  ::|:|: || |      |   ||||:       |||  |: ::::::
Db        242 INNFRQVQKFDERLVYTSFSQV--QVCTAAGLSLGIILSLALAGILGICIVVVVSIWLFR 299

Qy        313 RKIRKKRLENRKSVVFTSA-QATTEA 337
              ||  ||   : | |::  | :  |||
Db        300 RKGIKK--GDNKGVIYKPATKMETEA 323

Search completed: May  4, 2005, 15:10:02
Job time : 66 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:31:51 ; Search time 146 Seconds
(without alignments)
768.882 Million cell updates/sec

Perfect score: 1779
Sequence: 1 MLFSALLLEVIWILAADGGQ.....KRLENRKSVVFTSAQATTEA 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
2	1779	100.0	337	10	US-09-983-000A-27	Sequence 27, Appl
524	1779	100.0	337	14	US-10-174-587-268	Sequence 268, App
592	1779	100.0	337	14	US-10-063-742-74	Sequence 74, Appl
668	1779	100.0	337	14	US-10-013-909A-423	Sequence 423, App
736	1779	100.0	337	17	US-10-972-317-74	Sequence 74, Appl
737	1779	100.0	337	17	US-10-652-981-27	Sequence 27, Appl
738	1500	84.3	337	14	US-10-205-194-49	Sequence 49, Appl
739	1327.5	74.6	262	10	US-09-948-783-126	Sequence 126, App
740	1327.5	74.6	262	15	US-10-264-237-2058	Sequence 2058, Ap
741	1327.5	74.6	263	10	US-09-892-877-125	Sequence 125, App
742	940.5	52.9	194	10	US-09-989-442-86	Sequence 86, Appl
743	820	46.1	212	15	US-10-378-029-56	Sequence 56, Appl
744	696.5	39.2	354	15	US-10-295-027-296	Sequence 296, App
745	696.5	39.2	354	16	US-10-648-593-216	Sequence 216, App
746	562	31.6	459	9	US-09-772-719-2	Sequence 2, Appli
747	562	31.6	459	10	US-09-967-237-2	Sequence 2, Appli
748	562	31.6	459	14	US-10-301-822-12	Sequence 12, Appl
749	562	31.6	459	15	US-10-465-572-10	Sequence 10, Appl
750	562	31.6	459	15	US-10-295-027-306	Sequence 306, App
751	562	31.6	459	15	US-10-295-027-1239	Sequence 1239, Ap
752	562	31.6	459	15	US-10-241-814-16	Sequence 16, Appl
753	562	31.6	459	16	US-10-734-564-138	Sequence 138, App
754	562	31.6	459	16	US-10-888-694-2	Sequence 2, Appli
755	562	31.6	459	17	US-10-921-590-2	Sequence 2, Appli
756	562	31.6	610	9	US-09-783-708-1	Sequence 1, Appli
757	561.5	31.6	437	17	US-10-921-590-90	Sequence 90, Appl
758	536.5	30.2	283	15	US-10-108-260A-3974	Sequence 3974, Ap
759	535	30.1	377	10	US-09-967-237-87	Sequence 87, Appl
760	535	30.1	377	17	US-10-921-590-5	Sequence 5, Appli
761	533.5	30.0	256	9	US-09-772-719-51	Sequence 51, Appl
762	533.5	30.0	256	16	US-10-888-694-51	Sequence 51, Appl
763	533.5	30.0	257	10	US-09-967-237-51	Sequence 51, Appl
764	533.5	30.0	257	17	US-10-921-590-9	Sequence 9, Appli
765	533.5	30.0	277	17	US-10-921-590-101	Sequence 101, App
766	533.5	30.0	346	17	US-10-921-590-104	Sequence 104, App
767	531.5	29.9	358	17	US-10-921-590-92	Sequence 92, Appl
768	526.5	29.6	258	17	US-10-921-590-94	Sequence 94, Appl
769	507	28.5	308	15	US-10-287-226-356	Sequence 356, App
770	493	27.7	262	13	US-10-000-954-8	Sequence 8, Appli
771	482.5	27.1	255	15	US-10-099-322-304	Sequence 304, App
772	482.5	27.1	255	15	US-10-044-564-304	Sequence 304, App
773	465	26.1	232	17	US-10-921-590-69	Sequence 69, Appl
774	465	26.1	232	17	US-10-921-590-105	Sequence 105, App
775	442.5	24.9	242	15	US-10-231-913-284	Sequence 284, App
776	439.5	24.7	267	13	US-10-000-954-3	Sequence 3, Appli
777	423	23.8	309	14	US-10-165-603-9	Sequence 9, Appli
778	423	23.8	309	15	US-10-038-854-104	Sequence 104, App
779	422.5	23.7	262	15	US-10-108-260A-3082	Sequence 3082, Ap
780	422.5	23.7	262	15	US-10-433-802-1	Sequence 1, Appli
781	422.5	23.7	262	17	US-10-753-267-8	Sequence 8, Appli
782	421	23.7	294	9	US-09-925-299-945	Sequence 945, App
783	421	23.7	294	10	US-09-925-299-945	Sequence 945, App
784	420	23.6	259	13	US-10-000-954-5	Sequence 5, Appli
785	420	23.6	260	9	US-09-981-353-117	Sequence 117, App
786	419.5	23.6	308	15	US-10-038-854-103	Sequence 103, App
787	413.5	23.2	164	10	US-09-989-442-134	Sequence 134, App
788	410	23.0	288	9	US-09-750-913-12	Sequence 12, Appl
789	406	22.8	259	10	US-09-983-000A-25	Sequence 25, Appl
790	406	22.8	259	13	US-10-000-954-6	Sequence 6, Appli
791	406	22.8	259	17	US-10-652-981-25	Sequence 25, Appl
792	405	22.8	260	15	US-10-363-616-250	Sequence 250, App
793	405	22.8	421	9	US-09-938-270B-1	Sequence 1, Appli
794	398	22.4	305	15	US-10-038-854-105	Sequence 105, App
795	393	22.1	261	13	US-10-000-954-9	Sequence 9, Appli
796	386	21.7	1616	14	US-10-205-219-119	Sequence 119, App
797	385.5	21.7	170	9	US-09-772-719-54	Sequence 54, Appl
798	385.5	21.7	170	16	US-10-888-694-54	Sequence 54, Appl
799	383	21.5	274	15	US-10-220-120-215	Sequence 215, App
800	380.5	21.4	260	10	US-09-983-000A-26	Sequence 26, Appl
801	380.5	21.4	260	13	US-10-000-954-4	Sequence 4, Appli
802	380.5	21.4	260	17	US-10-652-981-26	Sequence 26, Appl
803	380.5	21.4	261	9	US-09-802-674-4	Sequence 4, Appli
804	380.5	21.4	261	9	US-09-981-353-80	Sequence 80, Appl
805	380.5	21.4	261	14	US-10-235-994-24	Sequence 24, Appl
806	380.5	21.4	261	16	US-10-408-765A-389	Sequence 389, App
807	380.5	21.4	263	14	US-10-106-698-4637	Sequence 4637, Ap
808	380.5	21.4	312	9	US-09-981-353-68	Sequence 68, Appl
809	380.5	21.4	312	14	US-10-165-603-11	Sequence 11, Appl
810	380.5	21.4	312	14	US-10-205-823-48	Sequence 48, Appl
811	380.5	21.4	312	15	US-10-116-275-259	Sequence 259, App
812	380.5	21.4	312	15	US-10-099-322-20	Sequence 20, Appl
813	380.5	21.4	312	15	US-10-099-322-86	Sequence 86, Appl
814	380.5	21.4	312	15	US-10-044-564-20	Sequence 20, Appl
815	380.5	21.4	312	15	US-10-044-564-86	Sequence 86, Appl
816	380.5	21.4	312	15	US-10-038-854-101	Sequence 101, App
817	376.5	21.2	242	14	US-10-069-434-1	Sequence 1, Appli
818	374.5	21.1	260	13	US-10-000-954-10	Sequence 10, Appl

819	373	21.0	266	15	US-10-099-322-88	Sequence 88, Appl
820	373	21.0	266	15	US-10-044-564-88	Sequence 88, Appl
821	373	21.0	268	13	US-10-000-954-7	Sequence 7, Appli
822	370	20.8	312	15	US-10-038-854-102	Sequence 102, App
823	365	20.5	374	10	US-09-983-000A-2	Sequence 2, Appli
824	365	20.5	374	17	US-10-652-981-2	Sequence 2, Appli
825	365	20.5	1113	15	US-10-295-027-1264	Sequence 1264, Ap
826	365	20.5	1359	15	US-10-295-027-1266	Sequence 1266, Ap
827	365	20.5	1448	15	US-10-295-027-376	Sequence 376, App
828	365	20.5	1448	15	US-10-295-027-1259	Sequence 1259, Ap
829	365	20.5	1456	15	US-10-295-027-374	Sequence 374, App
830	365	20.5	1456	15	US-10-295-027-1261	Sequence 1261, Ap
831	365	20.5	1493	15	US-10-295-027-1265	Sequence 1265, Ap
832	365	20.5	1494	15	US-10-295-027-380	Sequence 380, App
833	365	20.5	1494	15	US-10-295-027-1263	Sequence 1263, Ap
834	365	20.5	2308	13	US-10-000-954-2	Sequence 2, Appli
835	365	20.5	2314	9	US-09-816-703A-2	Sequence 2, Appli
836	365	20.5	2314	10	US-09-983-000A-6	GENERAL INFORMATI
837	365	20.5	2314	15	US-10-295-027-382	Sequence 382, App
838	365	20.5	2314	17	US-10-652-981-6	Sequence 6, Appli
839	365	20.5	2315	15	US-10-295-027-372	Sequence 372, App
840	365	20.5	2315	15	US-10-295-027-1260	Sequence 1260, Ap
841	365	20.5	2353	10	US-09-983-000A-4	Sequence 4, Appli
842	365	20.5	2353	17	US-10-652-981-4	Sequence 4, Appli
843	364.5	20.5	336	15	US-10-038-854-8	Sequence 8, Appli
844	363	20.4	289	14	US-10-074-475-239	Sequence 239, App
845	363	20.4	289	15	US-10-231-913-145	Sequence 145, App
846	363	20.4	290	15	US-10-231-913-143	Sequence 143, App
847	363	20.4	290	15	US-10-231-913-144	Sequence 144, App
848	363	20.4	291	15	US-10-231-913-146	Sequence 146, App
849	363	20.4	291	15	US-10-231-913-147	Sequence 147, App
850	359.5	20.2	262	15	US-10-099-322-89	Sequence 89, Appl
851	359.5	20.2	262	15	US-10-044-564-89	Sequence 89, Appl
852	354	19.9	294	15	US-10-099-322-87	Sequence 87, Appl
853	354	19.9	294	15	US-10-044-564-87	Sequence 87, Appl
854	351.5	19.8	1456	15	US-10-295-027-1262	Sequence 1262, Ap
855	347.5	19.5	248	15	US-10-287-226-354	Sequence 354, App
997	312	17.5	328	14	US-10-069-434-3	Sequence 3, Appli
1291	312	17.5	328	17	US-10-931-886-34	Sequence 34, Appl
1293	310.5	17.5	335	15	US-10-099-322-90	Sequence 90, Appl
1294	310.5	17.5	335	15	US-10-044-564-90	Sequence 90, Appl
1295	307	17.3	328	14	US-10-160-501-27	Sequence 27, Appl
1346	288.5	16.2	328	14	US-10-167-749-358	Sequence 358, App

Search completed: May 4, 2005, 15:19:18
Job time : 171 secs